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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN BONE MARROW(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human bone marrow is described. Also described are single exon nucleic acid probes expressed
in the bone marrow and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

CROSS REFERENCE TO RELATED APPLICATIONS

5 The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S.provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entirety.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20 The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_BONE_MARROW.txt,
25 created 24 January 2001, having 26,421,347 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30 The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

bone marrow and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence - and most importantly, but not exclusively, regions that
25 function to encode genes - to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

- Ismb* 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*, *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

- Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

- Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily to be confirmed experimentally.

- Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

- It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

- 5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

- Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality.
20 Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia
25 - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the bone marrow, particularly those diseases with polygenic etiology.

30

Summary of the Invention

- The present invention solves these and other problems in the art by providing methods and apparatus for
35 predicting, confirming, and displaying functional

information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

5 In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions
10 and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention,
15 there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs:
20 1 - 13,114 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

25 In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably
30 isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

35 In yet another embodiment, said set of single

exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,012 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include

polymethylacrylic, polyethylene, polypropylene,
polyacrylate, polymethylmethacrylate, polyvinylchloride,
polytetrafluoroethylene, polystyrene, polycarbonate,
polyacetal, polysulfone, celluloseacetate,
5 cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

10 In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is
15 packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression
20 analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 13,115 - 26,012, wherein the fragment hybridizes at high stringency to an expressed human gene.
25 In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,114.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from
30 human bone marrow which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone
35 marrow.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOS.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 26,013 - 38,628 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid

probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human bone marrow, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human bone marrow; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from

genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are
5 derived from mRNA from the bone marrow of said eukaryote,
said probe is a single exon probe having a fragment
identical in sequence to, or complementary in sequence to,
said predicted exon, said probe is included within a single
exon microarray in accordance with the first aspect of the
10 invention, and said fragment is selectively hybridizable at
high stringency.

In a eighth aspect of the invention, there is
provided a method of assigning exons to a single gene,
comprising:

15 identifying a plurality of exons from genomic
sequence in accordance with the seventh aspect of the
invention; and then

measuring the expression of each of said exons in
a plurality of tissues and/or cell types using
20 hybridization to single exon microarrays having a probe
with said exon,

wherein a common pattern of expression of said
exons in said plurality of tissues and/or cell types
indicates that the exons should be assigned to a single
25 gene.

In an ninth aspect of the invention, there is
provided a nucleic acid sequence as set out in any of SEQ
ID NOS: 1 - 26,012 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is
30 provided a peptide encoded by a sequence comprising a
sequence as set out in any of SEQ ID NOS: 13,115 - 26,012,
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
encoded by a sequence comprising a sequence set out in any
35 of SEQ ID NOS.: 1 - 13,114.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 26,013 - 38,628.

- 5 Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,013 - 38,628, or fragment thereof.

In another aspect, the invention provides means
10 for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated
15 sequence.

Detailed Description of the Invention

20 Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately
25 detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach
30 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the
35 term "microarray" and phrase "nucleic acid microarray"

further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);
5 in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid
10 microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution
15 phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the
20 sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop
30 codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

35 As used herein the term "exon" refers to the

consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

5 As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons
10 encoding the peptide are wholly contained within the exon.

 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a
15 nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

 As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present
20 within a target mRNA.

 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is
25 meant that it is homologous to the given sequence.

 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 ,
30 preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

 As used herein with respect to the visual display
35 of annotated genomic sequence, the term "rectangle" means

any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

- 5 As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

Brief Description of the Drawings

- The present invention is further illustrated with reference to the following non-limiting figures and
15 examples in which:

- FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in
20 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

- 25 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

- FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length
30 shown in black and PCR product length shown in dotted lines;

- FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color
35 hybridization to a genome-derived single exon microarray.

The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

5 FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured
10 tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

15 FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a
20 BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

 FIG. 9 presents a Mondrian of BAC AC008172 (bases
25 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

 FIG. 10 is a Mondrian of BAC A049839.

30 Methods and Apparatus for Predicting, Confirming,
 Annotating, and Displaying Functional Regions From Genomic
 Sequence Data

 FIG. 1 is a flow chart illustrating in broad
35 outline a process for predicting functional regions from

genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the

- htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).
- 5 Databases of genomic sequence from species other than human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.
- 10 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to,
- 15 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing
- 20 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which

25 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

- 30 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic
- 35 assay. Where the subsequent experimental assay is

bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

5 The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

10 Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by
15 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for
20 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

25 The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output
30 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational
35 substrates for, and performance of subsequent assay, of

functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

- 5 Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to
10 process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be
15 identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction
20 analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of
25 sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend
30 upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the
35 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were

static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query

20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or

codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the
5 undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence,
10 leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered
15 occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

20 Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived
25 from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the
30 input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,
35 where sequences with the desired function are identified

within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after
5 transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X
10 chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment,
15 for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described
20 become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene
25 prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and
30 GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For
35 the newly accessioned human genomic sequence input in

Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with
5 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase
10 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

15 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to
20 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report
25 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7%
30 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

35 Furthermore, consensus can be required among

different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process
5 can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence,
10 but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done
15 in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process
300 for identification of a subset thereof for functional
20 assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental
25 verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the
30 species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

35 Where such subsequent gene expression assay uses

amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify
5 and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that
10 subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message,
15 reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

20 The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

25 As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The
30 combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In
35 particular, the invention provides a novel method of

verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

5 Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is
10 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)
15 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500
20 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more
25 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400
30 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs
35 predicted from human genomic sequence according to the

methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
5 amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are
10 thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no
15 more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

20 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit
25 further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all
30 amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not
35 exceed about 25 nt in length. The "universal" priming

sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

- 5 Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 10 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 15 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

- The amplified nucleic acids can be attached 20 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

- 25 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 30 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

- As is well known in the art, microarrays 35 typically also contain immobilized control nucleic acids.

For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or
5 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural
10 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the
15 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates,
20 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using
30 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid
35 probe than can be achieved with spotting or lithography

techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such

microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the

desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST

5 approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

10 As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a
15 spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
20 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T,
25 where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical
30 derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the
35 probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include

artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even
5 smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning
10 artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide
15 greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the
20 optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the
25 range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often
30 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of
35 human chromosome 22, Dunham et al., *Nature* 402(6761):489-95

(1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from
5 algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-
10 derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure
15 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in
20 EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons
25 for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic
30 and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn
35 from noncoding regions. As discussed above, the additional

presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

5 The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

10 Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization
15 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

 In contrast, the longer probe length of the
20 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or
25 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

30 A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound
35 noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence

drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-

transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is

disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and

more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query -
5 including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200,
10 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such
15 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or
20 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

25 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the
30 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively
35 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the

sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from
5 GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method
10 and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to
15 report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where
20 display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by
25 pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83
30 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as
35 many as can discriminably be displayed, depending upon the

number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

- 5 However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-
- 10 selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

- Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted
- 15 functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the
- 20 results of such physical assay.

- Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function
- 25 by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

- Where the function desired to be identified is
- 30 protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe
- 35 immobilized on the support surface of the microarray. As

noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

5 Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in
10 process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically
15 need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

 Rectangle 87 as shown in FIG. 3 includes smaller
20 rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880
25 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

30 Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

 For example, where the function assayed and displayed is protein coding, the degree of shading of
35 rectangles 880 can be used to represent the degree of

sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as
5 many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of
10 expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which
15 often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right
20 borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical
25 assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays,
30 individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the
35 spectra of the Cy3 and Cy5 dyes conventionally used for

respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,114 of these ORFs in bone marrow.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in bone marrow is currently available for use in measuring the level of its ORF's expression in bone marrow.

Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations

in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies.

5 For example, cancers that originate in the bone marrow and lymphatic tissues such as the lymphomas, leukemias, and myeloma have been recognized as a major health concern. An estimated 632,000 Americans are presently living with lymphoma, leukemia or myeloma, and
10 over 110,000 new cases are anticipated each year. The new cases alone account for 11% of all cancer cases reported in the United States.

 Lymphoma is a general term for a group of cancers of lymphocytes that manifest in the tissues of the
15 lymphatic system. Eventually, monoclonal proliferation crowds out healthy cells and creates tumors which enlarge lymph nodes. Approximately 450,000 members of the U.S. population are living with lymphoma: 160,000 with Hodgkin disease (HD) and 290,000 with non-Hodgkin lymphoma.

20 Hodgkin disease (HD) is a specialized form of lymphoma, and represent about 8% of all lymphomas. HD can be distinguish in tissues by the presence of an abnormal cell called the Reed-Sternberg cell. Incidence rates of HD are higher in adolescents and young adults, but HD is
25 considered to be one of the most curable forms of cancer. Symptoms of HD include painless swelling of lymph glands, fatigue, recurrent high fever, sweating at night, skin irritations and loss of weight.

 Although an infectious etiology has been proposed
30 to account for the disproportionate incidence of HD among siblings reared together - particularly an association with Epstein Barr Virus (EBV) - multiple genetic contributions have also been suggested.

 As early as 1986, linkage to HLA was suggested,
35 with Klitz et al., Am. J. Hum. Genet. 54: 497-505 (1994)

reporting an overall association of the nodular sclerosing (NSHD) group with the HLA class II region. Results of the study suggested that susceptibility to NSHD is influenced by more than 1 locus within the class II region. Through a literature search, Shugart and Collins (2000), Europ. J. Hum. Genet. 8: 460-463 (2000), performed a combined segregation and linkage analysis on 59 nuclear families with HD and concluded that HD is most likely determined by both an HLA-associated major gene and other non-HLA genetic factors, in conjunction with environmental effects.

Non-Hodgkin lymphoma (NHL) is a malignant monoclonal proliferation of the lymphoid cells in the immune system, including bone marrow, spleen, liver and GI tract. The pathologic classification of NHL continues to evolve, reflecting new insights into the cells of origin and the biologic bases of these heterogeneous diseases. The course of NHL varies from indolent and initially well tolerated to rapidly fatal. Furthermore, common clinical symptoms of NHL, but rare in HD, are congestion and edema of the face and neck and ureteral compression.

Non-Hodgkin lymphoma (NHL) has been linked to a variety of specific genetic defects, including 26 mutated genes and at least 9 identified chromosomal translocations. Among the mutated genes are: ALK (2p23); API2 (MIHC, cIAP2) (11q22-q23); API4 (survivin, SVV) (17q25(?)); ATM (ATA, ATC) (11q22.3); BCL1 (11q13.3); BCL10 (CLAP, CIPER) (1p22); BCL2 (18q21.3); BCL6 (LAZ3, ZNF51) (3q27); BLYM (1p32); BMI1 (10p13); CCND1 (D11S287E, Cyclin D, PRAD1) (11q13); CD44 (MDU3, HA, MDU2) (11pter-p13); FRAT1 (10q23-q24(?)); FRAT2 (GBP) (10(?)); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LCPL (PLS2) (13q14.1-q14.3); MALT1 (MLT) (18q21); MUC1 (PUM, PEM) (1q21); MYBL1 (AMYB, A-MYB) (8q22); MYC (CMYC, C-MYC) (8q24.12-q24.13); NBS1 (8q21); NPM1 (B23) (5q35); PCNA (20p12); TIAM1 (21q22.1); and TP53 (p53, P53) (17q13.1).

Among the chromosomal abnormalities are: t(1;14)

(p22;q32); t(14;18)(q32;q21); t(3;14)(q27;q32);
t(6;14)(p25;q32); t(11;18)(q21;q21); t(1;14)(q21;q32);
t(2;5)(p23;q35); add(14q32) / dup(14p32); and
t(11;14)(q13;q32).

5 Additional genetic loci, as yet undiscovered, are
believed to account for other occurrences of NHL.

As another example, acute leukemia is a malignant
disease of blood-forming tissues such as the bone marrow.
It is characterized by the uncontrolled growth of white
10 blood cells. As a result, immature myeloid cells (in acute
myelogenous leukemia (AML)) or lymphoid cells (in acute
lymphocytic leukemia (ALL)) rapidly accumulate and
progressively replace the bone marrow; diminished
production of normal red cells, white cells, and platelets
15 ensues. This loss of normal marrow function in turn gives
rise to the typical clinical complications of leukemia:
anemia, infection, and bleeding.

If untreated, ALL is rapidly fatal; most patients
die within several months of diagnosis. With appropriate
20 therapy, many patients can be cured. The survival rate for
patients diagnosed with AML or ALL is 14% and 58%
respectively. However, the incidences of AML is expected
to be greater than ALL: an estimated 10,000 new cases of
AML, predominantly in older adults, is anticipated in the
25 U.S. alone, whereas 3,100 new cases of ALL are expected,
with 1,500 of these new cases occurring among children.

The etiology of acute leukemia is not known.
Although human T-cell lymphotropic virus type I (HTLV-I), a
causative agent of adult T-cell leukemia, and HTLV-II,
30 obtained from several patients with a syndrome resembling
hairy cell leukemia, have been isolated, the etiologic link
between HTLV and malignancy is uncertain. There is,
however, evidence which suggests a genetic predisposition
to incidences of acute leukemia.

35 For example, genetic disorders such as Fanconi

- anemia and Down syndrome appear to increase risk of acute leukemia, specifically, AML. Evidence supporting a chromosome 21 locus for acute myelogenous leukemia (AML) includes the finding of linkage to 21q22.1-q22.2 in a family with a platelet disorder and propensity to develop AML (Ho et al., Blood 87: 5218-5224 (1996), an increased incidence of leukemia in Down syndrome, and frequent somatic translocation in leukemia involving the CBFA gene on 21q22.3. In addition, Horwitz et al., Am. J. Hum. Genet. 61:873-881 (1997), suggest that a gene on 16q22 may be a second cause of acute myelogenous leukemia. Nonparametric linkage analysis gave a P-value of 0.00098 for the conditional probability of linkage. Mutational analysis excluded expansion of the AT-rich minisatellite repeat FRA16B fragile site and the CAG trinucleotide repeat in the E2F-4 transcription factor. Large CAG repeat expansion was excluded as a cause of leukemia in this family.

- Similarly, acute lymphoblastic leukemia (ALL) has been suggested to have a genetic predisposition. In particular, linkage to chromosome 9p has been reported by a number of groups. Chilcote et al., New Eng. J. Med. 313: 286-291 (1985), found that 6 of 8 patients with clinical features of lymphomatous ALL (LALL), a distinct category of ALL of T-cell lineage, had karyotypic abnormalities leading to loss of bands 9p22-p21. The mechanisms varied and included deletions, unbalanced translocations, and loss of the entire chromosome; only 1 of 57 patients without LALL had an abnormality of chromosome 9 at diagnosis. Kowalczyk et al., Cancer Genet. Cytogenet. 9:383-385 (1981), had earlier found changes in 9p in a subgroup of ALL cases. Chilcote et al. (1985) pointed out that there is a fragile site at 9p21 and raised the question of familial predisposition on this basis. This fragile site is the breakpoint in the translocation t(9;11)(p21-22;q23), which

is associated with acute nonlymphocytic leukemia with monocytic features, ANLL-AMoL-M5a. In a large series, Murphy et al., New Eng. J. Med. 313:1611 (1985), confirmed an abnormality of 9p in 10 to 11% of cases (33 out of more than 300) of acute lymphoblastic leukemia. The breakpoints in 9p clustered in the p22-p21 region. They could not, however, corroborate the specific association with T-cell origin or so-called lymphomatous clinical features. In addition, Taki et al., Proc. Natl. Acad. Sci. USA 96:14535 (1999), recently identified AF5q31, a new AF4-related gene, fused to MLL in infant ALL with ins(5;11)(q31;q13q23), and suspects that AF5q31 and AF4 might define a new family particularly involved in the pathogenesis of 11q23-associated-ALL.

As yet a further example of a disease affecting bone marrow with likely polygenic etiology is multiple myeloma (MM).

MM is a cancer of plasma cells, the final differentiated stage of B lymphocyte maturation. The malignant clone proliferates in the bone marrow and frequently invades the adjacent bone, producing extensive skeletal destruction that results in bone pain and fractures. Anemia, hypercalcemia, and renal failure are some clinical manifestations associated with MM.

MM causes 1% of all cancer deaths in Western countries. A genetic component to its etiology is suggested by disparate incidence among various groups in the country. Its incidence is higher in men than in women, in people of African descent relative to the U.S. population at large, and in older adults as compared to the young. It has been estimated that 14,000 new cases of myeloma will be diagnosed in the U.S., and over 11,000 persons will die from MM within the year.

Although, Kaposi's sarcoma-associated herpes virus has been associated with MM (Retig et al., Science

276:1851 (1997)), there is evidence that chromosomal abnormalities, such as the deletion of 13q14 and rearrangements of 14q increase the proliferation of myeloma cells.

- 5 Up to 30% of patients who suffer with MM have a balanced translocation, t(4;14)(p16.3;q32), that places the fibroblast growth factor receptor 3 (FGFR3) gene under the control of IgH promoter elements (Chesi et al., Nat. Genet. 16:260 (1997)). This results in increased expression of
10 FGFR3, a member of a family of tyrosine kinase receptors implicated in control of cellular proliferation.

- According to Zoger et al., Blood 95:1925 (2000), monoallelic deletions of the retinoblastoma-1 (rb-1) gene and the D13S319 locus were observed in 48 of 104 patients
15 (46.2%) and in 28 of 72 (38.9%) patients, respectively, with newly diagnosed MM. Fluorescence in situ hybridization (FISH) studies found that 13q14 was deleted in all 17 patients with karyotypic evidence of monosomy 13 or deletion of 13q but also in 9 of 19 patients with
20 apparently normal karyotypes. Patients with a 13q14 deletion were more likely to have higher serum levels of beta(2)-microglobulin (P=0.059) and a higher percentage of bone marrow plasma cells (P=0.085) than patients with a normal 13q14 status on FISH analysis. In patients with a
25 deletion of 13q14, myeloma cell proliferation was markedly increased. The presence of a 13q14 deletion on FISH analysis was associated with a significantly lower rate of response to conventional-dose chemotherapy (40.8% compared with 78.6%; P =.009) and a shorter overall
30 survival (24.2 months compared with > 60 months; P <.005) than in patients without the deletion.

- There are numerous other mutated genes and chromosomal abnormalities that may predispose to MM. Examples of such genes are: B2M (15q21-q22); CCND1
35 (D11S287E, Cyclin D, PRAD1)(11q13); CD19 (16p11.2); HGF

(HPTA) (7q21.1); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-23); LTA (TNFB, LT) (6p21.3); SDC1 (2p24.1); and TNF (TNFA, TNFSF2, DIF) (6p21.3). Examples of chromosomal abnormalities include: t(6;14) (p25;q32) and

5 t(11;14) (q13;q32).

Other significant diseases or disorders of the bone marrow are also believed, or likely to have, a genetic, typically polygenic, etiologic component. These diseases include, for example, chronic myeloid leukemia,

10 chronic lymphoid leukemia, polycythemia vera, myelofibrosis, primary thrombocythemia, myelodysplastic syndromes, Wiskott-Aldrich, lymphoproliferative syndrome, aplastic anemia, Fanconi anemia, Down syndrome, sickle cell disease, thalassemia, granulocyte disorders, Kostmann

15 syndrome, chronic granulomatous disease, Chediak-Higashi syndrome, platelet disorders, Glanzmann thrombasthenia, Bernard-Soulier syndrome, metabolic storage diseases, osteoporosis, congenital hemophagocytic syndrome.

The human genome-derived single exon nucleic acid

20 probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human bone marrow, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed

25 at detectable levels in human bone marrow, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging

30 of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given bone marrow disease, or to specific grades or stages thereof.

35 In one embodiment, the patient gene expression

profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's bone marrow (or cells cultured therefrom) to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the bone marrow of individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of diseases of bone marrow to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human bone marrow. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the bone marrow has been demonstrated are useful for both measurement in the bone marrow and for survey of expression in other tissues.

Significant among such advantages is the presence

of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc.*

- Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).
- Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer

Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in bone marrow. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity

sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA

- 5 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
- 10 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

- 15 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity
- 20 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and
- 25 WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

- 30 Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or
- 35 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable

of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are
5 required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,115 - 26,012, respectively, for probe SEQ ID
10 NOS. 1 - 13,114. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,115 - 26,012 individually
15 by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency
20 conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀tl DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20
25 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as
30 the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes
35 of the present invention is dictated by the proximity of

other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one
5 expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more
10 usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand
15 of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art
20 to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to
25 provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic
30 and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

35 And when intended for use in solution

hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent
5 labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates
10 thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

15 The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived
20 single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96
25 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3'
30 primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon
35 probes can usefully include a plurality of probes chosen

for the common attribute of expression in the human bone marrow.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be
5 chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be
10 used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

15 It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

20 The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human bone marrow. In preferred embodiments, the present invention provides human genome-derived single exon microarrays
25 comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 13,114.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived
30 single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression
35 measurements. Alternatively, at a given probe density, the

same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in
5 signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

10 Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,114 contains an open-reading frame, set forth
15 respectively in SEQ ID NOS.: 13,115 - 26,012, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,114 can be used, or that portion thereof in SEQ ID NOS. 13,115 - 26,012 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and
20 Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression &
25 Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically
30 synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN:
35 0199637245); Jones, Amino Acid and Peptide Synthesis

(Oxford Chemistry Primers, No 7) , Oxford Univ. Press
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles
of Peptide Synthesis (Springer Laboratory), Springer Verlag
(December 1993) (ISBN: 0387564314).

5 It is, therefore, another aspect of the invention
to provide peptides comprising an amino acid sequence
translated from SEQ ID NOS.: 13,115 - 26,012. Such amino
acid sequences are set out in SEQ ID NOS: 26,013 - 38,628.
Any such recombinantly-expressed or synthesized peptide of
10 at least 8, and preferably at least about 15, amino acids,
can be conjugated to a carrier protein and used to generate
antibody that recognizes the peptide. Thus, it is a
further aspect of the invention to provide peptides that
have at least 8, preferably at least 15, consecutive amino
15 acids.

The following examples are offered by way of
illustration and not by way of limitation.

20 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
in Human Genomic Sequence

Bioinformatics Results

25 All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

30 After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
35 GRAIL uses a neural network, GENEFINDER uses a hidden

Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic
5 DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION
10 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three
15 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two
20 criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single
25 gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not
30 span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments
35 fewer than 250 bp in length do not bind well to the amino-

modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

5 Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first
10 additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing
15 the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

 The ORFs were then PCR amplified from genomic
20 DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

 Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard
25 techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR
30 amplification was classified as successful if a single band appeared.

 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)
35 length and distribution of amplified PCR products, with ORF

length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median
5 size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

10 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of
15 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were
20 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR
25 and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material
30 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was
35 similarly found not to affect differential expression

ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis
--

Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message

pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

- 5 Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer
10 and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
15 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup
20 column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

- Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a
25 Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human Cot1 DNA, and 0.5 % SDS.

- Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C
30 overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

- 35 Slides were scanned using a Molecular Dynamics

Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

- 5 Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of
10 at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.
- 15 Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

- The relative expression signal for these probes
20 was then plotted as function of tissue or cell type, and is presented in FIG. 6.

- FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not
25 expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

- Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed"
30 products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were
35 expressed in all 10 tissues. The next most common class

(15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are
5 compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is
10 represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than
15 "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is
20 novel, with gray depicting nonidentical with significant homology (white: E values < $1e-100$; gray: E values from $1e-05$ to $1e-99$; black: E values > $1e-05$).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that
25 were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100;
30 HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose
35 expression was measurable in only a single of the tested

tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

10

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes

will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the

observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous

				system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to

				the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
 5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
 10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
 15 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed

down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in

choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm
Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

10

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

20 EXAMPLE 3

Representation of Sequence and Expression Data as a
"Mondrian"

For each genomic clone processed for microarray
5 as above-described, a plethora of information was
accumulated, including full clone sequence, probe sequence
within the clone, results of each of the three gene finding
programs, EST information associated with the probe
sequences, and microarray signal and expression for
10 multiple tissues, challenging our ability to display the
information.

Accordingly, we devised a new tool for visual
display of the sequence with its attendant annotation
which, in deference to its visual similarity to the
15 paintings of Piet Mondrian, is hereinafter termed a
"Mondrian". FIGS. 3 and 4 present the key to the
information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases
25,000 to 130,000 shown), containing the carbamyl phosphate
20 synthetase gene (AF154830.1). Purple background within the
region shown as field 81 in FIG. 3 indicates all 37 known
exons for this gene.

As can be seen, GRAIL II successfully identified
27 of the known exons (73%), GENEFINDER successfully
25 identified 37 of the known exons (100%), while DICTION
identified 7 of the known exons (19%).

Seven of the predicted exons were selected for
physical assay, of which 5 successfully amplified by PCR
and were sequenced. These five exons were all found to be
30 from the same gene, the carbamyl phosphate synthetase gene
(AF154830.1).

The five exons were arrayed, and gene expression
measured across 10 tissues. As is readily seen in the
Mondrian, the five chip sequences on the array show
35 identical expression patterns, elegantly demonstrating the

reproducibility of the system..

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in bone marrow tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical

structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
5 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,114 single exon probes, each fragment corresponding to an extension product from one of
10 the two amplification primers.)

The structures of the 13,114 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,114. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not
15 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,115 - 26,012, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
20 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant
25 expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give
30 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the
35 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining
5 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)
10 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +
15 (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any
20 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human bone marrow and thus
25 presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human bone marrow tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,115 - 26,012 was individually
30 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were
35 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.: The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs

in an exhaustive process based on the following criteria:

1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
5 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion
10 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the
15 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary:
in Example 2, *supra*, a BLAST E value of $1e-30$ was used as
20 the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously
25 been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
30 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
35 a proper subset of the data present within the attached

sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,114) and probe exon (SEQ ID NOs.: 13,115 - 26,012, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

- 5 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;
- (b) the most similar sequence provided by BLAST
- 10 query of the EST database, with accession number and BLAST E value for the "hit";
- (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and
- 15 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

20 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Bone marrow

- Table 4 (546 pages) presents expression, homology, and
- 25 functional information for the genome-derived single exon probes that are expressed significantly in human bone marrow.

30

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human bone marrow comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,114 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,115 - 26,012.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is
between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid
5 probes as claimed in any of claims 1 to 7, wherein at least
50% of said single exon nucleic acid probes lack
prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid
10 probes as claimed in any of claims 1 to 8, wherein at least
50% of said single exon nucleic acid probes lack
homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in any of claims 1 - 9 characterised in
that said set of probes is addressably disposed upon a
substrate.

11. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in claim 10 wherein said substrate is
selected from glass, amorphous silicon, crystalline silicon
and plastic.

12. A microarray comprising a spatially addressable set of
25 single exon nucleic acid probes as claimed in any of claims
1 - 11.

13. A single exon nucleic acid probe for measuring human
gene expression in a sample derived from human bone marrow
30 comprising a nucleotide sequence as set out in any of SEQ
ID NOS.: 1 - 13,114 or a complementary sequence or a
fragment thereof wherein said probe hybridizes at high
stringency to a nucleic acid molecule expressed in the
human bone marrow.

35

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,013 - 38,628, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.
- 15
16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 20
17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
- 25
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35
21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human bone marrow, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human bone marrow; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
 wherein said detectably labeled nucleic acids are derived
20 from mRNA from the bone marrow of said eukaryote, said
 probe is a single exon probe having a fragment identical in
 sequence to, or complementary in sequence to, said
 predicted exon, said probe is included within a microarray
 according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

- 5 25. A nucleic acid sequence as set out in any of SEQ ID
Nos: 1 - 26,012 which encodes a peptide.
26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 26,012.
- 10 27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 26,013 - 38,628.

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5830	18820	32103	3.19				
6138	25585	32443	1.89				
6167	19242	32473	2.11				
6556	19816		1.24				
6700	19757	33034	0.89				
6700	19757	33035	0.89				
7332	20303	33647	1.52				
7332	20303	33648	1.52				
7642	20002	33665	1.46				
7642	20002	33667	1.49				
8114	21051		0.61				
8398	21395	34774	1.55				
8530	21797	35218	1.21				
9212	22178	35603	0.37				
9212	22178	35609	0.37				
9212	22178	35610	0.37				
10126	23250	36526	0.69				
10341	23169	36653	1.44				
10383	23305	37702	0.91				
10675	23597	37693	0.49				
10675	23597	37694	0.49				
10784	23716	37216	0.6				
10784	23716	37217	0.6				
11043	24007		2.14				
11396	24314		1.61				
11897	24553	38232	1.82				
11920	24712		1.94				
12900	25302		1.5				
12988	25476	31730	1.34				
6170	18245	32477	15.3	9.8E+00 AJ230028.1	NT		Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8339	21368	34723	1.75	9.8E+00 U32716.1	NT		Hemophilus influenzae Rd section 31 of 163 of the complete genome
10000	23026	35502	0.47	9.8E+00 Y18900.1	NT		Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
10100	23026	35503	0.47	9.8E+00 Y18950.1	NT		Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
7184	20218	33549	0.86	9.8E+00 AF068530.1	NT		Galus gallus ornithine transcarbamylase (OTC) gene, exon 1

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Table 4
Single Exon Probes Expressed in Bone Marrow

[illegible]

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Table 4
Cytokines Expressed in Bone Marrow

Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6390	16448	33986	0.78	5.9E+00	F47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10138	20044	33987	0.47	5.9E+00	P13863	SWISSPROT	EXTENSION PRECURSOR (CELL WALL HYDROLYSIN- HIGH GLYCOPROTEIN)
11933	23958	37482	2.38	5.9E+00	P11860	SWISSPROT	PEPTIDYLASE (THIOAL-ACTIVATED CYTOSOLIN)
7115	20049	33951	1.1	5.4E+00	X02211	NT	Chicken alpha-cardiac actin gene
7116	20048	33952	1.1	5.4E+00	X02212	NT	Chicken alpha-cardiac actin gene
7652	26515	33952	0.84	5.4E+00	G94935	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8143	21020	34480	0.6	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4R) (PANCROATIC POLYPEPTIDE RECEPTOR 1) (PPI)
8202	21172		1.72	5.4E+00	Q10182	SWISSPROT	LIPOTELLIN PRECURSOR (V76) CONTAINS: LIPOTELLIN LV-AN; LIPOTELLIN LV-TC; LIPOTELLIN LV-2
8151	22117	35543	0.73	5.4E+00	P40379	SWISSPROT	REPI PROTEIN
9151	22117	35544	0.73	5.4E+00	P40379	SWISSPROT	REPI PROTEIN
10395	23318	36769	1.41	5.4E+00	Q17064	SWISSPROT	RHOOPSIN
10395	23318	36800	1.41	5.4E+00	Q17064	SWISSPROT	RHOOPSIN
4824	17841	30719	1.22	5.3E+00	L41126.1	NT	Bovine immunoglobulin-like virus surface envelope gene, 5' end, cds
6635	16935	30739	0.6	5.3E+00	P44779	SWISSPROT	HOMEOBOX PROTEIN CEF-20
8415	21394		3.5	5.3E+00	P54093	SWISSPROT	DNA POLYMERASE GAMMA (M) (TOCHOMORAL DNA POLYMERASE CATALYTIC SUBUNIT)
6395	22200		0.3	5.3E+00	Q53499.1	NT	Human septin HRPD01 gene for stress protein response cds
11950	24829	35426	1.84	5.3E+00	Q27608	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE FOR SYNTHESIS PRECURSOR
12063	24864	35556	2.34	5.3E+00	T27683.1	NT	3-carboxylate chromophore (1) (redshift frame) GSF YG3.141w
12093	24964	35560	2.34	5.3E+00	T27683.1	NT	3-carboxylate chromophore (1) (redshift frame) GSF YG3.141w
5539	18636		1.22	5.2E+00	U519484.1	EST_HUMAN	Proteinase inhibitor R19, noncovalent segment reverse transcriptase cDNA
10738	23650		0.78	5.2E+00	AF248070.1	EST_HUMAN	HYPOPHOSPHATE 61.1 XRD PROTEIN C2B22.83C IN CHROMOSOME 1
11527	24488		1.48	5.2E+00	Q10138	SWISSPROT	RHOOPSIN
8313	22778	35706	0.85	5.1E+00	P40379	SWISSPROT	COLGON N IMMUNITY PROTEIN MICROG N (IMMUNITY PROTEIN)
10194	23109	35992	3.07	5.1E+00	P50320	SWISSPROT	ZINC FINGER PROTEIN HRX (ALC-1)
11617	24585	35717	3.07	5.1E+00	P50320	SWISSPROT	ZINC FINGER PROTEIN HRX (ALC-1)
10554	24766	35714	0.65	5.0E+00	BF010443.1	EST_HUMAN	6018940407 NIH MGC. 17 Homo sapiens cDNA clone IMAGE:4124114.5
10554	24766	35714	0.65	5.0E+00	BF010443.1	EST_HUMAN	6018940407 NIH MGC. 17 Homo sapiens cDNA clone IMAGE:4124114.5
10736	23721	37219	3.70	5.0E+00	AF163464.2	EST_HUMAN	Genis familiis skeletal muscle channel OCCT (CLONT) mRNA, complete cds
11622	24690	39122	6.36	5.0E+00	Z53900.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162
10582	24514		0.63	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, Hfe gene, hereditary haemochromatosis
4090	17124		9.81	4.9E+00	AF185265.1	NT	Human aetiology haemochromatosis (NFTS) gene, complete cds
4090	17124		9.81	4.9E+00	AF185265.1	NT	Human aetiology haemochromatosis (NFTS) gene, complete cds

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Table 4
Types Expressed in Bone Marrow

Probe SEQ ID NO.	Gene SEQ ID NO.	ORF SEQ NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8454	21482	34876	0.53	4.8E-00	BF367009.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8456	21482	34876	0.53	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8458	161832	34876	0.51	4.8E-00	AF178007.1	EST_HUMAN	PAO-370547-311010-002-304 BT0547 Homo sapiens cDNA
8460	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8462	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8464	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8466	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8468	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8470	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8472	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8474	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8476	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8478	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8480	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8482	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8484	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8486	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8488	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8490	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8492	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8494	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8496	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8498	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8500	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8502	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8504	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8506	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8508	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8510	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8512	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8514	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8516	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8518	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8520	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890-011-c10 GN042 Homo sapiens cDNA
8522	161832	34876	0.51	4.8E-00	AF240768.1	EST_HUMAN	RC3-GM042-010890

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6046	25462	32334	0.84	41E+00	Q09185	CELLULAR TUMOR ANTIGEN P53
6046	25462	32335	0.84	41E+00	Q09185	CELLULAR TUMOR ANTIGEN P53
7916	20290	33633	0.76	41E+00	BE236948.1	B011107271 NIH JGOC-18 Homo sapiens cDNA clone IMAGE:3951534.5
7916	20297	33738	0.55	41E+00	EF247599.1	B018600071 NIH JGOC-58 Homo sapiens cDNA clone IMAGE:4080734.5
7923	20366	34254	7.87	41E+00	Q23810	YY1 PROTEIN PRECURSOR
8061	20366	34254	0.84	41E+00	AB041523.1	Paralogous yeastensis mRNA for calcineurin A, complete cds
8060	21002	34388	3.95	41E+00	P28694	GENE 68 PROTEIN
8065	21022	34399	3.95	41E+00	P28694	GENE 68 PROTEIN
8249	21218	34628	2.5	41E+00	U57903.1	Pan troglodytes noncoding sds LTR element in the RNUL2 locus
9868	22851	38310	0.52	41E+00	P11293	35S RIBOSOMAL PROTEIN S20
10031	22855	38426	2.43	41E+00	EF062453.1	R022765871 NIH JGOC-82 Homo sapiens cDNA clone IMAGE:433328.5
10096	23591		0.45	41E+00	P46114	CYCLO-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (CDKN1B)
10981	23901	37414	0.47	41E+00	C84242	CDKN1C1 (p21) CARRIER PROTEIN SYNTHASE III (BETA-KETOACYL-CoP SYNTHASE III) (KAS III)
11231	24184		2.3	41E+00	P09178	HYPOHEMICAL PROTEIN HVLFI
11317	24207		13.22	41E+00	BE335860.1	B016701071 NIH JGOC-71 Homo sapiens cDNA clone IMAGE:390051.5
3598	16602		0.7	41E+00	BE335860.1	GLC-INTERACTING PROTEIN 1
5334	20057	33361	0.94	41E+00	C34363	SUCRASE-ISOMALTAZE, INTES TINAL CONTAINS: SUCRASE; ISOMALTAZE
5334	20057	33362	0.94	41E+00	C34363	SUCRASE-ISOMALTAZE, INTES TINAL CONTAINS: SUCRASE; ISOMALTAZE
7123	20057	33363	1.01	41E+00	C34363	SUCRASE-ISOMALTAZE, INTES TINAL CONTAINS: SUCRASE; ISOMALTAZE
7123	20057	33364	1.01	41E+00	C34363	SUCRASE-ISOMALTAZE, INTES TINAL CONTAINS: SUCRASE; ISOMALTAZE
7983	20366	33715	1.47	41E+00	Q33910	CELL DIVISION PROTEIN FTSY HOMOLOG
8061	21002	34388	0.44	41E+00	Q14157	HYPOHEMICAL PROTEIN KIAA0144
10303	23228	36711	0.45	41E+00	Q81109	NITRIC-OXIDE SYNTHASE (NOS, TYPE 1) (NEURONAL NOS) (N-NOS)
10326	23448	36648	0.5	41E+00	AE02132.1	Ureaplasma urealyticum section 33 of 39 of the complete genome
10920	23542	37041	0.49	41E+00	Q00511	URICASE (URATE OXIDASE)
10920	23542	37042	0.49	41E+00	Q00511	URICASE (URATE OXIDASE)
11802	23667	37461	1.67	41E+00	P14548	CYTOCHROME C OXIDASE POLYPEPTIDE III
11875	24757	38540	2.98	41E+00	P07564	GENOME POLYPROTEIN CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5346	18252	31151	0.63	3.6E+00	Z89108.1	NT	Scalasin, complete genome (section 8 of 21) from 68561 to 120540
5327	18433	31165	0.73	3.6E+00	U51081.61	EST HUMAN	Scalasin, complete genome (section 8 of 21) from 68561 to 120540
8897	21863	35285	0.93	3.6E+00	U12397.1	EST HUMAN	HUM001593 Liver Hsp63 and Hsp70 Homo sapiens cDNA clone 1598
8897	21863	35286	0.93	3.6E+00	U12397.1	EST HUMAN	HUM001593 Liver Hsp63 and Hsp70 Homo sapiens cDNA clone 1598
8692	21698	35383	4.21	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 539 of the complete genome
8692	21698	35384	4.21	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 539 of the complete genome
10022	22949	36416	0.44	3.6E+00	U2775.1	NT	Citrona viscopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
10022	22949	36417	0.44	3.6E+00	U2775.1	NT	Citrona viscopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11200	24155		3.18	3.6E+00	M69705.1	NT	Escherichia coli glycerol phosphate dehydrogenase (gpd) gene, partial cds, and the translation start site has been verified (gpc), the translation start site has been verified (gpc), and repressor protein (gpr) genes, complete cds
6115	1783		1.1	3.6E+00	U2988.1	NT	Borrelia burgdorferi (strain 2001B) outer surface protein (ospC) gene, partial cds
6337	19133	32447	0.98	3.5E+00	U10748.1	EST HUMAN	X40068.1 Soares infant brain (NEB Homo sapiens cDNA clone IMAGE:3440 5'
8307	21023	34423	0.6	3.6E+00	P37508	SWISSPROT	5-OXOGLUTAMATE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE)
8904	21030	34428	0.54	3.6E+00	A1982102.1	EST HUMAN	cd9710.41 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:191887 3' similar to gp.104213
8124	21061	34460	0.96	3.6E+00	P24567	SWISSPROT	CELLULAR RETINAL DEHYDROGENASE-BINDING PROTEIN (HUMAN);
8829	21786		0.6	3.6E+00	P24567	SWISSPROT	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MSTR) mRNA
9387	22352	35782	0.91	3.6E+00	AA190698.1	EST HUMAN	THROMBOXANE SYNTHASE (TXA SYNTHASE) (TXS)
9387	22352	35783	0.91	3.6E+00	AA190698.1	EST HUMAN	THROMBOXANE SYNTHASE (TXA SYNTHASE) (TXS)
9850	22789	36240	0.96	3.5E+00	AL191553.2	NT	cd9680.4.1 Staphylococcus aureus cell 3' 837216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
1514	14546	27517	0.73	3.4E+00	AF24577.1	NT	cd9680.4.1 Staphylococcus aureus cell 3' 837216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
6803	19945	35241	0.49	3.4E+00	U77817.1	NT	cd9680.4.1 Staphylococcus aureus cell 3' 837216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
7866	20547	33007	2.90	3.4E+00	P04952	SWISSPROT	cd9680.4.1 Staphylococcus aureus cell 3' 837216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
7968	20507	34288	0.6	3.4E+00	P04952	SWISSPROT	cd9680.4.1 Staphylococcus aureus cell 3' 837216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
9025	21891		0.68	3.4E+00	U65406.1	NT	Arabis nemoralis RPB55r mRNA, complete cds
9428	22382	35831	0.73	3.4E+00	AJ250047.1	NT	Arabis nemoralis RPB55r mRNA, complete cds
9467	22431	35889	0.65	3.4E+00	AJ250047.1	NT	Arabis nemoralis RPB55r mRNA, complete cds
10027	23549	37049	2.69	3.4E+00	AF013167.1	NT	Arabis nemoralis RPB55r mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11881	24743	38327	2.80	3.4E+00/L7750.1	NT	NT	Homo sapiens D-George syndrome critical region, centromeric and
6186	19281	32428	1.03	3.3E+00/O09699	SWISSPROT	SWISSPROT	POTATIVE IRON ALCOHOL DEHYDROGENASE
8186	19281	32427	1.03	3.3E+00/O09699	SWISSPROT	SWISSPROT	POTATIVE IRON ALCOHOL DEHYDROGENASE
8225	21164	34601	0.9	3.3E+00/AF11108.2	NT	NT	Homo sapiens serine palmitoyl transferase, subunit I gene, complete cds, and unknown genes
10330	23751	37250	0.9	3.3E+00/AP0151.1	NT	NT	Bacillus halodurans genomic DNA, section 514
10330	23751	37251	0.9	3.3E+00/AP0151.1	NT	NT	Bacillus halodurans genomic DNA, section 514
301	13573	25495	1.83	3.2E+00/G9422.1	NT	NT	D-ribose 2P-50 POU genes
4051	13573	25495	0.84	3.2E+00/G9422.1	NT	NT	D-ribose 2P-50 POU genes
4769	17779	36874	1.93	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1).
6549	18778	31910	1.2	3.2E+00/R44924	SWISSPROT	SWISSPROT	SQUALENE-HOPENE CYCLASE
6549	18778	31911	1.2	3.2E+00/R44924	SWISSPROT	SWISSPROT	SQUALENE-HOPENE CYCLASE
6583	18778	31909	2.79	3.2E+00/P12763	SWISSPROT	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5593	18778	31901	2.79	3.2E+00/P12763	SWISSPROT	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
8439	19504	32754	1.66	3.2E+00/P16831	SWISSPROT	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
8439	19504	32755	1.66	3.2E+00/P16831	SWISSPROT	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
7603	20037	34185	0.71	3.2E+00/P04275	SWISSPROT	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8052	20869	34399	2.47	3.2E+00/Y13655.1	NT	NT	Chlamydomonas reinhardtii chloroplast DNA for psb, yf4, yf3, psb18 genes
8052	20869	34397	2.47	3.2E+00/Y13655.1	NT	NT	Chlamydomonas reinhardtii chloroplast DNA for psb, yf4, yf3, psb18 genes
8285	22350	36298	1.87	3.2E+00/M30393.1	SWISSPROT	SWISSPROT	PERIPLASMIC NIFE HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENYASE SMALL CHAIN)
8285	22350	36298	1.87	3.2E+00/M30393.1	SWISSPROT	SWISSPROT	PERIPLASMIC NIFE HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENYASE SMALL CHAIN)
10500	23422	36921	2.26	3.2E+00/AB10081.2	NT	NT	Saccharomyces cerevisiae genes for gnyf1, gnyf2, gnyf3, gnyf4, gnyf5, gnyf6, gnyf7, gnyf8, gnyf9, gnyf10, gnyf11, gnyf12, gnyf13, gnyf14, gnyf15, gnyf16, gnyf17, gnyf18, gnyf19, gnyf20, gnyf21, gnyf22, gnyf23, gnyf24, gnyf25, gnyf26, gnyf27, gnyf28, gnyf29, gnyf30, gnyf31, gnyf32, gnyf33, gnyf34, gnyf35, gnyf36, gnyf37, gnyf38, gnyf39, gnyf40, gnyf41, gnyf42, gnyf43, gnyf44, gnyf45, gnyf46, gnyf47, gnyf48, gnyf49, gnyf50, gnyf51, gnyf52, gnyf53, gnyf54, gnyf55, gnyf56, gnyf57, gnyf58, gnyf59, gnyf60, gnyf61, gnyf62, gnyf63, gnyf64, gnyf65, gnyf66, gnyf67, gnyf68, gnyf69, gnyf70, gnyf71, gnyf72, gnyf73, gnyf74, gnyf75, gnyf76, gnyf77, gnyf78, gnyf79, gnyf80, gnyf81, gnyf82, gnyf83, gnyf84, gnyf85, gnyf86, gnyf87, gnyf88, gnyf89, gnyf90, gnyf91, gnyf92, gnyf93, gnyf94, gnyf95, gnyf96, gnyf97, gnyf98, gnyf99, gnyf100, gnyf101, gnyf102, gnyf103, gnyf104, gnyf105, gnyf106, gnyf107, gnyf108, gnyf109, gnyf110, gnyf111, gnyf112, gnyf113, gnyf114, 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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mod Shifter (Tco) Htt BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10700	28922	37118	5.2	3.1E+00 P46985		SWISSPROT	DEOXYHYDROXY SYNTHASE (DHS)
11791	29948		1.98	3.1E+00 P39515		SWISSPROT	GENOME POLYPROTEIN CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS2C AND NS2D; HELICASE (NS3) RNA-DIRECTED RNA POLYMERASE (NS5) retroviral nuclear receptor isoform beta 2 (beta2), embryonal carcinoma cell line, PC97-A021, mRNA, 2871 nt
11811	24896		2.76	3.1E+00 S56951.1		NT	Homo sapiens hypophyseal pituitary PRO0889 (PRO0889) mRNA
2949	19069	28333	1.5	3.0E+00 J53386.1	602384	NT	Salmonella enterica serovar Typhimurium DNA methyltransferase and S-adenosyl methionine-dependent DNA methyltransferase (EC 2.9.9.2)
5411	18514	31922	0.78	3.0E+00 J53386.1		NT	Salmonella enterica serovar Typhimurium DNA methyltransferase and S-adenosyl methionine-dependent DNA methyltransferase (EC 2.9.9.2)
6708	19784	33263	0.78	3.0E+00 J53386.1		NT	Salmonella enterica serovar Typhimurium DNA methyltransferase and S-adenosyl methionine-dependent DNA methyltransferase (EC 2.9.9.2)
7198	19784	33263	0.78	3.0E+00 J53386.1		NT	Salmonella enterica serovar Typhimurium DNA methyltransferase and S-adenosyl methionine-dependent DNA methyltransferase (EC 2.9.9.2)
7423	20330	33734	0.69	3.0E+00 J53386.1		SWISSPROT	CYR61 PROTEIN PRECURSOR (GC461)
7623	20330	33734	0.69	3.0E+00 J53386.1		SWISSPROT	CYR61 PROTEIN PRECURSOR (GC461)
8258	22224		1.21	3.0E+00 J53386.1		NT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
10997	23678	37976	0.84	3.0E+00 Q56905		SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTTRANSFERASE) (ADOMET SYNTHETASE)
11008	23678	37467	1.85	3.0E+00 Q16181		SWISSPROT	QDC10 PROTEIN HOMOLOG
11331	24301	37827	4.64	3.0E+00 P51842		SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-F)
11351	24301	37828	4.64	3.0E+00 P51842		SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-F)
2028	10046	28059	2.33	2.9E+00 AE002248.2		NT	Chlamydomonas reinhardtii pncA gene, section 53 of 84 of the complete genome
6192	19296		0.6	2.9E+00 AB028033.1		NT	Bongaportia pedicularis mitochondrial DNA for 18S ribosomal RNA
7094	20028	33332	1.97	2.9E+00 J25879.1		NT	F-antigen gene for P-protein of the glyoxylate cleavage system
7418	20385	33734	6.15	2.9E+00 O14514		SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7418	20385	33734	6.15	2.9E+00 O14514		SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7689	20847	34011	5.32	2.9E+00 P46589		SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN) STRUCTURAL POLYPEPTIDE (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3)
8200	21170	34580	0.81	2.9E+00 P09844		SWISSPROT	STRUCTURAL POLYPEPTIDE (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3)
8200	21170	34581	0.82	2.9E+00 P09844		SWISSPROT	STRUCTURAL POLYPEPTIDE (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3)
8494	21403	34816	0.82	2.9E+00 BF544711.1		EST HUMAN	602374191 NC-COMP: Homo sapiens cDNA, clone IMAGE-4733089, 5'
14451	14484	27480	4.16	2.9E+00 AF186596.1		NT	Bacillus subtilis malA gene, partial cdc, chloroplast gene for chloroplast product

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	QVF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Database No.	Top Hit Source	Top Hit Description
1637	14689		2.87	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
7626	20492	33954	4.93	2.8E+00	8303724	NT	Mus musculus endonuclease (LOC35425), mRNA
8972	20496		0.56	2.8E+00	BE595182.1	EST_HUMAN	601942758F11N11_WG, 53 Homo sapiens cDNA clone IMAGE:3664607.5
11048	20492	33954	1.73	2.8E+00	8303724	NT	Mus musculus endonuclease (LOC35425), mRNA
233	13333	26256	13.36	2.7E+00	6079306	NT	Mus musculus per-leucine repeat gene 3 (Prlr3), mRNA
233	13333	26257	13.36	2.7E+00	6079306	NT	Mus musculus per-leucine repeat gene 3 (Prlr3), mRNA
6631	18727	31868	1.11	2.7E+00	L16005.1	NT	Homo sapiens apolipoprotein Kinase IV gene, exons 1 and 2
6405	21453		0.86	2.7E+00	U15947.1	NT	Homo sapiens apolipoprotein Kinase IV gene, exons 1 and 2
8319	22284		1.89	2.7E+00	AL116456.1	NT	Human placenta strain 14 cDNA library under conditions of mitogen-activated protein kinase (MAPK) stimulation
8787	21110	34510	0.94	2.7E+00	AW084191.1	EST_HUMAN	Human placenta strain 14 cDNA library under conditions of mitogen-activated protein kinase (MAPK) stimulation
10898	23798		1.89	2.7E+00	BE03327.1	EST_HUMAN	Human placenta strain 14 cDNA library under conditions of mitogen-activated protein kinase (MAPK) stimulation
4701	17722	36613	6.28	2.6E+00	AF056746.1	NT	Human placenta strain 14 cDNA library under conditions of mitogen-activated protein kinase (MAPK) stimulation
9527	18723	31863	2.04	2.6E+00	675601	NT	Mus musculus SRY-box containing gene 13 (Sry13), mRNA
9527	18723	31864	2.06	2.6E+00	675601	NT	Mus musculus SRY-box containing gene 13 (Sry13), mRNA
9528	18011		3.9	2.6E+00	V17063.1	NT	Myoblasts from fetal rat muscle
7803	26002		0.7	2.6E+00	AL24650.1	NT	Homo sapiens Sryr-5 and Sryr-6 genes
7987	20906		32.15	2.6E+00	AF23502.1	NT	Mus musculus SH2-containing isoform 5-phosphatase (Shp) gene, exons 16 through 27, and complete cds
8304	21365	34770	1.12	2.6E+00	AL132186.1	NT	Human placenta strain 14 cDNA library under conditions of mitogen-activated protein kinase (MAPK) stimulation
8304	21365	34771	1.12	2.6E+00	AL132186.1	NT	Human placenta strain 14 cDNA library under conditions of mitogen-activated protein kinase (MAPK) stimulation
10045	22042	36408	3.12	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
12841	20977		1.61	2.6E+00	6051933	NT	Homo sapiens ATP-binding cassette, sub-family B (MOTAP), member 4 (ABCB4), mRNA
12841	20977		2.58	2.6E+00	11416220	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1480	14463	27466	3.73	2.6E+00	AL271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
8911	18907	32188	2.32	2.6E+00	P13465	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5911	18907	32188	2.32	2.6E+00	P13465	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6901	19097	32187	1.49	2.6E+00	P13465	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6901	19097	32187	1.49	2.6E+00	P13465	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
9892	10944		0.86	2.6E+00	D30032.1	NT	Vibrio cholerae cdaA gene and cdaB gene for cholera toxin, complete cds
7960	20091	34293	0.35	2.6E+00	P17598	SWISSPROT	LATEIN-RELATED PROTEIN 1
8005	20091	34398	0.97	2.6E+00	AW049198.1	EST_HUMAN	Human placenta strain 14 cDNA library under conditions of mitogen-activated protein kinase (MAPK) stimulation
8095	21031	34429	0.51	2.6E+00	4502602	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTOL1) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8486	22423	35461	1.49	2.5E+00	D50307.1	NT	Rice DNA for ribidase C1, complete cds
10211	23136	36023	0.78	2.5E+00	BE23077.1	EST_HUMAN	6617579791 NH, MYC, 17 Homo sapiens cDNA clone IMAGE:353090 5'
12244	26033	37663	2.5	2.5E+00	AF28695.1	NT	Mus musculus EF14 gene, partial cds; LINK1 gene, complete cds; and ELN gene, partial cds
3026	16033	20009	1.1	2.4E+00	N24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4844	17690	30461	6.31	2.4E+00	490332	NT	Homo sapiens double C2-like domains, alpha (DC2A) mRNA
6126	19204	32427	3.82	2.4E+00	P02843	SWISSPROT	VITELLOGENIN PRECURSOR (YOLK PROTEIN 1)
7606	20567	33928	0.71	2.4E+00	BF667602.1	EST_HUMAN	6621208691 NH, MYC, 96 Homo sapiens cDNA clone IMAGE:4218012 5'
7606	20567	33928	0.71	2.4E+00	BF667602.1	EST_HUMAN	6621208691 NH, MYC, 96 Homo sapiens cDNA clone IMAGE:4218012 5'
8479	21448	34864	2.08	2.4E+00	P28942	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8479	21448	34864	2.08	2.4E+00	P28942	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8534	21522	34865	2.82	2.4E+00	AE001466.1	NT	Helicobacter pylori strain N6, region 17 of 132 of the complete genome
8698	21944		1.48	2.4E+00	AW87126.1	EST_HUMAN	RC2-PT0084-03.1254 Homo sapiens cDNA clone IMAGE:3133187 3'
9180	22146	35573	9.82	2.4E+00	P24091	SWISSPROT	ENDOGLYCANIN B PRECURSOR (CN1B)
10398	23320	36003	2.34	2.4E+00	P18973	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10398	23320	36004	2.34	2.4E+00	P18973	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10495	23348	36882	2.1	2.4E+00	X62311.1	SWISSPROT	XYLULOSE 5-EPIMERASE (XEL)
10604	23526		6.1	2.4E+00	P06969	SWISSPROT	XYLULOSE 5-EPIMERASE (XEL)
10685	23607	37100	1.97	2.4E+00	BE220702.1	EST_HUMAN	h33063.1 NO, CGAP, Xd11 Homo sapiens cDNA clone IMAGE:3133187 3'
10685	23607	37101	1.97	2.4E+00	BE220702.1	EST_HUMAN	h33063.1 NO, CGAP, Xd11 Homo sapiens cDNA clone IMAGE:3133187 3'
10985	23875	37368	1.4	2.4E+00	Q5148	SWISSPROT	IDENTIFICATION REGULATOR PROTEIN NRQ
11415	24339	37884	2.2	2.4E+00	Y1070.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKD operon and downstream
11517	24408		1.89	2.4E+00	AF068972.1	NT	Caprin locus alphaS2-casini type C gene, intron 15
11896	24682	38231	2.14	2.4E+00	AF158952.2	NT	Flagrin x transmembrane cytosolic ascorbate peroxidase (ApoSO) gene, ApoS-C allele, complete cds
12068	14293	27297	11.33	2.3E+00	Z46724.1	NT	G domesticus partial cytochrome c gene for cytochrome c
4147	17176		1.46	2.3E+00	AJ401081.1	NT	Bos taurus partial cytochrome c gene for cytochrome c
5934	18020		0.99	2.3E+00	N84245.1	EST_HUMAN	PROLYC-AROMATASE
7697	20545	34009	2.42	2.3E+00	6878554	NT	Rattus norvegicus ATPase, GTPase, GTPase, Ubiquitous (Atpase), mRNA
7853	20503		2.79	2.3E+00	P07189	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENPB)
8059	20995	34392	1.12	2.3E+00	P60295.1	NT	Mus musculus cDNA and protein homologous coding for DnaK and DnaJ
9405	22420	38689	0.84	2.3E+00		NT	Polypodium erianthum mitochondrion, complete genome
9523	22488	38936	2.03	2.3E+00	Q11127	SWISSPROT	ALPHA-1.3-GLUCOSYLTRANSFERASE (GALACTOSIDE 3-L-GLUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUT4)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10868	23876	37590	0.45	2.3E+00	P02481	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
11183	24113	37598	7.84	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SPNEXN)
11697	24718	38554	1.99	2.3E+00	P45631	SWISSPROT	HYPOTHETICAL 171.070 PROTEIN IN SPOLIC-CW1A INTERGENIC REGION
12072	24946	38559	2.34	2.3E+00	BF541087.1	EST_HUMAN	B02087.21.F1 NIH_JGC_38 Homo sapiens cDNA clone IMAGE:4008173 5'
12072	24946	38560	2.34	2.3E+00	BF541087.1	EST_HUMAN	B02087.21.F1 NIH_JGC_38 Homo sapiens cDNA clone IMAGE:4008173 5'
12443	25255	37628	6.31	2.3E+00	BE982337.1	EST_HUMAN	B0143387.3.F1 NIH_JGC_72 Homo sapiens cDNA clone IMAGE:3918493 5'
13077	25500		1.3	2.3E+00	A1261652.1	NT	Newcastle orcasin C protein alpha subunit (CNA-3) (gene-S) gene, complete cds
4065	17084	28861	142	2.2E+00	AF020328.1	NT	Regucalcin gamma Class 17 alpha synthase (C17a) gene, complete cds
4342	17380	32251	3.8	2.2E+00	D07071.1	NT	Ret gene for regulation, exon (non-coding exon)
4342	17380	32252	3.8	2.2E+00	D07071.1	NT	Ret gene for regulation, exon (non-coding exon)
5415	18516	31395	11.02	2.2E+00	Q88307	SWISSPROT	SORTIN-LIKE RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LIGAND-BINDING REPEATS) (INSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELAT... LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) >
5415	18516	31398	11.02	2.2E+00	Q88307	SWISSPROT	SORTIN-LIKE RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LIGAND-BINDING REPEATS) (INSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELAT... LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) >
5593	19038	32234	1.83	2.2E+00	BE927226.1	EST_HUMAN	RC3-OT0254-300960-022-406 OT0254 Homo sapiens cDNA
5593	19038	32235	1.83	2.2E+00	BE927226.1	EST_HUMAN	RC3-OT0254-300960-022-406 OT0254 Homo sapiens cDNA
6160	19255	32498	8.78	2.2E+00	BE250383.1	EST_HUMAN	RC3-OT0254-300960-022-406 OT0254 Homo sapiens cDNA
6469	19354	32604	3.91	2.2E+00	Q00335	SWISSPROT	MINOR VIBRION STRUCTURAL PROTEIN MV-2
6750	19804	33085	3.14	2.2E+00	F14159	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOTROPIN A)
7149	18381		3.5	2.2E+00	AJ364574.1	EST_HUMAN	hB602.21 NC. LOCAP
7539	20502	33661	0.95	2.2E+00	AA137027.1	EST_HUMAN	hB602.21 NC. LOCAP
7539	20502	33661	0.95	2.2E+00	AA137027.1	EST_HUMAN	hB602.21 NC. LOCAP
7653	20809	34187	18.24	2.2E+00	AA448012.1	EST_HUMAN	pcp510.17 Soar, full, Nucleo-HF, 3v Homo sapiens cDNA clone IMAGE:566143 5'
7653	20809	34287	0.95	2.2E+00	F54818	SWISSPROT	ALANINE RACEMASE
8439	21408	34820	0.89	2.2E+00	BE307159.1	EST_HUMAN	hB7H2.1 NIH_JGC_21 Homo sapiens cDNA clone IMAGE:2983207 3' similar to gbt-45836 Mouse
8439	21408	34821	0.89	2.2E+00	BE307159.1	EST_HUMAN	hB7H2.1 NIH_JGC_21 Homo sapiens cDNA clone IMAGE:2983207 3' similar to gbt-45836 Mouse
9697	22850		11.22	2.2E+00	BE741676.1	EST_HUMAN	hB7H2.1 NIH_JGC_21 Homo sapiens cDNA clone IMAGE:2983207 3' similar to gbt-45836 Mouse
9627	25998		2.53	2.2E+00	Q04708	SWISSPROT	TRANSFUSION TYF PROTEIN A

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10413	20335	36819	1.57	2.2E-000	AI280373.1	EST HUMAN	enr66003.x1 Source: placenta, 8dweeks 2NUPR62/91 Homo sapiens cDNA clone IMAGE:1659353 3' similar to gp10443 GLUTATHIONE PEROXIDASE (HUMAN);
10413	20335	36820	1.57	2.2E-000	AI280373.1	EST HUMAN	enr66003.x1 Source: placenta, 8dweeks 2NUPR62/91 Homo sapiens cDNA clone IMAGE:1659353 3' similar to gp10443 GLUTATHIONE PEROXIDASE (HUMAN);
10496	23376	36871	2.22	2.2E-000	AF26782.1	EST HUMAN	enr66003.x1 Source: placenta, 8dweeks 2NUPR62/91 Homo sapiens cDNA clone IMAGE:1659353 3' similar to gp10443 GLUTATHIONE PEROXIDASE (HUMAN);
10822	23743	37344	3.06	2.2E-000	AF163416.1	NT	347835597.1 NIH_XGC_37 Homo sapiens cDNA clone IMAGE:075391 5'
11786	23623	37421	3.23	2.2E-000	AF070911	SWISSPROT	PROGOLIN RECEPTOR (TAMMORE FALL URINARY GLYCOPROTEIN) (THP)
11837	24618	39415	6.31	2.2E-000	P10407	SWISSPROT	EARLY A2 KIDNEY PROTEIN, alpha gene, enhancer region and upstream region
571	16944	20555	12.39	2.1E-000	AF132612.2	NT	104139533.1 NIH_XGC_37 Homo sapiens cDNA clone IMAGE:2744550 3'
3601	16948		0.88	2.1E-000	AW44966.1	EST HUMAN	HYPOPHYSICAL PROTEIN MS302 HOMOLOG
6255	16328		0.88	2.1E-000	P75387	SWISSPROT	ALPHA 2HS GLYCOPROTEIN PRECURSOR (FETUIN A)
6860	20203	33532	3.45	2.1E-000	P70199	SWISSPROT	Homo sapiens cDNA, with glycine muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and
7225	20247	33381	0.61	2.1E-000	4803430	NT	transcripts
7246	19861	33278	5.97	3.1E-000	N29575.1	EST HUMAN	gk9810.x1 Source: melanocyte 2NHH1 Homo sapiens cDNA clone IMAGE:2701813 3' similar to gp.M5954
8842	21809		1.82	2.1E-000	AI123530.1	EST HUMAN	TRANSCRIPTION INITIATION FACTOR TF1D (HUMAN);
1201	14240	27197	1.38	2.0E-000	AF169527.1	NT	AUT28330.NT8R12 Homo sapiens cDNA clone NT8R12000871 5'
1201	14240	27198	1.38	2.0E-000	AF169527.1	NT	Homo sapiens p220-oxide (COKDEL) mRNA, complete cds
1372	14372	27142	1.15	2.0E-000	AF254027.1	NT	Homo sapiens p220-oxide (COKDEL) mRNA, complete cds
1378	14372	27142	3.42	2.0E-000	P25462	SWISSPROT	Cyclodextrin curcumin N-ox-A-Triase beta 1 subunit mRNA, complete cds
2189	15175	28195	4.96	2.0E-000	782735.1	NT	PUTATIVE RNA METHYLTRANSFERASE SP81
2189	15175	28196	4.96	2.0E-000	782735.1	NT	R-norvegicus mRNA for collagen alpha1 type I
4127	17160	30048	2.24	2.0E-000	AW684496.1	EST HUMAN	h13305.x1 NC_CGAP_GUT Homo sapiens cDNA clone IMAGE:2872188 3' similar to gp.X01677
4127	17160	30049	2.24	2.0E-000	AW684496.1	EST HUMAN	h13305.x1 NC_CGAP_GUT Homo sapiens cDNA clone IMAGE:2872188 3' similar to gp.X01677
7796	20750	34739	0.85	2.0E-000	P07566	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8358	21327	34739	3.84	2.0E-000	AB006976.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8358	21327	34740	3.84	2.0E-000	AB006976.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8358	21327	34740	3.84	2.0E-000	AB006976.1	NT	STRUCTURAL POLYPEPTIDE (CONTAINS NUCLEOCAPSID PROTEIN C; MEMBRANE
9274	22240	35668	3.22	2.0E-000	F31900.1	EST HUMAN	hSPD29703 TM6 Homo sapiens cDNA clone s4000117808
12756	29838	31427	4.52	2.0E-000	5834843	NT	Gallus gallus mitochondrion, complete genome

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	QIF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4826	17848	30746	0.98	1.9E+00	AF203468.1	NT	Dentio retro RhoG-like protein mRNA, complete cds
5979	16774	31945	4.52	1.9E+00	6754389	NT	Mus musculus insulin 1,4,5-bisphosphate receptor 1 (Ibr1) mRNA
5979	16774	31946	4.52	1.9E+00	6754389	NT	Mus musculus insulin 1,4,5-bisphosphate receptor 1 (Ibr1) mRNA
6219	16293	33527	1.05	1.9E+00	BE060955.1	EST - HUMAN	IRG-CT0083-07.096-022-032 CT0083 Homo sapiens cDNA
6810	16684		1.19	1.9E+00	AW84586.1	EST - HUMAN	CTD-BINDING SR-LIKE PROTEIN RAT
6912	16984		2.87	1.9E+00	Q60527	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8802	21789	35193	1.72	1.9E+00	P03467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8802	21789	35194	1.72	1.9E+00	P03467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9008	21972		3.6	1.9E+00	BF360268.1	EST - HUMAN	CAGE-MT014-010003-023-512 MT014 Homo sapiens cDNA
9248	22211		1.52	1.9E+00	Q57781	SWISSPROT	ARGININE DEIMINASE (AD) (ARGININE DHTDOLASE) (AD)
9896	22915	38360	0.33	1.9E+00	AA066725.1	EST - HUMAN	484404 st Stratagene lung (493.210) Homo sapiens cDNA clone IMAGE 554574 3' similar to contains Au
19328	23549	37354	0.83	1.9E+00	AF245268.1	NT	Impetigo element contains element L1 L1 Impetigo element
3198	16198	25077	1.5	1.9E+00	P21004	SWISSPROT	PROTEIN BB PRECURSOR
3197	16194	25103	10.61	1.9E+00	U04358.1	NT	3' UTR of P207942 copper transporting P-ATPase (cta) and ATP synthase apilin subunit (cta) genes, complete cds
3137	16194	25104	10.81	1.9E+00	U04358.1	NT	Synchrotron in P207942 copper transporting P-ATPase (cta) and ATP synthase apilin subunit (cta) genes, complete cds
5907	19032		1.84	1.9E+00	P16502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
8234	19295	32932	2.2	1.9E+00	BF311666.1	EST - HUMAN	601697954FT NH1_MGC_18 Homo sapiens cDNA clone IMAGE 4177384 5'
6536	19600		1.19	1.9E+00	BF683327.1	EST - HUMAN	602138479FT NH1_MGC_48 Homo sapiens cDNA clone IMAGE 4288272 5'
6904	19856	33253	1.02	1.9E+00	BF205652.1	EST - HUMAN	601862488FT NH1_MGC_7 Homo sapiens cDNA clone IMAGE 4139026 5'
7260	19995	33262	1.07	1.9E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7176	20442		0.7	1.9E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--(GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-GALACTOSYLTRANSFERASE)
8454	21423	34639	0.9	1.9E+00	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
6154	21423	34639	0.9	1.9E+00	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
6812	21779	35204	0.46	1.9E+00	P46834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8812	21779	35205	0.46	1.9E+00	P46834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8812	21779	35206	0.46	1.9E+00	P46834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8206	22172	39090	2.21	1.9E+00	Q43291	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (EHS)
9530	22493	39941	0.86	1.9E+00	R31042.1	EST - HUMAN	MT204MT Source placenta N20HP Homo sapiens cDNA clone IMAGE 135276 5'

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Single Exon Probes Expressed in Bone Marrow

Probe ID SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9617	25681	36009	0.84	1.8E+00	AJ189004.1	EST_HUMAN	D/O-OT003-07030-148-403 OT0030 Homo sapiens cDNA
10208	25133	36020	0.93	1.8E+00	FZ02039	SWISSPROT	CHITINASE D PRECURSOR
10816	25689	36041	2.28	1.8E+00	AI111049.1	NH	Homo sapiens PROK30 mRNA, complete cds
10919	25688	36042	0.75	1.8E+00	P44232	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12583	25608		8.17	1.8E+00	AF914254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12642	25526		3.93	1.8E+00	B930404	NT	Rattus norvegicus Atkin-related protein complex 1b (Acrpb1c) mRNA
1110	14154	27104	2.43	1.7E+00	GQ0114	SWISSPROT	LEVINURICAC (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2279	16262	28317	3.68	1.7E+00	AL51290.2	NT	cakr3kx.1 Soares NIHMPU_3.1 Homo sapiens cDNA clone IMAGE 197837.3'
2382	15300	28415	1.97	1.7E+00	AK111087.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
4487	17512	30400	0.9	1.7E+00	GQ0114	SWISSPROT	LEVINURICAC (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5884	17365	31659	1.66	1.7E+00	BE085846.1	EST_HUMAN	CABP-B10265-T71290-127-403 B10282 Homo sapiens cDNA
5924	17365	31660	1.66	1.7E+00	BE085846.1	EST_HUMAN	CABP-B10265-T71290-127-403 B10282 Homo sapiens cDNA
5925	17365	31660	1.66	1.7E+00	R08748.1	EST_HUMAN	CAB46 Fetal heart Homo sapiens cDNA clone C4548.6 and
6153	18210	32236	0.44	1.7E+00	Q07118	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TFI) (COUP-TF1)
6703	19759	33336	0.96	1.7E+00	P33816	SWISSPROT	(PYRUVATE DEHYDROGENASE LIPONAMIDE)PHOSPHATASE, MITOCHONDRIAL PRECURSOR
7428	20395	33746	1.01	1.7E+00	Q07303	SWISSPROT	HYPOHETICAL 380 KD PROTEIN IN CAT ZANDI INTERGENIC REGION
8167	21134	34466	1.01	1.7E+00	Q07303	SWISSPROT	HYPOHETICAL 380 KD PROTEIN IN CAT ZANDI INTERGENIC REGION
8367	21136	34466	1.01	1.7E+00	AF021336.1	NT	Mus musculus T-cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8367	21136	34476	1.21	1.7E+00	G75871.5	EST_HUMAN	Mus musculus T-cell alpha lymphocyte leukemia (T1041) mRNA
8397	21136	34775	0.84	1.7E+00	BF303053.1	EST_HUMAN	502071817FF1 NCBI CGAP Brn67 Homo sapiens cDNA clone IMAGE 421469.8
8887	21883	35273	0.54	1.7E+00	P44591.1	EST_HUMAN	501BM428F1 NH MGC 17 Homo sapiens cDNA clone IMAGE 414008.4
8974	21940		1.92	1.7E+00	P308000.1	EST_HUMAN	501BM428F1 NH MGC 17 Homo sapiens cDNA clone IMAGE 414008.4
9052	22018	35442	0.51	1.7E+00	G59053.3	NT	Mus musculus Ank-1 mRNA for erythrocyte enghym
9052	22018	35443	0.51	1.7E+00	U18832.1	NT	Mus musculus Ank-1 mRNA for erythrocyte enghym
9186	22132	35558	0.43	1.7E+00	U18832.1	NT	Fetuin nonregucis SA gene, partial cds
9504	25697	35609	2.37	1.7E+00	O00479	SWISSPROT	HOMEOBOX PROTEIN DLX3
9504	25697	35910	2.37	1.7E+00	O00479	SWISSPROT	HOMEOBOX PROTEIN DLX3
9665	22862		1.4	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
10331	24441		0.5	1.7E+00	AW953981.1	EST_HUMAN	EST395651 IMAGE reassessments, MAGO Homo sapiens cDNA

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Protein NO.	Eno SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
35	13158	28056	3.54	1.3E-001	U53449.1	NT	Rattus norvegicus jaw demineralization protein 2 (Jp2-2) mRNA, complete cds
204	13334	28258	2.63	1.5E-001	AE0022012	NT	Chlamydomonas reinhardtii AR33: section 32 of 84 of the complete genome
622	19307		2.04	1.3E-001	6752861	NT	Mus musculus a diethylglut and metalloprotease domain (ADAM) 15 (metagelidin) (Adam15), mRNA
1420	15427	28450	3.2	1.3E-001	UJ13402.1	NT	Pleurotus versipellis A RNA complete genome, isolate U
2522	15528	28547	2.17	1.3E-001	6678350	NT	Mus musculus T-cell lymphoma fixation and metastasis 1 (Tfm1), mRNA
3155	15427	28450	2.98	1.3E-001	UJ13402.1	NT	Pleurotus versipellis A RNA complete genome, isolate U
3396	19435	28302	0.92	1.3E-001	AE001846.1	NT	Drosophila melanogaster R1: section 82 of 228 of the complete chromosome 1
5817	18907	32090	0.82	1.3E-001	AE655301.1	EST_HUMAN	BT2010x1 NCJ_OGAP_G08 Homo sapiens cDNA clone IMAGE:2240897 similar to TR:000237.000237 HGF-1
5817	18907	32091	0.82	1.3E-001	AE655301.1	EST_HUMAN	BT2010x1 NCJ_OGAP_G08 Homo sapiens cDNA clone IMAGE:2240897 similar to TR:000237.000237 HGF-1
6546	19007	32369	2.71	1.5E-001	AF78793.1	EST_HUMAN	Y930407.01 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:37183 5
7393	20338	33688	1.48	1.5E-001	BE785386.1	EST_HUMAN	601476749P1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:383165 5
7985	20338	33688	16.72	1.5E-001	AF47779	SWISSPROT	HYPOHEALIN 18.140 PROTEIN IN RAT ADAL INTERFERON PRECURSOR
7985	20338	33689	16.72	1.5E-001	AF47779	SWISSPROT	HYPOHEALIN 18.140 PROTEIN IN RAT ADAL INTERFERON PRECURSOR
7998	20331	33580	0.7	1.5E-001	AA48226.1	EST_HUMAN	60210213T1 Soares testis 1N18 Homo sapiens cDNA clone IMAGE: 1407115 3
7850	20766	34172	0.78	1.5E-001	AD03254.1	EST_HUMAN	en70161.1 5' Endogenous cDNA from 5 T11 Homo sapiens cDNA clone IMAGE: 1664693 3 similar to Y930407.01 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:37183 5
8144	21081		0.97	1.5E-001	AF033887.1	NT	Homo sapiens (Homo) 1N18 Homo sapiens cDNA clone IMAGE:391181 5
8459	21428	34845	0.91	1.5E-001	BE374486.1	EST_HUMAN	Y930407.01 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:391181 5
8514	21482	34896	0.48	1.5E-001	AF034087.1	NT	Homo sapiens (Homo) 1N18 Homo sapiens cDNA clone IMAGE:391181 5
8991	21957	35382	1.08	1.5E-001	G02138.1	NT	Homo sapiens (Homo) 1N18 Homo sapiens cDNA clone IMAGE:391181 5
9670	22335		0.47	1.5E-001	AF033887.1	NT	Homo sapiens (Homo) 1N18 Homo sapiens cDNA clone IMAGE:391181 5
9489	22424	35853	0.95	1.5E-001	AF033887.1	EST_HUMAN	Y930407.01 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:391181 5
9838	22774	36229	0.91	1.5E-001	AF033887.1	EST_HUMAN	Y930407.01 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:391181 5
10262	23637		0.74	1.5E-001	AF033887.1	EST_HUMAN	Y930407.01 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:391181 5
10413	23334		6.14	1.5E-001	BF337694.1	EST_HUMAN	602039717F1 NCJ_OGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183695 5
10536	24778	36972	2.92	1.5E-001	AF001768.1	EST_HUMAN	2430926.1 Soares retina N24ZHR Homo sapiens cDNA clone IMAGE:381306 5
10536	24778	36973	5.98	1.5E-001	AF001768.1	EST_HUMAN	2430926.1 Soares retina N24ZHR Homo sapiens cDNA clone IMAGE:381306 5
11727	24613		0.71	1.5E-001	AA13417.1	EST_HUMAN	DKFZ567P243.1 5' 847 (synonym: hbr1) Homo sapiens cDNA clone DKFZ567P243.3
11861	24782	38180	1.63	1.5E-001	AF077880.1	EST_HUMAN	Maze mitochondrial RNA 18S Sur gene and RNA-Pol pseudogene
13122	24867	38553	1.53	1.5E-001	BE257652.1	EST_HUMAN	601109521F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3303477 5

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12892	29151		1.87	1.5E-00	8753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
12510	28599	31420	1.51	1.5E-00	U03480.1	NT	Human mRNA for KIAA0148 gene, partial cds
12723	29378		4.94	1.5E-00	AL45086.1	NT	Thermoplasma acidophilum complete genome, segment 3/6
12821	29143		1.33	1.5E-00	6978492	NT	Rattus norvegicus 5'-Lipoxygenase (ALOX5), mRNA
32	13152	26952	1.41	1.4E-00	7951688	NT	Human sapiens DKF278980M122 protein (DKF27898M122), mRNA
32	13152	26953	1.41	1.4E-00	7951688	NT	Human sapiens DKF27898M122 protein (DKF27898M122), mRNA
2285	15298	26953	0.9	1.4E-00	AF033357.1	NT	Helicobacter pylori glutamine synthetase (glutS) gene, complete cds
2341	15351		8.77	1.4E-00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2877	15973	28690	1.83	1.4E-00	X77453.1	NT	Human pallidum type 1 genomic DNA
2784	15778	28764	2.75	1.4E-00	AF064864.2	NT	Pigeon nuptius neobromatous type 1 (NF1), A-kinase anchor protein (AKAP4), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2784	15778	28765	2.75	1.4E-00	AF064864.2	NT	Pigeon nuptius neobromatous type 1 (NF1), A-kinase anchor protein (AKAP4), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3345	16396		0.83	1.4E-00	U543739	NT	Human sapiens KIAA0965 mRNA
4284	17313	30161	1.38	1.4E-00	AF000455.1	EST_HUMAN	CHX-1/NK005-145030.295-108 NK005 Homo sapiens cDNA
4284	17313	30162	1.38	1.4E-00	AF000455.1	EST_HUMAN	CHX-1/NK005-145030.295-108 NK005 Homo sapiens cDNA
4500	18144	28056	0.82	1.4E-00	AF033357.2	NT	Chlamydia muridarum, section 85 of 85 of the complete genome
4500	18144	28057	0.82	1.4E-00	AF033357.2	NT	Chlamydia muridarum, section 85 of 85 of the complete genome
4515	17528		1.58	1.4E-00	BE01147.4	EST_HUMAN	w45607.at NCL CGAP Part1 Homo sapiens cDNA clone IMAGE:287556.5
5065	18543	31461	5.92	1.4E-00	AF033357.3	EST_HUMAN	Human sapiens mRNA for KIAA1157 protein, partial cds
5065	18543	31462	5.92	1.4E-00	AF033357.3	EST_HUMAN	Human sapiens mRNA for KIAA1157 protein, partial cds
8430	19478	32725	3.05	1.4E-00	D11412	SWISSPROT	DNA TOPOISOMERASE II ALPHA
8430	19478	32726	4.2	1.4E-00	AF033357.1	NT	Human sapiens mRNA for KIAA0965 protein, complete cds
8527	20598		2.65	1.4E-00	Q62777	SWISSPROT	SYNAPSIN II
8552	19913	33875	2.65	1.4E-00	Q62777	SWISSPROT	SYNAPSIN II
8552	19913	33876	2.65	1.4E-00	Q62777	SWISSPROT	SYNAPSIN II
8781	19836	33110	0.86	1.4E-00	BE007970.1	EST_HUMAN	QVC-BN0148-050502-215-311 BN0148 Homo sapiens cDNA
8781	19836	33110	0.86	1.4E-00	BE007970.1	EST_HUMAN	QVC-BN0148-050502-215-311 BN0148 Homo sapiens cDNA
8998	20122	33436	0.86	1.4E-00	AF080057.1	EST_HUMAN	CHX-1/NK005-300300-132-312 NK005 Homo sapiens cDNA
8998	20122	33436	0.86	1.4E-00	AF080057.1	EST_HUMAN	CHX-1/NK005-300300-132-312 NK005 Homo sapiens cDNA
7503	20488	33529	2.02	1.4E-00	AJ133269.1	NT	Human sapiens capovirin-1/2 locus, Contig1, D7S1522 gene CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7521	20488	33848	1.15	1.4E-00	AF06790.1	EST_HUMAN	hca2103.at NCL CGAP CHX1 Homo sapiens cDNA clone IMAGE:291697.3 similar to contains Alu repetitive element
7552	20544	33904	0.86	1.4E-00	P56248	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7552	20544	33905	0.86	1.4E-00	P56248	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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Table 4
Single Exon Probes Expressed In[illegible]

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Table 4
Single Exon Probes Expressed in

Probe SEQ ID NO.	Emm SEQ ID NO.	ORF SEQ NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3611	19656	29574	1.02	1.3E+00	AF016044.1	NT	Fugu tubules germine-mimoblastic acid receptor beta subunit gene, partial cds, 5'UTR erythrocyte membrane protein (P56), synaptic vesicle-associated integral membrane protein (VAMP-1), microglial C-protease enhancer protein (P-OLCE) genes, complete cds
5824	18290	31152	0.98	1.3E+00	AF036052.1	SWISSPROT	Candida albicans partial mRNA for ribonucleotide reductase large subunit (rrt1 gene)
5825	18988	31657	1.08	1.3E+00	P10732	SWISSPROT	PHENOL ALIPHATIC P3 PROTEIN (PHENOL-ALIPHATIC P3 COMPONENT)
5794	18006	32055	0.92	1.3E+00	U02718.1	EST	Human extracellular 17 beta-hydroxysteroid dehydrogenase gene, complete cds
6063	19434	32365	0.54	1.3E+00	BF662626.1	EST	Homo sapiens H1b1, H1b2, H1b3, H1b4, H1b5, H1b6, H1b7, H1b8, H1b9, H1b10, H1b11, H1b12, H1b13, H1b14, H1b15, H1b16, H1b17, H1b18, H1b19, H1b20, H1b21, H1b22, H1b23, H1b24, H1b25, H1b26, H1b27, H1b28, H1b29, H1b30, H1b31, H1b32, H1b33, H1b34, H1b35, H1b36, H1b37, H1b38, H1b39, H1b40, H1b41, H1b42, H1b43, H1b44, H1b45, H1b46, H1b47, H1b48, H1b49, H1b50, H1b51, H1b52, H1b53, H1b54, H1b55, H1b56, H1b57, H1b58, H1b59, H1b60, H1b61, H1b62, H1b63, H1b64, H1b65, H1b66, H1b67, H1b68, H1b69, H1b70, H1b71, H1b72, H1b73, H1b74, H1b75, H1b76, H1b77, H1b78, H1b79, H1b80, H1b81, H1b82, H1b83, H1b84, H1b85, H1b86, H1b87, H1b88, H1b89, H1b90, H1b91, H1b92, H1b93, H1b94, H1b95, H1b96, H1b97, H1b98, H1b99, H1b100, H1b101, H1b102, H1b103, H1b104, H1b105, H1b106, H1b107, H1b108, H1b109, H1b110, H1b111, H1b112, H1b113, H1b114, H1b115, H1b116, H1b117, H1b118, H1b119, H1b120, H1b121, H1b122, H1b123, H1b124, H1b125, H1b126, H1b127, H1b128, H1b129, H1b130, H1b131, H1b132, H1b133, H1b134, H1b135, H1b136, H1b137, H1b138, H1b139, H1b140, H1b141, H1b142, H1b143, H1b144, H1b145, H1b146, H1b147, H1b148, H1b149, H1b150, H1b151, H1b152, H1b153, H1b154, H1b155, H1b156, H1b157, H1b158, H1b159, H1b160, H1b161, H1b162, H1b163, H1b164, H1b165, H1b166, H1b167, H1b168, H1b169, H1b170, H1b171, H1b172, H1b173, H1b174, H1b175, H1b176, H1b177, H1b178, H1b179, H1b180, H1b181, H1b182, H1b183, H1b184, H1b185, H1b186, H1b187, H1b188, H1b189, H1b190, H1b191, H1b192, H1b193, H1b194, H1b195, H1b196, H1b197, H1b198, H1b199, H1b200, H1b201, H1b202, H1b203, H1b204, H1b205, H1b206, H1b207, H1b208, H1b209, H1b210, H1b211, H1b212, H1b213, H1b214, H1b215, H1b216, H1b217, H1b218, H1b219, H1b220, H1b221, H1b222, H1b223, H1b224, H1b225, H1b226, H1b227, H1b228, H1b229, H1b230, H1b231, H1b232, H1b233, H1b234, H1b235, H1b236, H1b237, H1b238, H1b239, H1b240, H1b241, H1b242, H1b243, H1b244, H1b245, H1b246, H1b247, H1b248, H1b249, H1b250, H1b251, H1b252, H1b253, H1b254, H1b255, H1b256, H1b257, H1b258, H1b259, H1b260, H1b261, H1b262, H1b263, H1b264, H1b265, H1b266, H1b267, H1b268, H1b269, H1b270, H1b271, H1b272, H1b273, H1b274, H1b275, H1b276, H1b277, H1b278, H1b279, H1b280, H1b281, H1b282, H1b283, H1b284, H1b285, H1b286, H1b287, H1b288, H1b289, H1b290, H1b291, H1b292, H1b293, H1b294, H1b295, H1b296, H1b297, H1b298, H1b299, H1b300, H1b301, H1b302, H1b303, H1b304, H1b305, H1b306, H1b307, H1b308, H1b309, H1b310, H1b311, H1b312, H1b313, H1b314, H1b315, H1b316, H1b317, H1b318, H1b319, H1b320, H1b321, H1b322, H1b323, H1b324, H1b325, H1b326, H1b327, H1b328, H1b329, H1b330, H1b331, H1b332, H1b333, H1b334, H1b335, H1b336, H1b337, H1b338, H1b339, H1b340, H1b341, H1b342, H1b343, H1b344, H1b345, H1b346, H1b347, H1b348, H1b349, H1b350, H1b351, H1b352, H1b353, H1b354, H1b355, H1b356, H1b357, H1b358, H1b359, H1b360, H1b361, H1b362, H1b363, H1b364, H1b365, H1b366, H1b367, H1b368, H1b369, H1b370, H1b371, H1b372, H1b373, H1b374, H1b375, H1b376, H1b377, H1b378, H1b379, H1b380, H1b381, H1b382, H1b383, H1b384, H1b385, H1b386, H1b387, H1b388, H1b389, H1b390, H1b391, H1b392, H1b393, H1b394, H1b395, H1b396, H1b397, H1b398, H1b399, H1b400, H1b401, H1b402, H1b403, H1b404, H1b405, H1b406, H1b407, H1b408, H1b409, H1b410, H1b411, H1b412, H1b413, H1b414, H1b415, H1b416, H1b417, H1b418, H1b419, H1b420, H1b421, H1b422, H1b423, H1b424, H1b425, H1b426, H1b427, H1b428, H1b429, H1b430, H1b431, H1b432, H1b433, H1b434, H1b435, H1b436, H1b437, H1b438, H1b439, H1b440, H1b441, H1b442, H1b443, H1b444, H1b445, H1b446, H1b447, H1b448, H1b449, H1b450, H1b451, H1b452, H1b453, H1b454, H1b455, H1b456, H1b457, H1b458, H1b459, H1b460, H1b461, H1b462, H1b463, H1b464, H1b465, H1b466, H1b467, H1b468, H1b469, H1b470, H1b471, H1b472, H1b473, H1b474, H1b475, H1b476, H1b477, H1b478, H1b479, H1b480, H1b481, H1b482, H1b483, H1b484, H1b485, H1b486, H1b487, H1b488, H1b489, H1b490, H1b491, H1b492, H1b493, H1b494, H1b495, H1b496, H1b497, H1b498, H1b499, H1b500, H1b501, H1b502, H1b503, H1b504, H1b505, H1b506, H1b507, H1b5

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Table 4
bes Expressed in Bone Marrow

[illegible]

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3725	16787	28676	8.48	1.2E+00	U75002.1	NT	Mus muscularis subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4012	17051	28678	1.76	1.2E+00	BF73570.1	EST_HUMAN	MR3-FD175-05050-203-g0c.1 F10175 Homo sapiens cDNA
4327	16417	28343	1.09	1.2E+00	AF18940.1	NT	Homo sapiens LHX3 gene, intron 2
4498	17523	30457	2.12	1.2E+00	M87050.1	NT	Rattus ventralis cardiac A23 gene, exon 1, 23
4851	17574	30464	1.33	1.2E+00	AI101598.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4892	17613	30507	2.1	1.2E+00	AF106498.1	NT	Homo sapiens post-synaptic density 92 (DCA) gene, complete cds
4919	17640	30507	0.6	1.2E+00	U62200.1	NT	Human retinoblastoma protein (p105) gene, partial cds
5032	18094	30942	2.38	1.2E+00	P52228	SWISSPROT	Calmodulin-dependent protein kinase II (CDPKII) gene, partial cds
5032	18094	30943	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-III)
5032	18094	30944	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-II)
5032	18094	30945	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-I)
5032	18094	30946	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-IV)
5032	18094	30947	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-V)
5032	18094	30948	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-VI)
5032	18094	30949	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-VII)
5032	18094	30950	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-VIII)
5032	18094	30951	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-IX)
5032	18094	30952	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-X)
5032	18094	30953	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XI)
5032	18094	30954	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XII)
5032	18094	30955	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XIII)
5032	18094	30956	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XIV)
5032	18094	30957	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XV)
5032	18094	30958	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XVI)
5032	18094	30959	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XVII)
5032	18094	30960	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XVIII)
5032	18094	30961	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XIX)
5032	18094	30962	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XX)
5032	18094	30963	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXI)
5032	18094	30964	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXII)
5032	18094	30965	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXIII)
5032	18094	30966	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXIV)
5032	18094	30967	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXV)
5032	18094	30968	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXVI)
5032	18094	30969	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXVII)
5032	18094	30970	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXVIII)
5032	18094	30971	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXIX)
5032	18094	30972	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXX)
5032	18094	30973	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXI)
5032	18094	30974	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXII)
5032	18094	30975	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXIII)
5032	18094	30976	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXIV)
5032	18094	30977	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXV)
5032	18094	30978	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXVI)
5032	18094	30979	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXVII)
5032	18094	30980	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXVIII)
5032	18094	30981	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXIX)
5032	18094	30982	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXX)
5032	18094	30983	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXI)
5032	18094	30984	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXII)
5032	18094	30985	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXIII)
5032	18094	30986	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXIV)
5032	18094	30987	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXV)
5032	18094	30988	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXVI)
5032	18094	30989	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXVII)
5032	18094	30990	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXVIII)
5032	18094	30991	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXIX)
5032	18094	30992	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXX)
5032	18094	30993	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXI)
5032	18094	30994	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXII)
5032	18094	30995	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXIII)
5032	18094	30996	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXIV)
5032	18094	30997	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXV)
5032	18094	30998	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXVI)
5032	18094	30999	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXVII)
5032	18094	31000	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXVIII)
5032	18094	31001	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXIX)
5032	18094	31002	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXX)
5032	18094	31003	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXI)
5032	18094	31004	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXII)
5032	18094	31005	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIII)
5032	18094	31006	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIV)
5032	18094	31007	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXV)
5032	18094	31008	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVI)
5032	18094	31009	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVII)
5032	18094	31010	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVIII)
5032	18094	31011	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIX)
5032	18094	31012	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXX)
5032	18094	31013	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXXI)
5032	18094	31014	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXII)
5032	18094	31015	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIII)
5032	18094	31016	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIV)
5032	18094	31017	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXV)
5032	18094	31018	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVI)
5032	18094	31019	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVII)
5032	18094	31020	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVIII)
5032	18094	31021	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIX)
5032	18094	31022	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXX)
5032	18094	31023	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXXI)
5032	18094	31024	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXII)
5032	18094	31025	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIII)
5032	18094	31026	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIV)
5032	18094	31027	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXV)
5032	18094	31028	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVI)
5032	18094	31029	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVII)
5032	18094	31030	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVIII)
5032	18094	31031	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIX)
5032	18094	31032	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXX)
5032	18094	31033	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXXI)
5032	18094	31034	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXII)
5032	18094	31035	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIII)
5032	18094	31036	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIV)
5032	18094	31037	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXV)
5032	18094	31038	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVI)
5032	18094	31039	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVII)
5032	18094	31040	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVIII)
5032	18094	31041	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIX)
5032	18094	31042	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXX)
5032	18094	31043	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXXI)
5032	18094	31044	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXII)
5032	18094	31045	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIII)
5032	18094	31046	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIV)
5032	18094	31047	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXV)
5032	18094	31048	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVI)
5032	18094	31049	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVII)
5032	18094	31050	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVIII)
5032	18094	31051	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIX)
5032	18094	31052	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXX)
5032	18094	31053	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXXI)
5032	18094	31054	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXII)
5032	18094	31055	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIII)
5032	18094	31056	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXIV)
5032	18094	31057	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXV)
5032	18094	31058	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H4 PRECURSOR (CLONE PHRHS-XXXXXXVI)
5032	18094	31059	2.38	1.2E+00	P52228	SWISSPROT	HISTONE H

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Table 4
Genes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6228	2210a		0.58	1.2E+00	7708271	NT	Homo sapiens CQ3-30 protein (LOC51611). mRNA
6229	2210b	35777	1.08	1.3E+00	AW373720.1	EST_HUMAN	NR2-C70222-201089-001-07 C70222 Homo sapiens cDNA
6230	2210c	35778	1.08	1.2E+00	HA65981	EST_HUMAN	Y66060.1 Soares fetal liver system INF.S Homo sapiens cDNA
6231	2255a	35001b	0.98	1.2E+00	232980.1	NT	hERG2011 Soares fetal liver system INF.S Homo sapiens cDNA
6232	2255b	35001c	3.63	1.2E+00	232980.1	NT	R. communis gene for phosphatidylethanolamine phosphotransferase beta subunit
6233	2262a	35033	1.11	1.2E+00	D17146.1	EST_HUMAN	HUMHMT0A1 Liver HepG2 cell line. Homo sapiens cDNA clone hm07a01
6234	2262b	35033	3.52	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6235	2262c	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6236	2262d	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6237	2262e	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6238	2262f	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6239	2262g	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6240	2262h	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6241	2262i	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6242	2262j	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6243	2262k	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6244	2262l	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6245	2262m	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6246	2262n	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6247	2262o	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6248	2262p	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6249	2262q	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6250	2262r	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6251	2262s	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6252	2262t	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6253	2262u	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6254	2262v	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6255	2262w	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6256	2262x	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6257	2262y	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6258	2262z	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6259	2262aa	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6260	2262ab	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6261	2262ac	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6262	2262ad	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6263	2262ae	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6264	2262af	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6265	2262ag	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6266	2262ah	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6267	2262ai	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6268	2262aj	35700	3.32	1.2E+00	5458321	EST_HUMAN	H. sapiens ENO3 gene for muscle specific enolase
6269	2262ak	35700	3.32	1.2E+00	5458321	EST_HUMAN	

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	OSF SEQ ID NO.	Exon Signal	Max Similarity (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5715	18809	31987	0.96	1.1E+00	A1138882.1	EST_HUMAN	q885003.x1 Soares, basic_NH2 Homo sapiens cDNA clone IMAGE:1782800 3'
6211	10285	32517	1.63	1.1E+00	11418799	NT	Homo sapiens soluble carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6405	16473	32721	0.94	1.1E+00	AF197861.1	NT	Megastrola sulchra cytochrome b gene, complete cds, mitochondrial gene for mitochondrial product
8547	19008	32870	0.83	1.1E+00	R06037.1	EST_HUMAN	megastrola sulchra cytochrome b gene, complete cds, mitochondrial gene for mitochondrial product
8676	19029	33226	1.21	1.1E+00	AJ204004.1	NT	Mus musculus mRNA for ER protein 38 (EP38 gene)
7488	20434		0.88	1.1E+00	AF101091.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 25 through 28
7614	20479	33840	0.82	1.1E+00	U35961.1	NT	Mouse mRNA for protein 12-phospho-L-glutamate hydrolase
7732	20987	34050	1.83	1.1E+00	U72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7732	20987	34051	1.83	1.1E+00	U72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7754	20797	34076	8.13	1.1E+00	AL101566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7833	25591	34186	0.94	1.1E+00	11807960	NT	Mus musculus alien mating type information regulation 2, (S. cerevisiae, bomydys)like (SIR2), mRNA
8470	21439	34507	2.95	1.1E+00	BF320263.1	EST_HUMAN	923E982F.NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3246828 5'
8583	21531	34591	0.73	1.1E+00	AF176309.1	EST_HUMAN	h38h11.x2 NCI-GDAP_K211 Homo sapiens cDNA clone IMAGE:2186548 3'
9089	22539	35479	0.93	1.1E+00	AB030083.1	NT	Arabidopsis thaliana cellulosic microfibrillar GXY-like gene
9187	22133	35559	1.42	1.1E+00	BS00750.1	NT	VH-epitope-epitope/glycoprotein 8 antibody/424 heavy chain variable region [human, mRNA Partial, 376 nt]
9278	22244	35973	0.45	1.1E+00	A079444.1	EST_HUMAN	ca5403.x1 Soares, NHMPu, S1 Homo sapiens cDNA clone IMAGE:1077248 3'
9722	21115		0.84	1.1E+00	BE384876.1	EST_HUMAN	8072787F.NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9846	22913	36376	0.95	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
10040	22987		0.89	1.1E+00	U12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
10130	23036	36534	0.95	1.1E+00	U76301.1	NT	Yersinia pseudotuberculosis paeA, paeF, adhesin (paeA), chaperone (paeB), and other (paeC) genes, complete cds
10292	23117	36901	1.38	1.1E+00	AB022015.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10327	23222	36706	5.55	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10337	23291	36757	20.32	1.1E+00	0754021	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10897	23797	37287	1.09	1.1E+00	P73769	SWISSPROT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10989	23909	37422	0.83	1.1E+00	BF343844.1	EST_HUMAN	DNA MIA/TAH REPAIR PROTEIN MUTS
10989	23909	37422	0.83	1.1E+00	BF343844.1	EST_HUMAN	92201488F.NCI_GDAP_Bred4 Homo sapiens cDNA clone IMAGE:4150068 5'
11012	23877	37502	2.03	1.1E+00	11067364	NT	92201488F.NCI_GDAP_Bred4 Homo sapiens cDNA clone IMAGE:4150068 5'
11084	24027		3.83	1.1E+00	AF065942.1	NT	Homo sapiens KIAA0629 gene product (KIAA0628), mRNA Kiaapromoter fuzumae cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11435	18340		4.65	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11439	24382	37921	3.12	1.1E+00	AF012892.1	NT	Perlecanin crissum cytosolic glucose-6-phosphate dehydrogenase 1 (G6PDPH1) mRNA, complete cds
11439	24382	37922	3.12	1.1E+00	AF012892.1	NT	Perlecanin crissum cytosolic glucose-6-phosphate dehydrogenase 1 (G6PDPH1) mRNA, complete cds
11803	24649	38227	3.44	1.1E+00	AB095869.1	EST_HUMAN	w7861.t1 Source: NPL T_CGC S1 Homo sapiens cDNA clone IMAGE:2381548.3
12439	25202		3.12	1.1E+00	P07066	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12539	25203	31807	1.55	1.1E+00	AF216896.1	NT	Taenia solium immunogenic protein T176 mRNA, partial cds
12691	25705		2.26	1.1E+00	AF234189.1	NT	Dichytolium discoidium isopentenyl pyrophosphate isomerase (Dip) mRNA, complete cds
99	13215		1.55	1.0E+00	U25808.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	13224	26148	1.68	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for alpha-thalassaemia, complete cds
418	13491		3.03	1.0E+00	AB021884.1	NT	Mercurialis polymorpha genes for 26S rRNA, SS rRNA, 16S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
578	13947	29560	2.22	1.0E+00	AJ251880.1	NT	Mercurialis polymorpha genes for 26S rRNA, SS rRNA, 16S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
879	13741	29606	0.74	1.0E+00	AL183418.2	NT	Homo sapiens chromosome 21 segment RS21C018
879	13742		1.35	1.0E+00	AF125894.1	NT	Aedes aegypti much-like protein MUC1 mRNA, complete cds
1388	15890		3.53	1.0E+00	D80416.1	NT	V. carteri AggCm mRNA
1771	14800	27780	0.97	1.0E+00	AB060531.1	NT	Pleurocid inhibitory virus RNA for nonstructural
2403	15498	29521	1.42	1.0E+00	P48355	SWISSPROT	polyprotein, capsid protein precursor, complete cds
2403	15498	29522	1.42	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2987	15946	29881	4.42	1.0E+00	P24008	SWISSPROT	DNA GYRASE SUBUNIT B
2987	15946	29882	4.42	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STERIOD 4-DEHYDROGENASE 1 (STERIOD 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2978	16038		0.91	1.0E+00	O14228	SWISSPROT	3-OXO-5-ALPHA-STERIOD 4-DEHYDROGENASE 1 (STERIOD 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3212	16257	29190	1.08	1.0E+00	AA028453.1	EST_HUMAN	HYPOPHYSICAL PROTEIN 87/90 PROTEIN CBF12.08C IN CHROMOSOME 1
3813	13216		0.93	1.0E+00	U25808.1	NT	cdgpa11 Source: Ipsi, Ipsi, N28H3.3w Homo sapiens cDNA clone IMAGE:1032830.3 similar to
3932	16736	29640	1.33	1.0E+00	AJ223816.1	NT	WPC-CD3A.3 OE4124 contains element MER22 MER22 repetitive element;
4037	17131	30024	0.73	1.0E+00	AF223941.1	NT	Xenopus laevis rhodopsin gene, complete cds
4943	17333		0.73	1.0E+00	8922245	NT	Aquatic bispous mRNA for tyrosinase
4943	17333		0.73	1.0E+00	8922245	NT	Homo sapiens calcium channel alpha 1E subunit (CACNA1E) gene, exons 7-8, and partial cds, alternatively spliced
4943	17333		0.73	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4943	17333		0.73	1.0E+00	8922245	NT	Homo sapiens chromosome 21 segment RS21C047
5033	18095		0.91	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase II, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5354	18469	31328	3.23	1.0E+00	Z97022.1	NT	Hordium vulgare gene encoding catalase proteinase
5949	19035	32228	5.05	1.0E+00	AF248054.1	NT	Bot taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5949	19035	32229	5.05	1.0E+00	AF248054.1	NT	Bot taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6067	19148	32360	1.44	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA 1 PCA contig fragment No. 5
6238	19309	32541	4.52	1.0E+00	P04501	SWISSPROT	FIBRINOLYTIC
8243	18016	32546	1.71	1.0E+00	AW452782.1	EST_HUMAN	U1-HB3-8x-400-U1.1 NC, CGA2, SUG2 Homo sapiens cDNA clone IMAGE:3088089 3'
6637	16695	32972	2.12	1.0E+00	U79502.1	NT	Mus musculus subunit-like serine protease LPS (CPS) gene, exons 1 to 9, partial cds
6691	19748	33025	0.68	1.0E+00	AF104069.1	NT	Homo sapiens cell cycle protein (CYCLIN) gene, exons 2 through 3
6760	19841		0.68	1.0E+00	P46506	SWISSPROT	SNB-1 (P46506) NC, UGC 7 Homo sapiens cDNA clone IMAGE:335352 5'
6873	19887	33155	0.71	1.0E+00	BE797718.1	EST_HUMAN	80133 (BE797718) NC, UGC 7 Homo sapiens cDNA clone IMAGE:335352 5'
6873	19887	33156	0.71	1.0E+00	BE797718.1	EST_HUMAN	80133 (BE797718) NC, UGC 7 Homo sapiens cDNA clone IMAGE:335352 5'
6944	20168	33491	1.17	1.0E+00	Y12541.1	NT	Human proteinase 3, partial cds
7033	18365	31282	0.84	1.0E+00	U63721.1	NT	Human elastin (ELN) gene, partial cds, and LMW-kinesin (LMK1) gene, complete cds
7345	20316	33681	1	1.0E+00	S62770.1	NT	Insulin-like growth factor-binding protein 4 (IGFBP4) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (B-LCAM)
7719	20576		8.7	1.0E+00	P20773	SWISSPROT	B-C-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE)
7719	20576	34339	1.52	1.0E+00	AF162851.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7719	20576	34340	1.52	1.0E+00	AF162851.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
8165	21103		6.07	1.0E+00	AA775193.1	EST_HUMAN	80176208.1 (Stratagene) Lung (8017210) Homo sapiens cDNA clone IMAGE:808791 3'
8165	21103	34630	0.67	1.0E+00	BF070231.1	EST_HUMAN	802183762.1 NIH, MGCC, B3 Homo sapiens cDNA clone IMAGE:429427 5'
8204	21263	34673	1.48	1.0E+00	BE688267.1	EST_HUMAN	80144950.1 NIH, MGCC, B5 Homo sapiens cDNA clone IMAGE:394805 5'
8204	21263	34674	1.48	1.0E+00	BE688267.1	EST_HUMAN	80144950.1 NIH, MGCC, B5 Homo sapiens cDNA clone IMAGE:394805 5'
8461	18685		1.22	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for R-acylglycerol transferase III, complete cds
8693	21981	35094	2.31	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDROLYTIC-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MIF) [INCLUDES: 2-ENOYL-COA HYDRA TASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8693	21981	35095	2.31	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDROLYTIC-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MIF) [INCLUDES: 2-ENOYL-COA HYDRA TASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8821	21788		0.83	1.0E+00	P61784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBQUITIN THIOLESTERASE 11) (UBQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBQUITINATING ENZYME 11)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5969	10094	32234	0.78	9.8E-01	Q09832	SWISSPROT	PROBABILE OXIDOREDUCTASE ZK1290.3 IN CHROMOSOME 11
9616	25590		1.4	9.8E-01	U65697.1	NT	Lyso-papain (acidic) putative M1T copy 1 metalloprotease gene
9013	22734		3.02	9.8E-01	Q28942	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
11099	24032	37366	1.48	9.8E-01	AJ005026.1	NT	Dinlo retro mRNA for Eph-like receptor tyrosine kinase nk6
524	13695	26813	1.12	9.8E-01	P22667	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2305	15317		1.28	9.8E-01	AJ003106.1	NT	Caillietin locus UBE1 gene derived retrocopy on the Y chromosome
2813	15505		1.28	9.8E-01	AF174644.1	NT	Xenopus laevis rbc GTPase mRNA, complete cds
7405	20374	33726	4.12	9.8E-01	AJ302156.1	NT	Enterobacteriaceae sp. J0883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate J0883
7406	20374	33726	4.12	9.8E-01	AJ302156.1	NT	Enterobacteriaceae sp. J0883 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate J0883
7807	20350	34235	0.98	9.8E-01	BF334763.1	EST_HUMAN	801468337F11N1.YGCC.98 Homo sapiens cDNA clone IMAGE:3660048 5'
7807	20350	34237	0.98	9.8E-01	BF334763.1	EST_HUMAN	801468337F11N1.YGCC.98 Homo sapiens cDNA clone IMAGE:3660048 5'
10094	22535	35156	0.88	9.8E-01	P38832	SWISSPROT	PHOSPHOGLUCOSE (GLUCOSE PHOSPHOMUTASE) (P-GM)
10094	22535	35156	0.88	9.8E-01	P38832	SWISSPROT	PHOSPHOGLUCOSE (GLUCOSE PHOSPHOMUTASE) (P-GM)
11336	24255	37813	0.95	9.8E-01	U62555.1	EST_HUMAN	801102861F11N1.YGCC.98 Homo sapiens cDNA clone IMAGE:3571847 3'
11336	24255	37813	0.95	9.8E-01	U62555.1	EST_HUMAN	801102861F11N1.YGCC.98 Homo sapiens cDNA clone IMAGE:3571847 3'
11336	24259	37814	2.06	9.8E-01	BE536705.1	EST_HUMAN	801102861F11N1.YGCC.98 Homo sapiens cDNA clone IMAGE:3559730 5'
							Homo sapiens X28 gene, a putative ALU element containing dual specificity tyrosine phosphatase 9 (DUSP9), fibronectin protein 1 like (FBLN1), Cdc42-binding protein kinase 1 (CBK1), creatine transporter (CTR1), CDM protein (CDM), adrenocorticotrophic protein 3
12545	25298		1.41	9.8E-01	U92111.2	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9, 10, 11, 12 and optional segments b, c, d and e, partial cds
7396	20336	33665	2.3	9.7E-01	U26716.1	NT	Trilium asiaticum stipe root resistance protein Y10 (Y10) gene, complete cds
8648	21815	35255	1.81	9.7E-01	AF149112.1	NT	Salmonella typhimurium adenosine-methyltransferase (moa) and restriction endonuclease (moa)
8654	21821	35241	1.33	9.7E-01	M60544.1	NT	UHH-BJ44-97-2-J1 at NCI QCAP S483 Homo sapiens cDNA clone IMAGE:3085140 3'
11505	24427		3.97	9.7E-01	BF511205.1	EST_HUMAN	Dichobalium discoloratum CARR3 gene, promoter region
12117	24067	38360	2.26	9.7E-01	U87514.1	NT	PM2JUM0035-240305-005-412 U00033 Homo sapiens cDNA
44895	17511	31065	1.98	9.6E-01	AV1769674.1	EST_HUMAN	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA
8749	18168		0.9	9.6E-01	Z70356.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2684
8647	18937	32121	3.85	9.6E-01	Z70356.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2684
8910	19662	33268	0.57	9.6E-01	Z07341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
8735	21703		1.21	9.6E-01	X58275.1	NT	P. fluorescens complete gene map of plasmid-like DNA (pF4)
9203	22109	35660	0.51	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps27 gene, complete cds

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9446	22410	35847	0.44	0.6E-01	AF228343.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cyclic filicase transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
11848	24731	38317	3.04	0.6E-01	AF175205.1	EST_HUMAN	AF175205 NP2 Homo sapiens cDNA clone NP204366 5'
11848	24731	38318	3.04	0.6E-01	AF175205.1	EST_HUMAN	Homo sapiens centromere protein 2 (CEP2) mRNA
12223	25090		2.19	0.6E-01	11421722	NT	Sphingomyelinase 2 (SMPD2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
12839	25874	31416	3.03	0.6E-01	U91423.1	NT	Homo sapiens C12orf136 protein (LOC51003) mRNA
2484	15488	26512	1.03	0.5E-01	7705891	NT	901618031 NH, MGC, 21 Homo sapiens cDNA clone IMAGE:358473 5'
3796	16836	20741	2.39	0.5E-01	BE022440.1	EST_HUMAN	347690301 NH, MGC, 21 Homo sapiens cDNA clone IMAGE:358473 5'
3796	16836	20742	2.39	0.5E-01	BE022440.1	EST_HUMAN	347690301 NH, MGC, 21 Homo sapiens cDNA clone IMAGE:358473 5'
6834	22919	35748	0.88	0.5E-01	AF119102.1	EST_HUMAN	RC1-CTD285-241198-011-B22 C10288 Homo sapiens cDNA
9481	22428	35853	1.1	0.5E-01	AF1081102.1	EST_HUMAN	RC1-CTD285-241198-011-B22 C10288 Homo sapiens cDNA
11574	24512	36059	1.15	0.5E-01	BE216717.1	EST_HUMAN	RC1-CTD285-241198-011-B22 C10288 Homo sapiens cDNA
11780	25835	37456	1.32	0.5E-01	AF156200.1	EST_HUMAN	UHL-B12-4492-03-031-11 NCI, GAP, 57 Homo sapiens cDNA clone IMAGE:272167 3'
3274	16269		3.77	0.5E-01	AF156200.1	NT	Actinella clathrinase RNA polymerase beta subunit (rpb3) gene, partial cds
3281	16269		3.77	0.5E-01	AF156200.1	NT	Actinella clathrinase RNA polymerase beta subunit (rpb3) gene, partial cds
3281	16269		3.77	0.5E-01	AF156200.1	NT	Actinella clathrinase RNA polymerase beta subunit (rpb3) gene, partial cds
8217	22183	35616	0.88	0.5E-01	BE07241.1	NT	Human F-2-gamma-receptor (FCGR2A) gene, exon 4
12490	25235		2.89	0.5E-01	BE781251.1	EST_HUMAN	Human F-2-gamma-receptor (FCGR2A) gene, exon 4
12838	26790		1.89	0.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (erbb3) oncogene homolog (EGFR) mRNA
1745	27976		1.34	0.5E-01	AF242882.1	NT	Homo sapiens phytoerythrin-Cdk hydroxylase (PHH) gene, exon 5
2041	15835	28983	1.01	0.5E-01	BE071172.1	EST_HUMAN	RC5-B10503-271198-011-B01 B10503 Homo sapiens cDNA
17102	20903		0.82	0.5E-01	N20216.1	NT	Scirpus pallidus virus type 2, complete genome
4058	17102	26924	0.82	0.5E-01	N20216.1	NT	Scirpus pallidus virus type 2, complete genome
5073	19768	31040	1.47	0.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5761	18854	33034	3.92	0.3E-01	J36185.1	NT	Spodoptera frugiperda methyltransferase/hydroxylase dehydrogenase mRNA, complete cds
7554	20517		0.76	0.3E-01	AF270548.1	NT	Plasmodium falciparum mature parasite-inferred erythrocyte surface antigen (MESA) gene, complete cds
8402	21371	34779	1.75	0.3E-01	AA874040.1	EST_HUMAN	ca06905.s1 NCI, GAP, 57 Homo sapiens cDNA clone IMAGE:1383357
9165	22131		0.95	0.3E-01	AF081881.1	NT	Xenopus laevis COCH zinc finger protein C3H2 (C3H2) mRNA, complete cds
9269	22265	35855	0.91	0.3E-01	AF191834.2	NT	Krabapple Italian DNA chromosome 1, contig fragment 16.34
12503	25028	31713	1.34	0.3E-01	11440286	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (100) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12645	25534		3.29	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein PL34 mRNA, complete cds
13033	18037	20231	3.14	9.2E-01	BEG22702.1	EST_HUMAN	6014419381 NIH_MGC_72 Homo sapiens cDNA, clone IMAGE:381614.3
9908	18896		1.73	9.2E-01	7105410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6101	19180	32360	4.04	9.2E-01	BF037866.1	EST_HUMAN	6014611531 NIH_MGC_68 Homo sapiens cDNA, clone IMAGE:3804461.5
6789	19843	33127	0.51	9.2E-01	U68703.1	NT	N crassa vspH-RNA synthase (vsh-20um-3) gene
10018	22945	36412	0.77	9.2E-01	AL161860.2	NT	Arabidopsis thaliana RNA, chromosome 4, contig fragment No. 85
10105	20031	36509	1.21	9.2E-01	6871677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
19528	23550	37050	3.42	9.2E-01	11439685	NT	Homo sapiens lysosomal aspartase-like protein 1 (LAP-1), mRNA
10780	29701	37180	1.84	9.2E-01	BF930351.1	EST_HUMAN	7686603.ct NOI_GGAP_XG81 Homo sapiens cDNA, clone IMAGE:378219.3 similar to SW:NU561_TRYBB
12031	28407	38501	1.34	9.2E-01	BF132402.1	EST_HUMAN	P45490 TM6H-UBIQUITONE DIOXIDOREDUCTASE CHAIN 3
1629	14882	27638	2.31	9.1E-01	766781.1	EST_HUMAN	59162012121 NIH_MGC_58 Homo sapiens cDNA, clone IMAGE:4052018.5
2134	15151		2.06	9.1E-01	6622036	NT	Y65201.1 St. Soraes testis liver spliced 1N1F3 Homo sapiens cDNA, clone IMAGE:121389.3 similar to contains
2362	15583	28602	1.12	9.1E-01	AF032919.1	NT	HLA sequence element
3216	18273	29165	1.11	9.1E-01	726418.1	EST_HUMAN	Phasmodonts fluorescent DNA polymerase II (cmse) gene, complete cds
3216	18273	29166	1.11	9.1E-01	726418.1	EST_HUMAN	AB2003695 Infanti brain L1.N1L array of Dr. M. Soares 1N1B Homo sapiens cDNA, clone LLAB20036.5
8321	19943	33602	1.69	9.1E-01	U36033.1	NT	AB2003695 Infanti brain L1.N1L array of Dr. M. Soares 1N1B Homo sapiens cDNA, clone LLAB20036.5
6556	10712	32660	2.94	9.1E-01	U65704	SWISSPROT	Human cdk2 cell stimulating factor homologous (SDFH) mRNA, complete cds
7527	20778	34152	18.4	9.1E-01	AA809523.1	EST_HUMAN	INTERALPHA-1RY25IN INHIBITOR HEAVY CHAIN3 PRECURSOR (IT1HEAVY CHAIN H3)
8011	20849	34442	2.58	9.1E-01	U72665.1	NT	cd51 IgG3 at NOI_GGAP_G031 Homo sapiens cDNA, clone IMAGE:1335882.3
10538	22438	36955	0.45	9.1E-01	P28432	SWISSPROT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
12598	23667		10.31	9.1E-01	AF550113.1	NT	P80.CO1LIN
4406	17434	30319	1.77	9.0E-01	AF006910.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
7622	20582	33948	0.55	9.0E-01	U42547.1	NT	Homo sapiens nuclear 11-alpha gene, partial cds
7652	20612		1.32	9.0E-01	U36821.1	NT	Danio rerio L1 class homeodomain protein (lmo) mRNA, complete cds
9704	22657	35112	0.55	9.0E-01	AF080761.1	NT	Xenopus laevis gene for aldolase, complete cds
10189	23114	38508	0.44	9.0E-01	U39702.1	NT	Danio rerio semaphorin 2 is mRNA, complete cds
							Myoplasma genitalium section 24 of the complete genomes
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1
							(PUT1) gene, partial cds; mitotic-specific chromosome segregation protein SMO1 homolog (SMO1) gene, complete cds; and calcium channel alpha-1 subunit
9781	18873	32054	2.37	8.9E-01	AF021081.1	NT	Rabbit MHC fragment RLA-DF DNA
8377	19418		1.28	8.9E-01	X00906.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Human Ref BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3913	19683	29760	1.38	8.9E-01	U46724.1	NT	Drocephila melanogaster met in (Dmefin) mRNA, complete cds
5007	18276	31091	2.6	8.9E-01	BE47509.1	EST_HUMAN	RC1H10229-160300.019-05 H10229 Homo sapiens cDNA
8001	18084	32263	7.79	8.9E-01	X00547.1	NT	Chicken lipoprotein lipase gene
8001	18084	32264	7.79	8.9E-01	X00547.1	NT	Chicken lipoprotein lipase gene
8515	26661	32835	0.94	8.9E-01	S78772.1	NT	polyprotein (Coxsackie B4 virus GB4, hostemia, E2, originally derived from Edwards GB4 human strain, Genome RNA, Complete, 7397 nt)
8597	19920	33275	1.7	8.9E-01	AF143732.1	NT	Cratichneumon recombination activating protein 1 (RAG-1) gene, partial cds
8597	19920	33276	1.7	8.9E-01	AF143732.1	NT	Cratichneumon recombination activating protein 1 (RAG-1) gene, partial cds
7770	20723	33216	0.81	8.9E-01	AF030991.1	NT	Brachycephalus pinnatus 28S rDNA, sequence 1 of 131 of the complete genome
8230	21228	34767	1.29	8.9E-01	U011816.1	NT	Brachycephalus pinnatus 28S rDNA, sequence 2 of 131 of the complete genome
8274	21346	34767	1.29	8.9E-01	U011816.1	NT	Brachycephalus pinnatus 28S rDNA, sequence 2 of 131 of the complete genome
10715	20637	37120	1.35	8.9E-01	AB000796.1	NT	Arabis holboellii 28S rDNA, sequence 1 of 172 of the complete genome
12038	26377	37130	1.44	8.9E-01	AL112832.1	NT	Archaeoglobus fulgidus, sequence 128 of 172 of the complete genome
6839	18940	33235	1.5	8.9E-01	AF143732.1	NT	Brachycephalus pinnatus 28S rDNA, sequence 1 of 131 of the complete genome
7598	20721	34093	2.49	8.9E-01	BE47509.1	EST_HUMAN	RC1H10229-160300.019-05 H10229 Homo sapiens cDNA, contig IMAGE3463505.5
8323	21282	34760	0.42	8.9E-01	AL161722.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 88
8761	21278	35151	0.93	8.9E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8761	21278	35151	0.93	8.9E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8848	21816	35268	0.57	8.9E-01	AL243213.1	NT	Homo sapiens partial E-H14 receptor gene, exons 2 to 5
10715	20637	37120	1.35	8.9E-01	AB000796.1	NT	Cyanidium caldarium gene for SsgC, complete cds
10715	20637	37130	1.35	8.9E-01	AB000796.1	NT	Cyanidium caldarium gene for SsgC, complete cds
12655	26869	37130	2.25	8.9E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVBP1), mRNA
12572	25283	36993	1.37	8.9E-01	5907009	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4762	17802	30893	0.85	8.9E-01	AF039715.2	NT	Fowl adenovirus 8, complete genome
5571	22641	31627	2.68	8.9E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5571	22641	31628	2.68	8.9E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
8107	21044	34443	0.51	8.9E-01	AF051142.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
10317	23241	34443	0.51	8.9E-01	AF051142.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
12005	24882	33478	1.54	8.9E-01	AL224837.1	NT	Pyrococcus abyssi complete genome, segment 6/8
7413	19304	26749	3.01	8.9E-01	NR0437.1	NT	Human collagenase type IV (CLG4) gene, exon 4
3111	19188	29078	3.15	8.9E-01	AL161065.2	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3823	19963	29767	0.83	8.9E-01	AB010879.1	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 18
4040	17078	29778	0.83	8.9E-01	AB010879.1	NT	Nicotiana glauca mRNA for chloroplast ribosomal protein L10, complete cds
5341	18446	31160	2.42	8.9E-01	AL161540.2	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5341	18446	31160	2.42	8.9E-01	AL161540.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 40

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3472	16518	29440	3.97	8.1E-01	AF050086.1	NT	Homo sapiens MHC class I region
5792	19884	32066	0.51	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSHR) (MELANOTROPIN RECEPTOR)
6448	19513	32763	0.84	8.1E-01	U10760.1	NT	(MELANOCORTIN-1) RECEPTOR (MCH-R)
8777	19832	33114	2.47	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2(X) chain (COL12A2) gene, partial cds
8777	19832	33116	2.47	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN MB-9
7185	20708	34077	0.95	8.1E-01	Q04777	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN MB-9
							CYTOSOLIC PROTEIN B
8243	21212	34618	1.12	8.1E-01	AF22713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico) gene, partial cds; putative sodium channel (Nuch) and putative amylose-related protein (Amyrel) genes, complete cds, and putative serine-enriched protein (Spre) gene, partial cds
8243	21212	34618	1.12	8.1E-01	AF22713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico) gene, partial cds; putative sodium channel (Nuch) and putative amylose-related protein (Amyrel) genes, complete cds, and putative serine-enriched protein (Spre) gene, partial cds
8938	21822	35210	0.81	8.1E-01	AF001317.1	NT	Bacillus halodurans genomic DNA, section 1114
8938	21822	35250	0.81	8.1E-01	AF001317.1	NT	Bacillus halodurans genomic DNA, section 1114
							2001063.1 NC_003971 Homo sapiens cDNA clone IMAGE289248 3' similar to SW1LYAR, MOUSE
9122	22068	33518	1.13	8.1E-01	AF242647.1	EST_HUMAN	MDM288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, (MDM2) b7a 3 subunit
10484	22408	38002	0.84	8.1E-01	P08426	SWISSPROT	PROBABLE E4 PROTEIN
10778	22907	37106	0.42	8.1E-01	N84541.1	EST_HUMAN	KG97272 Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K19872 5' similar to EST(GLOE COPE1)
11812	24897	38277	4.05	8.1E-01	BE028558.1	EST_HUMAN	RC3-10086-220000-026-r10 TN0080 Homo sapiens cDNA
11812	24897	38277	4.05	8.1E-01	BE028558.1	EST_HUMAN	RC3-10086-220000-026-r10 TN0080 Homo sapiens cDNA
12288	25109	31639	1.73	8.1E-01	AE001711.1	NT	Thermoplasma maritima section 23 of 138 of the complete genome
178	13279	26210	3.32	8.0E-01	AJ271670.1	NT	Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15
288	13383	26210	6.97	8.0E-01	AJ132772.1	NT	Bos taurus full and full genes
2051	15070	26085	1.72	8.0E-01	BF530962.1	EST_HUMAN	60207247941 NC_003971 Homo sapiens cDNA clone IMAGE4210691 5'
3093	18151	26260	1.41	8.0E-01	AF000193.1	NT	Samit bovine insulin receptor (SBO27) gene, partial cds
3324	18375	26260	2.38	8.0E-01	AF127697.1	NT	Mus musculus gene for cytoskeletal glycoprotein, complete cds
4563	17588	30479	6.45	8.0E-01	AF127697.1	NT	Neisseria meningitidis serogroup A strain 22961 complete genome, segment 777
8322	21291		2.31	8.0E-01	AF127697.1	NT	G. gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
8870	21837	35259	1.05	8.0E-01	Y11095.1	EST_HUMAN	RC3-10086-220000-021-H05 NN1012 Homo sapiens cDNA
11303	24253	37779	1.58	8.0E-01	Q02763	SWISSPROT	Rice stripe virus RNA 3
							CREB-BINDING PROTEIN

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Probe SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
454 13327	26457	0.76	7.6E-01	D11476.1	NT	Lymnatic dipter nuclear polyhedrosis virus gene for DNA polymerase, complete cds
716 13778		0.76	7.6E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 98 of the complete genome
1002 14641		23.05	7.6E-01	AB040985.1	NT	Homo sapiens mRNA for KIAA1463 protein, partial cds
1063 14695		1.28	7.6E-01	U32789.1	NT	Hemophilus influenzae Rd section 54 of 183 of the complete genome
2272 15285	28311	7.35	7.6E-01	AB004916.1	NT	Oryzidactylus curticulus mRNA for mitogunin29, complete cds
2273 15286	28312	2.35	7.6E-01	AF110449.1	NT	Danio rerio Tpa-associated protein 1 (Tpa) mRNA, complete cds
3526 16574	22487	3	7.6E-01	AF228694.1	NT	Galus repto SOX2 transcription factor (SOX2) mRNA, complete cds
4330 17358		0.84	7.6E-01	BE263912.1	EST_HUMAN	60116203ST NIH XGC-7 Homo sapiens cDNA clone IMAGE335785 5'
4642 17693	30551	1.15	7.6E-01	67537459	NT	Mus musculus enigma (Enig), mRNA
4642 17693	30552	1.15	7.6E-01	67537459	NT	Mus musculus enigma (Enig), mRNA
5244 18252	31123	1.03	7.6E-01	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative activin-like protein and cyclic fibrinogen transmembrane conductor-regulated (COTR) gene, section 1 of 2 of the complete cds, and unknown gene
6479 19544	32792	0.76	7.6E-01	U39746.1	NT	Human HMG CoA synthase, complete cds
8446 21415	34828	3.37	7.6E-01	X00096.1	NT	Human HMG CoA synthase, complete cds
6905 22857	35519	4.3	7.6E-01	U01912.1	NT	Human HMG CoA synthase, complete cds
10409 23331	35516	4.3	7.6E-01	P16719	SWISSPROT	Small hydrophobic protein
10451 23373	35564	0.82	7.6E-01	AF100660.1	EST_HUMAN	AV700890 SKC Homo sapiens cDNA clone SKCORE12 3'
10977 27797	37298	0.82	7.6E-01	AB000931.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keelo-L-thiamine reductase, complete cds
11350 28330		2.61	7.6E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11546 28487	36441	2.62	7.6E-01	P19222	SWISSPROT	NEURAL CADHERIN PRECURSOR (N-CADHERIN)
877 13832		0.76	7.6E-01	U33765.1	EST_HUMAN	HSC1K1041 normalized infant brain cDNA Homo sapiens cDNA clone c-1404
2263 15286	28320	0.35	7.6E-01	AF095667.1	EST_HUMAN	ES1371637 MAGI, resequenced, MAGI Homo sapiens cDNA
4730 17750	30442	1.35	7.6E-01	U97035.1	NT	Rattus norvegicus transmembrane receptor Unc5c1 mRNA, complete cds
5075 18365		0.8	7.6E-01	AF175333.1	EST_HUMAN	RC3-012524-130100-022-c02 012524 Homo sapiens cDNA
6167 19252	33468	2.5	7.6E-01	AF115856.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds
6344 19419	32655	1.04	7.6E-01	P05231	SWISSPROT	INTERLEUKIN-3 PRECURSOR (IL-3) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYPER-DOXA GROWTH FACTOR)
8603 19554	32619	0.72	7.6E-01	AF045066.1	NT	Thermoplasma acidophilum complete genome, segment 4/6
8635 21803	35221	1.29	7.6E-01	BF106527.1	EST_HUMAN	7B4005.x1 Soares, NSF, FG, BW, OT, PA, 3' ST Homo sapiens cDNA clone IMAGE525176 3'
5166 22511	36002	1.34	7.6E-01	Y10156.1	NT	D. discoideum rncAq gene
5687 22840	36097	0.52	7.6E-01	4828873	NT	Homo sapiens nucleoporin 214 kD (NUP214), mRNA
10183 23405		1.01	7.6E-01	U328452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MCL-ALPHA1)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12589	25948		2.32	7.8E-01	U26260.1	NT	Arabidopsis thaliana 1-aminocyclopropylcarboxylate synthase (ACS5) gene, complete cds
145	13248	26177	6.69	7.7E-01	AF184948.1	NT	Lyoprotein hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
							Mus musculus major histocompatibility locus class II region, major histocompatibility protein class II alpha chain (Malpha) and major histocompatibility protein class II beta chain (Ebeta) genes, complete cds; butyrophilin-like (NGB), butyrophilins
727	13788		3.26	7.7E-01	AF590167.1	NT	CITRATE SYNTHASE
2724	19718	28736	2	7.7E-01	Q33915	SWISSPROT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetyl-galactosaminyltransferase 7 (GALNAcT-7) (GALNAcT-7) mRNA, complete cds
3369	16418		0.78	7.7E-01	8392403	NT	Homo sapiens PRO1975 mRNA, complete cds
3854	19638	29576	3.03	7.7E-01	AF118938.1	NT	Gallus gallus japonica sub-species japonica beta-actin mRNA, partial cds
4425	17452	30243	3.84	7.7E-01	AF190488.1	NT	Caenorhabditis elegans beta-actin mRNA, partial cds
4435	17452	30243	3.84	7.7E-01	AF190488.1	NT	Caenorhabditis elegans beta-actin mRNA, partial cds
5640	19736	31669	1.25	7.7E-01	P18533	SWISSPROT	RAPIFOSF INTERASE (INTERASE)
5640	19736	31669	1.25	7.7E-01	P18533	SWISSPROT	RAPIFOSF INTERASE (INTERASE)
8065	19147	32359	0.83	7.7E-01	R08900.1	EST_HUMAN	X24692 at Sscas (see last column) TMS1 Homo sapiens cDNA, clone IMAGE:127163.9
10204	23129	36516	0.72	7.7E-01	AB02134.1	NT	Daphnia magna hemoglobin gene cluster (Hb3, Hb1 and Hb2 genes), complete cds
12447	22927		5.53	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
8218	19292	33225	4.49	7.6E-01	AF055910.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
8218	19292	33225	4.49	7.6E-01	AF055910.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
9917	19724	32969	0.65	7.6E-01	P37938	SWISSPROT	MA TINC-TYPE PROTEIN N-ALPHA_24
7029	19351	31248	0.98	7.6E-01	A233399.1	EST_HUMAN	sq14512.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA, clone IMAGE:2030976
7029	19351	31282	0.88	7.6E-01	A233399.1	EST_HUMAN	sq14512.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA, clone IMAGE:2030976
7252	19987	33295	0.89	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-lactalbumin receptor mRNA, complete cds
5400	21069	34779	1.33	7.6E-01	AF146793.2	NT	Mus musculus neomycin U precursor (NmU) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and HBAR (Hbar) gene, complete cds
8464	21433	34849	1.92	7.6E-01	885752	NT	Mus musculus actinin (Actin-pending), mRNA
8464	21433	34850	1.92	7.6E-01	885752	NT	Mus musculus actinin (Actin-pending), mRNA
8668	21336	36036	0.43	7.6E-01	Q01068	SWISSPROT	GLUTAMATE (NM2A) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 3C) (NR2C) (NM2A2C)
8668	21336	36036	0.43	7.6E-01	Q01068	SWISSPROT	GLUTAMATE (NM2A) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 3C) (NR2C) (NM2A2C)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) H BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9318	22283	35714	1.01	7.8E-01	6783577	NT	Mac-1-related G-proteins P430_20a, phosphatidyl inositol, type a (Cp230a), mRNA
9834	22578	35028	5.25	7.8E-01	P03372	SWISSPROT	MUSCULINUS CISTYCHOLINE RECEPTOR M2
9834	22578	35029	5.25	7.8E-01	P03372	SWISSPROT	MUSCULINUS CISTYCHOLINE RECEPTOR M2
11685	24651	38220	2.09	7.8E-01	P03372	NT	H1 sapiens mRNA for overexpression IN70
11685	24651	38220	2.09	7.8E-01	P03372	NT	H1 sapiens mRNA for overexpression IN70
12020	24697	38230	3.05	7.8E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	25046	38230	3.8	7.8E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0855 protein, partial cds
514	13585		1.57	7.3E-01	AF163307.2	NT	Homo sapiens chromosome 21 segment HS21C01
585	13854	26588	1.01	7.8E-01	AF020503.1	NT	Homo sapiens FRAB3 common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7764	20717	34780	0.78	7.8E-01	AF020703.1	NT	Drosophila melanogaster Kriblin kinase receptor protein (eph) mRNA, complete cds
12515	25247		4.45	7.8E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
13027	25575	31697	1.57	7.8E-01	AE00823.1	NT	Methanobacterium thermophilum from basins 317950 to 328792 (section 29 of 148) of the complete genome
1132	14175	27124	1.35	7.4E-01	AF08146.1	EST_HUMAN	h14005.x1 NC_023435 Homo sapiens cDNA clone IMAGE:2167577 3 similar to contains Alu repetitive element contains element MIR repetitive element
2380	13389	26581	0.93	7.4E-01	AF112338.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
3738	18781	25693	18.81	7.4E-01	AF112338.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
3919	19559	28972	2.01	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calculata-nRf-a (nRf-a) and Calculata-nRf-b (nRf-b) genes, complete cds
4340	17367	30260	0.99	7.4E-01	AF163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8178	21149	34553	1.04	7.4E-01	AF161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
8178	21149	34554	1.04	7.4E-01	AF161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
8880	21946	35370	0.78	7.4E-01	BF146036.1	EST_HUMAN	502018465F1 NC_023435 Homo sapiens cDNA clone IMAGE:4154340 5'
9063	22029		0.64	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, transcribed alternative untranslated exon
8462	22416	33584	7.09	7.4E-01	BE147603.1	EST_HUMAN	50179328F1 NH_MGC_9 Homo sapiens cDNA clone IMAGE:3584171.5
9511	22474	35919	1.14	7.4E-01	AA187666.1	EST_HUMAN	597970.1 a) Stragene adenoviral cell library clone IMAGE:425297 3' similar to SW17CQ3_MOUSE P43352 1-CD34 (CD34) cDNA, THE TA SUBMIT
10767	23988	37188	0.74	7.4E-01	11224933	NT	Homo sapiens NT-REN-45 antigen (LOC41133) mRNA
12171	25021		4.49	7.4E-01	6753277	NT	Homo sapiens NT-REN-45 antigen (LOC41133) mRNA
12284	25101		1.54	7.4E-01	AA172641.1	EST_HUMAN	112284.1 NT_023435 Homo sapiens cDNA clone IMAGE:2043883 3'
3999	17038		0.84	7.3E-01	AP000062.1	NT	Arabidopsis thaliana genomic DNA, section 87
4647	17688	30555	0.97	7.3E-01	AE031166.1	NT	Borrelia burgdorferi (section 12 of 70) of the complete genome

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Probe SEQ ID NO.	Exon SEQ ID NO.	OFF SEQ ID NO.	Exon Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4728	17749	30841	4.57	7.3E-01	AF228421.1	NT	Homo sapiens HT017 mRNA, complete cds
5135	18144	31024	1.18	7.3E-01	043103	SWISSPROT	PERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6781	18015	33094	6.03	7.3E-01	L38772.1	NT	Mus musculus antigen (CD72) gene
6781	18015	33095	6.03	7.3E-01	L38772.1	NT	Mus musculus antigen (CD72) gene
7301	25878	33908	0.92	7.3E-01	AJ011418.1	NT	Cycloperon esculentum mRNA for ubiquitin activating enzyme
7892	20660	34014	0.53	7.3E-01	Z14133.1	NT	D melanogaster: Cdc mRNA for clathrin heavy chain
7794	20748	34119	7.48	7.3E-01	U28511.1	NT	V alginolyticus sucrose (scsB) gene, complete cds
7794	20748	34120	7.48	7.3E-01	U28511.1	NT	V alginolyticus sucrose (scsB) gene, complete cds
8115	21032	34490	0.51	7.3E-01	U34831.1	NT	Mus musculus alpha1 integrin gene, exon 7
11759	24687	35267	3.11	7.3E-01	AA078015.1	EST_HUMAN	225008.01 Storaar, Wal, Jnr, Jansen, NF-13, S1 Homo sapiens cDNA clone IMAGE 437799 3
832	13089	35268	3.11	7.3E-01	AA078015.1	EST_HUMAN	225008.01 Storaar, Wal, Jnr, Jansen, NF-13, S1 Homo sapiens cDNA clone IMAGE 437799 3
1974	14935	27997	3.23	7.2E-01	X77400.1	NT	Rattus norvegicus insulin factor-2 kinase (IR-2B) mRNA, complete cds
2488	18472	28465	1.31	7.2E-01	AB003003.1	NT	Rattus norvegicus insulin factor-2 kinase (IR-2B) mRNA, complete cds
3030	16137	28465	1.47	7.2E-01	AF198100.1	NT	Rattus norvegicus insulin factor-2 kinase (IR-2B) mRNA, complete cds
3407	18513	20424	2.46	7.2E-01	AF095806.1	NT	Cardia intestinalis veratrin-specific surface protein (vspt47.4) gene, sps47-6/4-1 allele, complete cds
4833	17820	30714	2.69	7.2E-01	D90314.1	NT	Limonchordates gene for succinate phosphatase (EO 2.4.1.7)
5159	18168	31046	1.57	7.2E-01	AF198778.1	NT	Homo sapiens transcription factor GHM enhancer 3, JH41 protein, JH4 protein, T54 protein, JH40 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophycin genes, complete cds, and L-type calcium channel alpha
5159	18168	31047	1.57	7.2E-01	AF198778.1	NT	Homo sapiens transcription factor GHM enhancer 3, JH41 protein, JH4 protein, T54 protein, JH40 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophycin genes, complete cds, and L-type calcium channel alpha
7421	20398	33739	0.78	7.2E-01	U69833.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8797	21784	35189	1.34	7.2E-01	AF205051.1	NT	Cytoskeleton RING-finger binding protein mRNA, partial cds
8514	22279	37123	0.52	7.2E-01	AF143776.1	EST_HUMAN	AV74373 CS Homo sapiens cDNA clone CBMAFD06 5
10795	23627	37123	2.59	7.2E-01	BF970061.1	EST_HUMAN	60211837 PF NH2_MGC_56 Homo sapiens cDNA clone IMAGE 4270381 5
11091	24031	37574	3.38	7.2E-01	U68623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12523	19343	31281	1.43	7.2E-01	U02568.1	NT	Dichocaulis viviparus nematode polyprotein antigen precursor (DVA) mRNA, complete cds
12700	25340	31281	5.56	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 87
693	13755	29684	13.3	7.4E-01	D21070.1	NT	Rare cathepsin mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RA1), complete cds
3075	18132	29045	13.21	7.4E-01	AJ270777.1	NT	Homo sapiens partial TGF-beta gene for T-cell transcription factor-4, exons 15-18

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4238	17285	30161	3.29	7.1E-01	7305360	NT	Mus musculus dogapin (Dog), mRNA
4239	17285	30162	3.29	7.1E-01	7305360	NT	Mus musculus dogapin (Dog), mRNA
6059	19139	32350	1.55	7.1E-01	BF981034.1	EST_HUMAN	6021545871 NIH_XLOC_83 Homo sapiens cDNA clone IMAGE:626344 5'
6059	19139	32351	1.55	7.1E-01	BF981034.1	EST_HUMAN	6021545871 NIH_XLOC_83 Homo sapiens cDNA clone IMAGE:626344 5'
7137	20113	33428	0.62	7.1E-01	U36232.1	NT	Drosophila melanogaster 5'-untranslated region of the gene for the protein
8833	21801	34916	0.49	7.1E-01	U36232.1	EST_HUMAN	Y58860.91 Soares Cell line taken NY-13 Homo sapiens cDNA
9088	22054	35477	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-31 1587-3917256-11-409 5' 10287 Homo sapiens cDNA
9088	22054	35478	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-31 1587-3917256-11-409 5' 10287 Homo sapiens cDNA
10214	23139	36028	1.29	7.1E-01	BE694405.1	EST_HUMAN	6074683071 NIH_XLOC_70 Homo sapiens cDNA clone IMAGE:3569485 5'
10214	23139	36029	1.13	7.1E-01	U36261.1	NT	Human cell receptor gamma chain cDNA, 5' part
12499	25773	37226	2.34	7.1E-01	AA421462.1	EST_HUMAN	206011.11 Soares RNA for KIA0851 protein, partial cds
1233	14270	27226	1.13	7.0E-01	AB014814.1	NT	Homo sapiens cDNA clone IMAGE:289708 3' similar to
1233	14270	27226	1.13	7.0E-01	AB014814.1	NT	Homo sapiens cDNA clone IMAGE:289708 3' similar to
2455	15460	26482	1.09	7.0E-01	N62412.1	EST_HUMAN	192363.11 Soares multiple, subcloned, 2N8HNSP Homo sapiens cDNA clone IMAGE:289708 3' similar to
2455	15460	26483	1.09	7.0E-01	N62412.1	EST_HUMAN	192363.11 Soares multiple, subcloned, 2N8HNSP Homo sapiens cDNA clone IMAGE:289708 3' similar to
3098	18108	37043	2.11	7.0E-01	U36301.2	NT	coronin A1, repetitive element
6952	17433	37043	0.85	7.0E-01	AB01319.1	NT	Homo sapiens chromosome 21 segment H321C101
6952	17433	37043	0.85	7.0E-01	AB01319.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
9721	21869	37043	0.51	7.0E-01	AE000553.1	NT	Echthra cell K12/M1655 section 143 of 400 of the complete genome
9871	22624	38377	0.52	7.0E-01	U33985.1	NT	Coccardium aculeatum mannitol-specific phosphotransferase system (PTS) system, mUA, mIR, mIF, and mID genes, complete cds
9871	22624	38378	0.52	7.0E-01	U33985.1	NT	Coccardium aculeatum mannitol-specific phosphotransferase system (PTS) system, mUA, mIR, mIF, and mID genes, complete cds
11454	24397	37043	1.71	7.0E-01	AV783942.1	EST_HUMAN	AV783942 MDS Homo sapiens cDNA clone MDSCHED 5'
11454	24397	37043	1.71	7.0E-01	AV783942.1	EST_HUMAN	AV783942 MDS Homo sapiens cDNA clone MDSCHED 5'
13036	26811	31638	1.35	7.0E-01	6800462	NT	Bacteriophage N15 v10n, complete genome
971	14023	26979	12.59	6.9E-01	U69874.1	NT	Candida albicans squelone epoxide (CABERG1) gene, complete cds and translational regulator gene, partial cds
971	14023	26977	12.59	6.9E-01	U69874.1	NT	Candida albicans squelone epoxide (CABERG1) gene, complete cds and translational regulator gene, partial cds
1313	14349	27315	2.22	6.9E-01	AA593350.1	EST_HUMAN	m2860a1 NCI_CGAP_Gast1 Homo sapiens cDNA clone IMAGE:1065178 3'
3233	10298	29210	1.8	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 1 of 95 of the complete genome
5249	19257	31726	0.82	6.9E-01	AV1714502.1	EST_HUMAN	AV1714502 DOB Homo sapiens cDNA clone DBA1D12 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Single (Top) Ht BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8878	18687	32198	0.8	8.9E-01	AB035932.1	NT	Brachyotomus belcheri BNU33 mRNA for nothard edin, complete cds
8104	19193	32402	0.55	8.9E-01	Y18278.1	NT	Desaphie melanogaster mRNA for A-type anchor protein DNAPAP500, partial
8508	19570	32622	1.5	8.9E-01	BE26768.1	EST_HUMAN	08177/333F1 NT, MGC_17 Homo sapiens cDNA clone IMAGE352328 5'
8312	21281	34602	3.39	8.9E-01	AL191573.2	NT	Xanthopsylla trilineata DNA chromosome 4, contig fragment No. 99
8312	21281	34603	3.39	8.9E-01	AL191573.2	NT	Xanthopsylla trilineata DNA chromosome 4, contig fragment No. 99
8528	22486	34603	0.73	8.9E-01	AF118945.1	NT	Entomobrya cristallina cation transporting ATPase (tapase) gene, partial cds
10033	22890	35447	0.95	8.9E-01	AF120315.1	NT	Musa acuminata peptase (pase) 1 (PL1) mRNA, complete cds
10033	22890	35448	0.95	8.9E-01	AF120315.1	NT	Musa acuminata peptase (pase) 1 (PL1) mRNA, complete cds
11337	24536	38916	2.03	8.9E-01	AF03913.1	NT	Homo sapiens DNA gene, complete cds
11337	24536	38917	2.03	8.9E-01	AF03913.1	NT	Homo sapiens DNA gene, complete cds
12145	25796		3.91	8.9E-01	D89958	SWISSPROT	FORHEAD BOX PROTEIN (C2) FORHEAD-RELATED PROTEIN FKHL16 (MESENCHYMALE FORK HEAD PROTEIN1) (MHP-1) (MHP-1) TRANSCRIPTION FACTOR FKHL16
938	14011	26964	1.52	8.9E-01	AF017764.1	NT	Gardia intestinalis carboxamide lyase gene, complete cds
2632	15578		1.38	8.9E-01	D86917.1	NT	Synchoecia sp. POC863 complete genome. 2727_341863-357470
2840	14851	27827	1.5	6.8E-01	AA85475.1	EST_HUMAN	475643.1 Soares, arylsulfoxide, NASHA Homo sapiens cDNA clone IMAGE102256 3' similar to gp-X59411.1 mval ALCOHOL DEHYDROGENASE CLASS II P1 CHAIN (HUMAN);
4032	17623	30518	1.75	6.8E-01	J00762.1	NT	Rat (Rattus norvegicus) protein gene: exon II and flanks
5698	22923	39368	1.97	8.9E-01	AB037765.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11424	24398	37903	1.77	6.8E-01	AJ276975.1	NT	Slagonospora evansii bgl1 gene for beta-glucosidase, exons 1-4
11424	24398	37904	1.77	6.8E-01	AJ276975.1	NT	Slagonospora evansii bgl1 gene for beta-glucosidase, exons 1-4
11430	24393	37909	1.82	6.8E-01	AF038936.1	NT	Musa muscicola zinc finger protein (Peg3) mRNA, complete cds
11430	24393	37939	1.82	6.8E-01	AF038936.1	NT	Musa muscicola zinc finger protein (Peg3) mRNA, complete cds
11931	24812	38407	1.46	8.9E-01	AF110520.1	NT	Musa muscicola major histocompatibility complex region NG27, RPS28, RPS28, NADH oxidoreductase, NG22, RPS18 genes, complete cds, Sacm21 gene, partial>
11931	24812	38408	1.49	8.9E-01	AF110520.1	NT	Musa muscicola major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG22, RPS18 genes, complete cds, Sacm21 gene, partial>
298	13392	26520	25.45	8.7E-01	AF13864.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
336	13428	26550	28.03	8.7E-01	AF13864.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1927	14691		1.07	8.7E-01	MT1213.1	NT	Quail fast skeletal muscle troponin gene, complete cds

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar EST E Value	Top Hit Accession No.	Top Hit Source	Top Hit Descriptor
2157	15179	28192	1.79	6.7E-01	AA45184.1	EST_HUMAN	zx2p12.1 Source: cclaf1_fetus_N2b1P8_9w Homo sapiens cDNA clone IMAGE768310.3' similar to contains element TAT1 repetitive element.
2176	15966	28213	2.65	6.7E-01	AF189073.1	NT	Drosophila melanogaster HsRSC gene, complete cds; NUDMC isoform (Nimmo) gene, complete cds, alternatively spliced; isoform factor (Relief) gene, complete cds, alternatively spliced
3009	16097	29887	3.95	8.7E-01	6876580	NT	Utrn musculus Vwfut1.13ch3 androme protein (Wap) mRNA
4481	17593	30395	0.78	8.7E-01	X74421.1	NT	Sluc1a2 mRNA for glucose-6-phosphate dehydrogenase
5002	18018	30603	0.97	8.7E-01	AF079710.1	EST_HUMAN	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
5597	18893	31651	0.77	8.7E-01	J04835.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
5597	18893	31652	0.77	8.7E-01	J04835.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
6073	19154	32396	0.93	8.7E-01	AE07485.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
6456	19521	32771	1.28	8.7E-01	9635335	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
6456	19521	32772	1.28	8.7E-01	9635335	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
7537	20900	33771	4.57	8.7E-01	EV04968.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
7537	20900	33772	4.57	8.7E-01	EV04968.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
7953	20528	33884	0.93	8.7E-01	AE01485.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
10953	23425	37778	0.93	8.7E-01	AF04549.1	EST_HUMAN	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
11305	24250	37778	0.93	8.7E-01	AF04549.1	EST_HUMAN	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
11791	23842	37778	0.93	8.7E-01	AF04549.1	EST_HUMAN	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
11958	24411	38441	0.93	8.7E-01	AF04549.1	EST_HUMAN	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
2505	19312	29339	1.92	6.6E-01	AF076240.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
2711	19703	29721	1.4	6.6E-01	AF156038.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
3501	16546	29474	1.41	6.6E-01	4509830	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
3670	16713	29528	4.37	6.6E-01	V07595.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
4136	17169	31134	0.96	6.6E-01	U91328.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
5238	18266	31134	1.13	6.6E-01	AL161572.2	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
5282	18289	31150	0.95	6.6E-01	AF25002.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
5282	18289	31151	0.95	6.6E-01	AF25002.1	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
6466	19551	32778	0.93	6.6E-01	698057	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
6466	19551	32778	0.93	6.6E-01	AF090506.1	EST_HUMAN	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
7919	20960	34281	3.57	6.6E-01	AF074000.1	EST_HUMAN	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
8502	21878	35504	0.98	6.6E-01	AL163778.2	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'
10023	22590		1.56	6.6E-01	AL163778.2	NT	hsp90.2.1.1 NC_CGAP 2017 Homo sapiens cDNA clone IMAGE2574588.3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12746	25395	31768	1.76	8.EE-01	AE04382.1	NT	Vitro chondrase chromosome II, section 39 of 83 of the complete chromosome
6822	18884	32077	0.98	8.EE-01	U75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
624	13869	29007	0.98	8.EE-01	U75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3448	19493	29412	4.63	8.EE-01	AB04125.1	NT	Mus musculus gene for Tcd2, complete cds
4311	17340	30220	4.28	8.EE-01	A272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5102	18112	30984	3.71	8.EE-01	U2892.1	NT	Phaeosolus vulgaris ATPase gamma subunit mRNA, nuclear genes encoding mitochondrial protein, partial cds
5204	18213	31088	1.13	8.EE-01	Z70326.1	NT	H1 sapiens mRNA for immunoglobulin heavy chain variable region (IGL4L6, VH, 450DP-71)
5516	25640	31851	2.13	8.EE-01	P16480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWIN5F COMPLEX COMPONENT SNF5)
6802	18884	32077	0.98	8.EE-01	AL16349.2	NT	Homo sapiens chromosome 21 segment H821049
6807	19359	33234	1.24	8.EE-01	D85443.1	NT	Chicken mRNA for T134Ds melanosomal matrix protein, complete cds
7841	20785	34153	0.84	8.EE-01	D04753.1	NT	Wntless (y-related oncogene) gene (each 1) transcribed selectively in pre-B lymphocytes
7830	20813	34223	0.89	8.EE-01	U19382.1	EST_HUMAN	Wntless (y-related oncogene) gene (each 1) transcribed selectively in pre-B lymphocytes
10707	23722	37111	1.03	8.EE-01	T8904.1	EST_HUMAN	M23002.1 (3' untranslated region) NPL3 home sapiens cDNA clone IMAGE:108847.3
10859	23621	37111	2.2	8.EE-01	AF11679.1	NT	Mus musculus small GTP-binding protein G425 (G425) gene, complete cds
10907	20953	37487	2.19	8.EE-01	H97553.1	EST_HUMAN	Wntless (y-related oncogene) gene (each 1) transcribed selectively in pre-B lymphocytes
11045	24009	37535	2.86	8.EE-01	AA001287.1	EST_HUMAN	no1607.61 NCL CGAP Photo Homo sapiens cDNA clone IMAGE:3179740.3
11143	24163		3.43	8.EE-01	AF136078.1	EST_HUMAN	AL136078 P.LAGE1 Homo sapiens cDNA clone IMAGE:100748.3
11925	24806	38380	2.3	8.EE-01	AF014115.1	NT	Phaeosolus vulgaris cytochrome c oxidase subunit II, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
11970	24846	38445	1.47	8.EE-01	AF140837.1	NT	Fugu nup160 L2 small nuclear ribonucleoprotein auxiliary factor subunit-related protein (L2A-F1-352), 19 kDa GAG adaptor protein adaptor (AP19), and phosphotyrosine kinase alpha 2 subunit (PHK42) genes, complete cds; leish protein (KELCH1) and leish p2
12130	24999	38604	1.61	8.EE-01	AF161590.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 76
12554	25276		2.65	8.EE-01	BE465050.1	EST_HUMAN	h74101 NCL CGAP L204 Homo sapiens cDNA clone IMAGE:3179740.3
252	13349	26776	10.51	8.EE-01	U48948.1	NT	Oreochromis melanogaster Bcl-2 protein, light chain mRNA, complete cds
3470	16516	26437	3.26	8.EE-01	U48948.1	NT	Mus musculus dyx11 (DAG1) gene, exons 1 and 2 and complete cds
3975	18914	26623	1.34	8.EE-01	AB016827.1	NT	Homo sapiens mRNA for KIAA1807 protein, partial cds
4519	17544	30430	0.69	8.EE-01	U12486.1	NT	M.musculus win gene
4519	17544	30431	0.69	8.EE-01	U12486.1	NT	M.musculus win gene
5192	16201	31073	1.71	8.EE-01	H85837.1	EST_HUMAN	ypb06c11 Scores refine N2654R Homo sapiens cDNA clone IMAGE:222066.5
8800	21629	39353	1.57	8.EE-01	AE001247.1	NT	Trepone pallidum section 83 of 87 of the complete genome

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Exon Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10448	23371	38583	6.94	6.4E-01	U82828.1	NT	Homo sapiens <i>hmx</i> (hmx) gene, complete cds
10464	23360	38579	1.18	6.4E-01	BF670405.1	EST HUMAN	Homo sapiens <i>hmx</i> (hmx) gene, complete cds
12966	25342	38579	5.78	6.4E-01	AF759212.1	EST HUMAN	Homo sapiens <i>hmx</i> (hmx) gene, complete cds
434	13508	28442	3.27	6.4E-01	AF759212.1	SWISSPROT	HYPERBETIC PROTEIN PRECURSOR (CLONE PHIP-III)
538	13507	28425	2.19	6.3E-01	U33889.1	NT	Hemophilus influenzae N4 section 1 of 105 of the complete genome
2171	15187	28208	3.4	6.3E-01	U81138.1	NT	Stigella haereri multi-subunit resistance locus
2583	15584	28603	2.72	6.3E-01	U75531.1	NT	Stigella haereri multi-subunit resistance locus
2393	15584	28604	2.72	6.3E-01	U75531.1	NT	Stigella haereri multi-subunit resistance locus
3029	19087	32490	0.8	6.3E-01	U71775.1	NT	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
6182	19257	33089	0.87	6.3E-01	BE503905.1	EST HUMAN	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
6753	19807	33089	1.07	6.3E-01	U77788.1	NT	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
8895	21833	35586	3.17	6.3E-01	BE503905.1	EST HUMAN	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
9238	22204	35586	0.8	6.3E-01	BE503905.1	EST HUMAN	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
9575	22537	35586	1.07	6.3E-01	U77788.1	NT	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
9575	22716	38771	2.85	6.3E-01	BE503905.1	EST HUMAN	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
10298	22228	38771	0.83	6.3E-01	BE503905.1	EST HUMAN	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
10792	22713	37215	1.53	6.3E-01	U77000.1	NT	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
10895	23815	37221	0.85	6.3E-01	U77000.1	NT	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
11400	24345	37278	1.52	6.3E-01	AA87715.1	EST HUMAN	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
11853	24359	38470	6.95	6.3E-01	AA87715.1	EST HUMAN	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
11734	24359	38470	1.79	6.3E-01	AF7003	SWISSPROT	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
12195	24359	38470	2.09	6.3E-01	AF7003	SWISSPROT	Lycaena didyma morphogenetic protein 1 (BMP-1) mRNA, partial cds
12359	24349	31008	6.44	6.3E-01	9910263	NT	Homo sapiens <i>hmx</i> (hmx) gene, complete cds
12359	24349	31008	1.81	6.3E-01	AF105227.1	NT	Homo sapiens <i>hmx</i> (hmx) gene, complete cds
12370	25845	32255	3.19	6.3E-01	AF105227.1	NT	Homo sapiens <i>hmx</i> (hmx) gene, complete cds
5970	10055	32255	2.75	6.3E-01	AF105227.1	NT	Homo sapiens <i>hmx</i> (hmx) gene, complete cds
7737	20862	34117	1.12	6.3E-01	AF105227.1	NT	Homo sapiens <i>hmx</i> (hmx) gene, complete cds
7701	25930	34117	1.12	6.3E-01	AF105227.1	NT	Homo sapiens <i>hmx</i> (hmx) gene, complete cds
8844	21812	35034	8.41	6.3E-01	AF105227.1	EST HUMAN	Homo sapiens <i>hmx</i> (hmx) gene, complete cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4277	17246		1.51	6.0E-01	AF036895.1	NT	Human sapiens Ndc13 (NOTCH3) gene, exons 26, 27, and 28
4279	17308	30187	0.99	6.0E-01	AB02319.1	NT	Yab1 monkey lung, full cDNA, BamHI restriction fragment E, M and partial C, partial and complete cds
5333	19438	31327	2.14	6.0E-01	P20386	SWISSPROT	(D3) DOPAMINE RECEPTOR
5374	19914	31547	2.22	6.0E-01	AF139713.1	EST_HUMAN	U4-H-B1, sub-a-10-4-JUL-1 NCL CGAP_S343 Homo sapiens cDNA clone IMAGE:274819.3
5669	19746	33022	2.68	6.0E-01	U38813.1	NT	Musca domestica histidine-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
8818	19872	33181	0.67	6.0E-01	Q04912	SWISSPROT	MACROPHAGE STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P184-RON)
6988	20211	33550	0.78	6.0E-01	U0284.1	NT	(CDW195) (CD19 ANTIGEN)
6988	20211	33540	0.78	6.0E-01	U0284.1	NT	Strongyloides purpuratus, leishman light chain isoform 2 mRNA, complete cds
7577	20359	33598	5.51	6.0E-01	A127769.1	NT	Strongyloides purpuratus, leishman light chain isoform 2 mRNA, complete cds
8461	21430	34847	4.55	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8461	21430	34848	4.55	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10182	23107	36589	1.84	6.0E-01	AB008182.1	NT	Human sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10336	23558		1.69	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER0 (PEROXIN-3)
10749	23671		0.46	6.0E-01	BE83778.1	EST_HUMAN	RC2-FN0094-190700-017-008 FN0094 Homo sapiens cDNA
11878	24760	33845	2.79	6.0E-01	A1420623.1	EST_HUMAN	108697.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:2069521.3
12638	25322	31768	1.87	6.0E-01	U1421603	NT	Human sapiens nuclear factor (erythroid-derived 2-like 3) (NFE2L3), mRNA
12731	25384		2.78	6.0E-01	AA706957.1	EST_HUMAN	ZB95p05.s1 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:482776.3
12948	25771	31522	4.71	6.0E-01	Q055303	NT	Mus musculus cAMP-inhibited phosphodiesterase (Pde3a), mRNA
12948	25771		3.4	6.0E-01	BE157817.1	EST_HUMAN	RC1-H10375-035000-015-003 H10375 Homo sapiens cDNA
1002	14053	27009	0.97	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3283	10337	26269	4.95	5.9E-01	AL183267.2	NT	Human sapiens chromosome 21 segment HS21C087
3283	10337	26267	4.95	5.9E-01	AL183267.2	NT	Human sapiens chromosome 21 segment HS21C087
4280	17276		4.09	5.9E-01	AF182765.1	NT	Rattus norvegicus cecron 2 mRNA, partial cds
8009	19587	32943	1.45	5.9E-01	AF085440.2	NT	Human sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7481	20447	33800	2.44	5.9E-01	AB023486.1	NT	Human sapiens gene for histamine H2 receptor, promoter region and complete cds
8332	21301	34718	0.46	5.9E-01	Q50911.1	NT	Synchytrium sp. PC08603 complete genome, 1327, 157660-1719403
8945	21951	35375	0.48	5.9E-01	D15922.1	NT	Lepidoptera pneumophila gene for non-superoxide dismutase, complete cds
9901	22933	36314	0.89	5.9E-01	AF033204.2	NT	Chlamydia trachomatis strain KUW310x, major outer membrane protein (omp1) gene, complete cds

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Table 4
Cytokines Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Top Hit (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12273	21198		0.66	5.9E-01	P04683	SWISSPROT	EG PROTEIN
10948	22470	36965	1.19	5.9E-01	PQ3294	SWISSPROT	VASCULAR ENDOTHelial CADHERIN PRECURSOR (VE-CADHERIN) (CAHERIN-9)
11031	23095	37526	2.48	5.9E-01	QX0203	SWISSPROT	THYMIDYLATE KINASE (TMP KINASE)
11037	24091	37526	49.8	5.9E-01	AF197941.1	EST	Xenopus laevis nucleolar protein tyrosine phosphatase della (XPTP-D) mRNA, complete cds
11309	24259	37765	24.8	5.9E-01	AF197941.1	EST	P4H-DT0041-100100-002-003 D70041 Homo sapiens cDNA
11236	24467	38021	1.93	5.9E-01	AF096426.1	NT	Male apurine strain SPRET161 CD48 antigen (CD48) gene, partial cds
11237	25108	31830	1.23	5.9E-01	L42320.1	NT	Oryzias latipes SPRET161 anti-Tyrosin (alpha 1 A1) gene, promoter region
12297	25239	31830	2.86	5.9E-01	AB017705.1	SWISSPROT	Aspergillus oryzae pycG gene for extracellular 5'-phosphate deacetylase, complete cds
12541	25290		6.24	5.9E-01	FA4626	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS MAP1 LIGHT CHAIN LC2]
12747	25394		1.28	5.9E-01	PA472	SWISSPROT	SMI PROTEIN
2824	14948	27944	1.28	5.9E-01	7903200	EST	Male muscular low density lipoprotein B (Ldb), mRNA
1571	15572	28362	1	5.9E-01	BF095738.1	NT	P01832747F1 NIH JGCG, 58 Homo sapiens cDNA clone IMAGE:40716131
4059	17048	29954	4.42	5.9E-01	AB000077.1	EST	Vigna radiata mRNA for protein tyrosinphosphatase, complete cds
4542	17565	30482	0.84	5.9E-01	AE002152.1	NT	Unpublished yeast/yeast section 53 of 59 of the complete genome
1448	19550		0.75	5.9E-01	Q10689	SWISSPROT	POTENTIAL 5'3' EXONUCLEASE
9609	19705	31862	0.75	5.9E-01	Q10689	SWISSPROT	SHingella sonnei DNA for 28 ORFs, complete cds
8308	10370	32816	1.82	5.9E-01	D70689.1	EST	HUM006088 Homo placentae plactae pJA4* (TF-lysin) Homo sapiens cDNA clone GEN:500606 5'
8445	10570	32760	3.70	5.9E-01	D50601.1	NT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
5985	20208		2.55	5.9E-01	SE5901.1	NT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
8219	21188		2.83	5.9E-01	HA1571.1	EST	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
2132	21382	34982	0.29	5.9E-01	AE020051.1	EST	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
8423	21392	34983	0.39	5.9E-01	AE020051.1	EST	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
8532	21500	34915	2.37	5.9E-01	P14326	SWISSPROT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
8532	22036	34917	2.37	5.9E-01	P14326	SWISSPROT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
8532	22038	34940	9.77	5.9E-01	AF197741.1	EST	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
8532	22038	34940	0.82	5.9E-01	Q10689	SWISSPROT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
8532	22038	35119	0.82	5.9E-01	Q10689	SWISSPROT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
8532	22038	35119	0.82	5.9E-01	Q10689	SWISSPROT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
8532	22038	35119	0.82	5.9E-01	BF031903.1	EST	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
11334	24284	37906	6.9	5.9E-01	A133213.1	EST	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
11334	24320		2.98	5.9E-01	BF700252.1	NT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
14176	24419		1.81	5.9E-01	BF700252.1	NT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
1482	14525	27496	1.11	5.7E-01	PF077	SWISSPROT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
1482	14525	27497	1.11	5.7E-01	PF077	SWISSPROT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)
3056	18113		0.77	5.7E-01	6755333	NT	phf3.017.017.M-Phase INDUCED PHOSPHATASE 2 (HUMAN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Exon Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3327	16302	29214	1.38	5.7E-01	Q9WTL2	SWISSPROT	POTATIVE TRANSCRIPTION FACTOR OVOLIKE 1 (MOV1A)
3515	16351		2.79	5.7E-01	AB059503.1	NT	Populus americanae pates-2 mRNA for 1-aminocyclohexane-1-carboxylate synthase, complete cds
3922	16962	28076	1.05	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (B/957-2A151) mRNA, partial cds
5213	18222	31097	11.22	5.7E-01	4595060	NT	Homo sapiens T cell receptor alpha chain (B/957-2A151) mRNA, partial cds
6490	19555	32805	4.36	5.7E-01	BF059415.3	EST_HUMAN	Homo sapiens T cell receptor alpha chain (B/957-2A151) mRNA, partial cds
6989	19922	33216	0.82	5.7E-01	AA194291.1	EST_HUMAN	Homo sapiens T cell receptor alpha chain (B/957-2A151) mRNA, partial cds
7042	18374	31262	1.33	5.7E-01	AA111440.1	NT	Homo sapiens T cell receptor alpha chain (B/957-2A151) mRNA, partial cds
8041	20078	34374	0.93	5.7E-01	AF00373	SWISSPROT	Proteinase 3, human
8303	21272		0.91	5.7E-01	AA205183.1	NT	Proteinase 3, human
8723	21991		0.52	5.7E-01	AF058567.1	EST_HUMAN	Proteinase 3, human
10168	23084	35580	1.22	5.7E-01	AF058567.1	EST_HUMAN	Proteinase 3, human
10168	23084	35581	1.22	5.7E-01	AF058567.1	EST_HUMAN	Proteinase 3, human
10460	23661	37376	0.72	5.7E-01	BF040962.1	EST_HUMAN	Proteinase 3, human
12252	25078		1.49	5.7E-01	BF040962.1	EST_HUMAN	Proteinase 3, human
1389	14341	27008	1.6	5.7E-01	AF007732.1	NT	Proteinase 3, human
3376	16428	26351	1.53	5.7E-01	AB018283.2	NT	Proteinase 3, human
3376	16428	26352	1.53	5.7E-01	AB018283.2	NT	Proteinase 3, human
4298	17297	30741	0.77	5.7E-01	D83135.1	NT	Proteinase 3, human
5205	18214	31089	0.93	5.7E-01	BF032377.1	EST_HUMAN	Proteinase 3, human
8165	25121	35550	1.69	5.7E-01	AF084703.1	EST_HUMAN	Proteinase 3, human
8165	25121	35551	1.69	5.7E-01	AF084703.1	EST_HUMAN	Proteinase 3, human
8730	22759	36211	1.23	5.7E-01	AB038182.1	NT	Proteinase 3, human
12153	25011		3.4	5.7E-01	BE088280.1	EST_HUMAN	Proteinase 3, human
12270	25092	38176	1.73	5.7E-01	AA460335.1	EST_HUMAN	Proteinase 3, human
12636	18341	31290	1.51	5.7E-01	AF011581.2	NT	Proteinase 3, human
12662	28340		3.05	5.7E-01	AF050508	SWISSPROT	Proteinase 3, human
13060	25596		4.95	5.7E-01	BF073929.1	EST_HUMAN	Proteinase 3, human
13110	25630		1.33	5.7E-01	AA460335.1	EST_HUMAN	Proteinase 3, human
1216	14254	27212	0.82	5.7E-01	893912	NT	Proteinase 3, human
2712	15706	28722	5.31	5.7E-01	P06341	SWISSPROT	Proteinase 3, human

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2712	15706	28723	5.31	5.5E-01	P03841	SWISSPROT	GAG POLYPROTEIN (CONTAINS INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOCAPTEIN P10)
2828	13687	28906	0.78	0.9E-01	3902089	NT	Homo sapiens superfamily viraloid activity 2 (S. cerevisiae homolog), like (SKIV2), mRNA
2879	10138	29271	1.48	5.9E-01	H46219.1	EST_HUMAN	Putative 21 Source adult brain VZV-06857 Homo sapiens cDNA clone IMAGE:178266 3'
3204	10138	29271	4.73	5.9E-01	AF221240.1	NT	Rabbit anti pathomeasur, complete genome
3704	10707	29281	2.24	5.9E-01	H46756	SWISSPROT	PO3-RELATED ANTIGEN-1
5209	18218	31694	1.98	5.9E-01	U68397.1	NT	Bos taurus MHC class II beta-chain B2A-DIB1 gene, partial cds
7487	20433	33769	0.86	5.9E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class II region/butyrophilin-like protein gene, partial cds; NucleoRNP, and tetraodon X(TN0) genes, complete
7487	20433	33769	0.98	5.9E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class II region/butyrophilin-like protein gene, partial cds; NucleoRNP, and tetraodon X(TN0) genes, complete
7504	20469	35181	0.67	5.9E-01	AB016808.1	NT	CREB-PP, and tetraodon X(TN0) genes, complete
8702	21759	35181	0.66	5.9E-01	AF017090.1	EST_HUMAN	CREB-PP, and tetraodon X(TN0) genes, complete
10125	22051	37160	0.69	5.9E-01	U88415.1	NT	Grasshopper hemaphysal fever virus strain SPU 4116/93 nucleocapsid gene, complete cds
10743	23665	37160	0.87	5.9E-01	T05947.1	EST_HUMAN	Grasshopper hemaphysal fever virus strain SPU 4116/93 nucleocapsid gene, complete cds
146	13249	28778	9.02	5.4E-01	7857266	NT	Homo sapiens KIAA0029 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0029), mRNA
146	13249	28779	9.02	5.4E-01	7857266	NT	Homo sapiens KIAA0029 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0029), mRNA
587	13655	26569	1.34	5.4E-01	AF22006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds, and unknown genes
587	13655	26570	1.34	5.4E-01	AF22006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds, and unknown genes
1278	14311	27772	2.99	5.4E-01	AF069087.1	EST_HUMAN	Q1V4-NN00040-070400-190-04 NN00040 Homo sapiens cDNA
2116	15133	28204	2.81	6.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2285	15279	28204	2.28	5.4E-01	AJ270682.1	EST_HUMAN	Drosophila melanogaster mRNA for 15'15' beta carotene dioxygenase (beta-dio gene)
5740	18834	33214	0.91	5.4E-01	AJ054237.1	EST_HUMAN	PM2-CH00050-03000-008-c10 CN0030 Homo sapiens cDNA
6315	16985	33228	0.8	5.4E-01	AB025917.1	NT	Rattus norvegicus gene for TIS11, complete cds
7228	20248	33582	0.77	5.4E-01	BE065922.2	EST_HUMAN	0010027061 NH1_MGC_71 Homo sapiens cDNA clone IMAGE:390690 3'
7558	20321	33577	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RIB5 gene encoding DGP synthase
7658	20321	33579	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RIB5 gene encoding DGP synthase

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7590	20923	33881	1.76	5.4E-01	Q64423	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA)
10349	23273		1.83	5.4E-01	BF572396.1	EST HUMAN	[INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
11414	24358	37893	2.19	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE (NADPH)[NRK]
11632	24688	38159	1.82	5.4E-01	AAV373984.1	EST HUMAN	Q17431 1053627199-058084 910536 Homo sapiens cDNA
11841	24821	38416	3.29	5.4E-01	Q160675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11841	24821	38417	3.29	5.4E-01	Q160675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
12215	26054		3.88	5.4E-01	AB59398.1	EST HUMAN	w67694.XT NCL_OGAP_U11 Homo sapiens cDNA clone IMAGE:242702.3 similar to g31473-462 LAMIN A (HUMAN).
517	13598	26593	1.86	5.3E-01	AF018413.1	NT	Homo sapiens U.S. class III region containing hrasch X (hwasch-X) gene, partial cds; cytochrome P450 21A hydroxylase (CYP21B), component C2 (C2) genes >
2150	15168	28121	0.97	5.3E-01	K411819.1	NT	Brassica oleracea var. capitata thiosphalase D2 (PLD2) gene, complete cds
2150	15168	28181	0.97	5.3E-01	K411819.1	NT	Brassica oleracea var. capitata thiosphalase D2 (PLD2) gene, complete cds
2794	19783	28531	8.62	5.3E-01	4506326	NT	Homo sapiens protein tyrosine phosphatase, cytosolic-type, zeta polypeptide 1 (PTFRZ1) mRNA
2794	19783	28532	8.62	5.3E-01	4506326	NT	Homo sapiens protein tyrosine phosphatase, cytosolic-type, zeta polypeptide 1 (PTFRZ1) mRNA
2807	19783	28533	3.26	5.3E-01	AF037658.1	NT	Homo sapiens secreted C-type lectin precursor (LSC1), gene, complete cds
5439	17433		1.33	5.3E-01	U39687.1	EST HUMAN	Mycobacterium genitalium section 9 of 51 of the complete genome
5439	17433	31569	2.06	5.3E-01	AB20921.1	EST HUMAN	2422012.y5 Soares ovary tumor Nsi-OT Homo sapiens cDNA clone IMAGE:740711.5
5533	18031	31570	2.06	5.3E-01	AB20921.1	EST HUMAN	2422012.y5 Soares ovary tumor Nsi-OT Homo sapiens cDNA clone IMAGE:740711.5
5633	18729	31980	0.76	5.3E-01	AA153072.1	EST HUMAN	2422019.r1 Soares, NHHMPL_S1 Homo sapiens cDNA clone IMAGE:660112.5
5633	18729	31981	0.76	5.3E-01	AA153072.1	EST HUMAN	2422019.r1 Soares, NHHMPL_S1 Homo sapiens cDNA clone IMAGE:660112.5
9729	18826	32003	2	5.3E-01	BE645620.1	EST HUMAN	7673412.XT NCL_OGAP_P28 Homo sapiens cDNA clone IMAGE:3288118.5 similar to gpJ02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9729	18823	32004	2	5.3E-01	BE645620.1	EST HUMAN	7673412.XT NCL_OGAP_P28 Homo sapiens cDNA clone IMAGE:3288118.5 similar to gpJ02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9295	22221		1.94	5.3E-01	U11800.2	NT	Rodulid purpuris rubicosa 1,5-bisphosphatase (bcl) gene, partial cds; chloroplast gene for chloroplast product
9307	22272	33703	0.76	5.3E-01	BF433959.1	EST HUMAN	7671612.XT NCL_OGAP_L024 Homo sapiens cDNA clone IMAGE:3 similar to contains element MER29 repetitive element.
9307	22272	33704	0.76	5.3E-01	BF433959.1	EST HUMAN	7671612.XT NCL_OGAP_L024 Homo sapiens cDNA clone IMAGE:3 similar to contains element MER29 repetitive element.

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Emission Signal	Max Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10572	25484	36965	0.74	5.3E-01	AB64210.1	EST_HUMAN	w54002.x1 NC1_GGAP_M4165 Homo sapiens cDNA clone IMAGE:2551276 3' similar to
10977	23987	37410	0.17	5.3E-01	11429833	NT	SW COX4_HUMAN P0874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11086	24787	36354	5.19	5.3E-01	BE666201.1	EST_HUMAN	Homo sapiens nucleoside 24 and (CIN) (NUP214), mRNA
12144	25775	26523	4.97	5.3E-01	AA616953.1	EST_HUMAN	6813396971 NHK_M052_53 Homo sapiens cDNA clone IMAGE:3682176 5'
917	13975	26523	16.24	5.2E-01	20770.1	NT	eg310405.1 NC1_GGAP_B7 Homo sapiens cDNA clone IMAGE:1441378 3' similar to gb:202811
1108	14209	27163	7.86	5.2E-01	60WV30	SWISSPROT	APOLIPROTEIN D PRECURSOR (HUMAN);
1108	14235	27160	3.01	5.2E-01	AF224402.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
2162	14927	28181	3.18	5.2E-01	AL183853.2	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
3136	15103	27102	2.88	5.2E-01	AB578263.2	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
3251	15103	27102	1.14	5.2E-01	U737436.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
3416	15444	26424	1.39	5.2E-01	AL116780.1	NT	Homo sapiens mRNA for KUCA740 protein, partial cds
3458	15554	26424	2.72	5.2E-01	AA984105.1	EST_HUMAN	Homo sapiens chromosome 21 segment 14521008
3549	15591		1	5.2E-01	AF120269.1	NT	Homo sapiens chromosome 21 segment 14521008
5160	19189		1.04	5.2E-01	AL183281.2	NT	Human sapiens chromosome 21 segment 14521008
6729	19830	32009	1.02	5.2E-01	AA934261.1	EST_HUMAN	z244005.17 Spares, serous, fibroblast, NHRSF Homo sapiens cDNA clone IMAGE:325169 3'
10089	25700	35480	0.64	5.2E-01	U02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10089	25700	35480	0.64	5.2E-01	U02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10262	22027	35701	0.52	5.2E-01	AA194516.1	EST_HUMAN	z205005.17 Spares, serous, fibroblast, NHRSF Homo sapiens cDNA clone IMAGE:325169 3'
10387	23309	35787	1.76	5.2E-01	AF143562.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13031	25576		6.82	5.2E-01	P16516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
919	13684	26002	2.34	5.1E-01	U58505.1	NT	Human adrenocortical medulla gene, exons 3 to 12
649	13715	26537	3.53	5.1E-01	U233944.1	NT	Polyomavirus vimentin (strain P1 v1) 16S rRNA gene
649	13715	26537	3.53	5.1E-01	U233944.1	NT	Polyomavirus vimentin (strain P1 v1) 16S rRNA gene
1600	14682		1.28	5.1E-01	U07895.1	NT	R-nor-epididymus mRNA for mammalian fucose protein
4103	17137	30032	4.61	5.1E-01	AB58485.1	EST_HUMAN	w38312.x1 NC1_GGAP_U7 Homo sapiens cDNA clone IMAGE:2427253 3'
4216	17245		0.57	5.1E-01	P66900	SWISSPROT	TRANSCRIPTION REPAIR COUPLING FACTOR (TRCF)
6848	19417	32658	0.57	5.1E-01	BE441068.1	EST_HUMAN	501050300671 NHK_M052_53 Homo sapiens cDNA clone IMAGE:3460000 5'
5407	19475		0.63	5.1E-01	U712228.1	EST_HUMAN	AV712228 DCA Homo sapiens cDNA clone DCAUAP07 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7102	20039	33339	1.52	5.1E-01	R80873.1	EST_HUMAN	Y64408.41 Spores plasmid N22HP Homo sapiens cDNA clone IMAGE:146872 3'
8919	21884	35059	0.62	5.1E-01	AV069881.1	EST_HUMAN	OV4-S10023-160400-1174601 ST0023 Homo sapiens cDNA
8919	21884	35100	0.62	5.1E-01	AV069881.1	EST_HUMAN	OV4-S10023-160400-1174601 ST0023 Homo sapiens cDNA
10043	22970	39437	4.3	5.1E-01	J05441.1	NT	Human regenerating protein (reg) gene, complete cds
10046	22973	39440	3.2	5.1E-01	W22802.1	EST_HUMAN	6681 Human retina cDNA Tsp60gI-cleaved subunit Homo sapiens cDNA, not directional
10321	23443	39841	0.89	5.1E-01	M94379.1	NT	Human carboxy ester lipase (CEL) gene, complete cds
12284	25088	38174	2.09	5.1E-01	BF540777.1	EST_HUMAN	6020674711 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:4065742 5'
12368	25709		2.47	5.1E-01	BF603007.1	EST_HUMAN	6015989391 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3825737 5'
12811	26310		3.62	5.1E-01	BF49982.1	EST_HUMAN	head110101 NOT_GMAP_Dm23 Homo sapiens cDNA clone IMAGE:3402175 5' similar to contains element
2144	15161	28176	0.97	5.0E-01	4895532	NT	17A11 reductive element 1
2144	15161	28177	0.97	5.0E-01	4895532	NT	Homo sapiens postmitotic segregation increased 2.5 kb 9 (PMS2.9), mRNA
						NT	Homo sapiens postmitotic segregation increased 2.5 kb 9 (PMS2.9), mRNA
						NT	Buchnera apterous genome (B. apterous) containing (chaperone Hsp70) gene, DNA biosynthesis initiating complete cds; and termination factor Rho (rho) genes>
2154	15170	28197	2.39	5.0E-01	AF098210.1	NT	
2154	15170	28198	2.39	5.0E-01	AF098210.1	NT	Buchnera apterous genome fragment containing (chaperone Hsp70) gene, DNA biosynthesis initiating protein (gpah), ATP aporeon (hsp70AHHEB), and putative chromosome replication protein (gdaA) genes, complete cds; and termination factor Rho (rho) genes>
2172	15193		0.31	5.0E-01	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3761	16322	29714	0.8	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain Igm mRNA, antibody 365p.138, partial cds
3872	16327	29768	1	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain Igm mRNA, antibody 365p.138, partial cds
3887	16327	29835	2.74	5.0E-01	AB030310.1	NT	Rattus norvegicus lagged protein mRNA, complete cds
6801	19653		0.84	5.0E-01	BF576198.1	EST_HUMAN	Homo sapiens mRNA for KIAA1184 protein, partial cds
7026	20659	34256	0.68	5.0E-01	AL161549.2	NT	6021326221 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4271639 5'
7026	20659	34257	0.68	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7026	20659	34257	0.68	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8875	21842	35604	1.87	5.0E-01	BF107848.1	EST_HUMAN	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
9018	21884		0.59	5.0E-01	BF107848.1	EST_HUMAN	6018238501 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:405448 3'
9813	21336	34338	3.16	5.0E-01	BF317212.1	EST_HUMAN	6019038711 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:405448 3'
9983	22910	36375	1.31	5.0E-01	P35573	SWISSPROT	GLYCOSYL DEBRANCHING ENZYME (GLYCOSYL DEBRANCHER) (INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANOTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 5-ALPHA-D-GLUCOSIDASE))
9983	22910	36376	1.31	5.0E-01	P35573	SWISSPROT	GLYCOSYL DEBRANCHING ENZYME (GLYCOSYL DEBRANCHER) (INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANOTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 5-ALPHA-D-GLUCOSIDASE))

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Asses- sion No.	Top Hit Database Source	Top Hit Descrip- tor
107368	23878		1.38	5.0E-01 BE6927.8.1	EST_HUMAN	101:446242F1.NH.MGC_36 Homo sapiens cDNA clone IMAGE:3649408 9'	
120802	29113		0.28	3.0E-01 AY026715.1	NT	Mus musculus MYC OX-2 antigen homolog gene, exons 2-5, and complete cds	
13004	26548		2.21	5.0E-01 AL183302.2	NT	Homo sapiens chromosome 21 segment H82C102	
13011	25543		5.0	5.0E-01 U19391	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11	
700	13840	26705	2.03	4.9E-01 F51472.1	EST_HUMAN	XG237924F1.NH.MGC_32 Homo sapiens cDNA clone IMAGE:4243360 5'	
1698	14700	27075	2.75	4.9E-01 U02865.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 bp	
5480	19880	31491	0.99	4.9E-01 U02865.1	NT	Chimpanzee cDNA for putative nuclear protein A (SP-4) mRNA, complete cds	
6153	19228	32457	2.67	4.9E-01 AF020831.1	SWISSPROT	FIBRILLIN-1 (FIBRILIN3)	
1938	19228	32458	2.67	4.9E-01 AF020831.1	NT	Homo sapiens cDNA clone IMAGE:102503 3'	
7685	20043	34007	1.69	4.9E-01 AB042051.1	NT	Oryza sativa subunit 3 (DAGK3) gene, exon 10	
7972	20911	34001	0.7	4.9E-01 U10008	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-NACETYLGUCOSAMINYL TRANSFERASE	
7972	20911	34302	0.7	4.9E-01 U10008	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-NACETYLGUCOSAMINYL TRANSFERASE	
9341	22306		1.77	4.9E-01 BF200791.1	EST_HUMAN	80187486F1.NH.MGC_54 Homo sapiens cDNA clone IMAGE:4192503 5'	
9542	22505	33954	0.99	4.9E-01 AW339505.1	EST_HUMAN	h60602-11.Sovera.NF_1_2_GRC_31 Homo sapiens cDNA clone IMAGE:2607268 3' similar to TR-095714	
9851	26009		2.64	4.9E-01 10946883	NT	O65714-1.HERC2...	
10681	23603	37097	0.86	4.9E-01 AF03380.1	NT	Mus musculus adenylM cyclase 1 (Adoryl) cDNA, partial cds	
10688	23608	37314	0.97	4.9E-01 X50000.1	NT	H. sapiens cDNA for BCL7A gene and BCL7AIGH locus fusion	
12195	25541		1.41	4.9E-01 AF176912.1	EST_HUMAN	Homo sapiens neurotrophin-1B cell stimulating factor-3 gene, complete cds	
12607	25953		0.43	4.9E-01 AA13562.1	EST_HUMAN	ng22811.1.NC1_GGAP_Cyt10 Homo sapiens cDNA clone IMAGE:1144552 3'	
5565	19881	31849	8.83	4.8E-01 U02867.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds	
6836	19886	33194	0.99	4.8E-01 U02867.1	NT	Mus musculus slow skeletal muscle troponin T (Tnnt1) gene, complete cds	
6846	19886		3.82	4.8E-01 AA09078.1	EST_HUMAN	nu8509 at NC1_GGAP_Ant Homo sapiens cDNA clone IMAGE:127513	
7138	20871		1.96	4.8E-01 5031950	NT	Homo sapiens chromosome 21 segment H82C1009	
7029	20872	34281	0.78	4.8E-01 AL103209.2	NT	Homo sapiens chromosome 21 segment H82C1009	
8037	20874	34369	3.96	4.8E-01 AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4	
8337	20874	34370	3.96	4.8E-01 AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4	
8227	21209	34611	0.98	4.8E-01 AB02744.1	EST_HUMAN	177710.16 Sovera breast 2N4H8at Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element	
9500	22504		0.97	4.8E-01 BE15148.1	EST_HUMAN	PM1-IT0380:207289-3014-H10380 Homo sapiens cDNA	
10386	23281		0.99	4.8E-01 BF398653.1	EST_HUMAN	502194297F1.NH.MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'	
11081	24043		1.75	4.8E-01 X83932.1	NT	S.cerevisiae ORF4 from chromosome X	

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID/NO.	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12277	25096		1.65	4.8E-01	AI16927.2	NT	Homo sapiens chromosome 21 segment H521.C037
13065	25737		3.32	4.8E-01	AI16279.5	NT	Thymopontin cDNA (IMAGE:149011) 3' similar to
13065	25766		1.49	4.8E-01	AI16294.1	NT	Chromoprotein 18
0964	19721	32096	6.88	4.7E-01	BF217173.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:406387.5'
7241	19876	33273	0.92	4.7E-01	AI162434.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
8197	21077	34577	0.99	4.7E-01	111414.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
8197	21077	34578	0.99	4.7E-01	111414.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
9430	22984	35884	0.57	4.7E-01		NT	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
11193	24143		4.78	4.7E-01	K162873.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
11422	24503		1.74	4.7E-01	K162873.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
11613	24551	38111	1.74	4.7E-01	B152506.3	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
11704	24693	38246	1.49	4.7E-01	AI169048.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
12399	25713		1.49	4.7E-01	B5867793.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
12399	25713		1.49	4.7E-01	B5867793.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
3798	19783	29739	1.93	4.6E-01	B5979515.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
3798	19783	29739	1.93	4.6E-01	B5979515.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
4739	19196	29710	1.53	4.6E-01	B5963300.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
4739	19196	29710	1.53	4.6E-01	B5963300.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5409	18503	31503	1	4.6E-01	B1313693.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5409	18503	31503	1	4.6E-01	B1313693.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5445	18645	31566	3.33	4.6E-01	Q09043	SWISSPROT	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5445	18645	31567	3.33	4.6E-01	Q09043	SWISSPROT	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5925	18721	31580	1.95	4.6E-01	BE724791.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5639	18735	31597	3.12	4.6E-01	A1247678.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5639	18735	31598	3.12	4.6E-01	A1247678.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5647	18743	31609	1.46	4.6E-01	P20250	SWISSPROT	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5730	18824		0.85	4.6E-01	AF121214.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
5821	18911		0.78	4.6E-01	B121747.1	EST HUMAN	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
8002	19085	32395	0.51	4.6E-01	D28215.1	NT	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
0386	19454	32699	0.92	4.6E-01	AF1000894.1	NT	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'
0861	19633	33231	0.52	4.6E-01	AF110340.1	NT	470260.AT Source: testis, NBT Homo sapiens cDNA clone IMAGE:178564.3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
2381	15940	28957	5.38	4.5E-01	AA677386.1	EST_HUMAN	255022.s1 Source: fetal liver, spleen, thymus, S1 Homo sapiens cDNA clone IMAGE:454170.3
3328	18370	25000	3.85	4.5E-01	005793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3359	18438	25084	1.62	4.5E-01	AF126378.1	NT	Mus musculus alpha polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4090	17068		1.23	4.5E-01	C26247	SWISSPROT	COLLAGEN ALPHA 2(V) CHAIN
4101	17135	30030	1.12	4.5E-01	U79808.1	EST_HUMAN	aa6902.x1 Barred point HPLR85 Homo sapiens cDNA clone IMAGE:2583480.3
4205	18325		4.08	4.5E-01	AW673485.1	EST_HUMAN	1060902.x1 Source: NFL_T, GSC, S1 Homo sapiens cDNA clone IMAGE:3041810.3
4840	17995	30884	1.09	4.5E-01	BE83445.2	EST_HUMAN	6916572581.NH, MGC, 87 Homo sapiens cDNA clone IMAGE:3869263.3
5628	18724	31985	1.33	4.5E-01	AW69814.1	EST_HUMAN	QV22-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
5790	18814		1.74	4.5E-01	000956	SWISSPROT	COAT PROTEIN
7644	20604	33660	0.93	4.5E-01	M37038.1	NT	Rat nuclear proteins B23.1 and B23.2
7697	20811	34188	2.84	4.5E-01	AB88849.1	EST_HUMAN	W32902.x1 NCI_OGAP_U18 Homo sapiens cDNA clone IMAGE:2426618.3 similar to TR-052623 Q02628
7697	20830	34255	0.61	4.5E-01	P50070	SWISSPROT	SWISNF COMPLEX 170 KDA SUBUNIT 1
8050	21818		0.87	4.5E-01	M32651.1	NT	D melanogaster Shwz protein mRNA, complete cds
8745	21714	35137	3.86	4.5E-01	AB48896.1	EST_HUMAN	1255311.x1 NCI_OGAP_O35 Homo sapiens cDNA clone IMAGE:232644.3
8905	21871	35287	0.74	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
9133	22069		1.72	4.5E-01	11444786	NT	Homo sapiens hypoblastin protein DKFZ5947G183 [DKFZ5947G183], mRNA
9351	22318	35742	0.78	4.5E-01	AE000218.1	NT	Escherichia coli K12 MG1655 section 108 of 400 of the complete genome
10300	23225		0.89	4.5E-01	9830816	NT	Bombay mori nuclear polyhedrosis virus, complete genome
10881	22761	37281	26.2	4.5E-01	M68006.1	EST_HUMAN	EST102331 Fetal brain, Striatum (026836208) Homo sapiens cDNA clone HBC0Y17
10881	22761	37282	26.2	4.5E-01	M68006.1	EST_HUMAN	EST102331 Fetal brain, Striatum (026836208) Homo sapiens cDNA clone HBC0Y17
11212	24165	37695	2.3	4.5E-01	AW591271.1	EST_HUMAN	xc14701.x1 NCI_OGAP_U18 Homo sapiens cDNA clone IMAGE:2703865.3 similar to SW-INT6_MOUSE
12105	25955		5.3	4.5E-01	BE671451.1	EST_HUMAN	Q64552 VIRAL INTEGRATION SITE PROTEIN INT-8 (1)
12349	25144		1.48	4.5E-01	O19838	SWISSPROT	6071440201T1 NH1_MGC_88 Homo sapiens cDNA clone IMAGE:3862861.5
12452	25211		1.54	4.5E-01	A132045.1	NT	OUT AT FIRST PROTEIN
12681	25478		6.22	4.5E-01	11422069	NT	Thelastin amide 2H12 gene
2052	15071		2.23	4.5E-01	6980503	NT	Homo sapiens testis-specific kinase 2 (TEK2), mRNA
2388	15405	28430	7.02	4.5E-01	P49765	SWISSPROT	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3326	16377	29258	1.36	4.E-01	AF508790.1	NT	Rattus norvegicus SynGAP-5 mRNA, complete cds
3328	16377	29259	1.36	4.E-01	AF508790.1	NT	Rattus norvegicus SynGAP-5 mRNA, complete cds
3330	16381	29302	1.78	4.E-01	BF936728.1	EST_HUMAN	791602.7 nt NCI CGAP: BF98 Homo sapiens cDNA clone IMAGE:335795.5
4282	17391	32502	1.75	4.E-01	BE337670.1	EST_HUMAN	69127139P1NH1 JGC: 44 Homo sapiens cDNA clone IMAGE:356938.5
5464	18894	31603	1.83	4.E-01	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5484	18894	31608	1.83	4.E-01	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5772	18894	32043	1.77	4.E-01	555016.1	NT	muslin (mln, Stragun-Dowsey, null-locus-related protein) epithelium, mRNA, Partial, 350 nt
5790	18892	32044	1.82	4.E-01	AY724083.1	EST_HUMAN	AY724083 G.CC Homo sapiens cDNA clone IMAGE:356510.3 similar to TR:Q23168 Q23169
5844	19145	32336	1.42	4.E-01	AI198413.1	EST_HUMAN	584413.1 NCI CGAP: BF925 Homo sapiens cDNA clone IMAGE:356510.3 similar to TR:Q23168 Q23169
5844	19145	32337	1.42	4.E-01	AI198413.1	EST_HUMAN	584413.1 NCI CGAP: BF925 Homo sapiens cDNA clone IMAGE:356510.3 similar to TR:Q23168 Q23169
6369	19436	32680	1.9	4.E-01	AW080795.1	EST_HUMAN	UNKNOWN PROTEIN
6482	19437		1.17	4.E-01	AA776132.1	EST_HUMAN	648211.1 Strabagun schizoblast S11 Homo sapiens cDNA clone IMAGE:356510.3 similar to gb:M16038
7627	20487	33500	0.85	4.E-01	AE000571.1	NT	HYDROLYSIN-PROTEIN KINASE LVN (HUMAN)
8773	21143		12.56	4.E-01	Z11679.1	NT	Helicobacter pylori 26695 strain NCTC 11637 section 19 of 134 of the complete genome
9116	22091	33509	0.74	4.E-01	AA055427.1	EST_HUMAN	S. Libermann mRNA for induced sodium lip protein (partial)
9200	22469	33613	0.72	4.E-01	AF112540.1	NT	25603.3 at Strabagun color (6637203) Homo sapiens cDNA clone IMAGE:509836.3
9538	22501	33949	0.56	4.E-01	AW612578.1	EST_HUMAN	HV-1 isolate 0810746 from USA, envelope glycoprotein (env) gene, partial cds
9645	22560	36038	1.21	4.E-01	O62838	SWISSPROT	H30508.4 NCI CGAP: K411 Homo sapiens cDNA clone IMAGE:254422.3 similar to
10321	23245	36725	2.1	4.E-01	AI268550.1	EST_HUMAN	SW:ASHB: HUMAN P5201 DNA MISMATCH REPAIR PROTEIN MSH6
10322	23246		3.91	4.E-01	P28822	SWISSPROT	ZINC FINGER XCHROMOSOMAL PROTEIN
10457	23378	36872	5.07	4.E-01	P35500	SWISSPROT	93609.x1 NCI CGAP: Luf8 Homo sapiens cDNA clone IMAGE:191021.3
10740	23962	37195	1.27	4.E-01	S78424.1	NT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10740	23962	37197	1.27	4.E-01	S78424.1	NT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
12432	25198	31824	5.76	4.E-01	697874.1	NT	bata-HK4H-K-ATPase beta-subunit (beta, Genomic, 8885 nt, segment 2 of 2)
12851	25465	31727	2.83	4.E-01	9527142	NT	bata-HK4H-K-ATPase beta-subunit (beta, Genomic, 8885 nt, segment 2 of 2)
12887	25535		1.43	4.E-01	PF4725	SWISSPROT	Beta-HK4H-K-ATPase beta-subunit (beta, Genomic, 8885 nt, segment 2 of 2)
4111	13464	26419	2.46	4.E-01	AF165218.1	NT	Autographa californica nucleopolydnavirus, complete genome
4111	13464	26420	2.46	4.E-01	AF165218.1	NT	UV EXCISION REPAIR PROTEIN PCD3 HOMOLOG A (HHR23A)
16071	14639	27618	0.86	4.E-01	AW86550.1	EST_HUMAN	Callitriche jacquii MW/LW spin gene, upstream flanking region
							Q14-SN024-20400-183-501 SN024 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2863	15942		1.83	4.3E-01	AW63296.1	EST_HUMAN	CM2-071000-071030-037 -cd1 171003 Homo sapiens cDNA
3073	16130	28042	0.94	4.3E-01	AW69477.1	EST_HUMAN	MRQ-BN0076-27000-008-g04 BN0070 Homo sapiens cDNA
4178	17209	30095	1.32	4.3E-01	U00094.1	NT	Human c-metrasin 1 gene and flanks
4435	13464	26419	1.83	4.3E-01	AF155218.1	NT	Callitrix jacchus MYL1W open gene, upstream flanking region
4435	13464	26420	1.63	4.3E-01	AF155218.1	NT	Callitrix jacchus MYL1W open gene, upstream flanking region
8154	18164		1.17	4.3E-01	8693520	NT	Xenopus laevis g1.12.1 open gene, upstream flanking region
5291	15208	31157	1.10	4.3E-01	BE780182.1	EST_HUMAN	h64610.01 Y1 NC_CGAP_GUT Homo sapiens cDNA clone IMAGE:387725 5'
5438	18540	31449	0.89	4.3E-01	U48534	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5438	18540	31450	0.89	4.3E-01	U48534	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5500	18075	32273	1.15	4.3E-01	BE101555.1	EST_HUMAN	QV1-H10538-070500-191-c08 H10838 Homo sapiens cDNA
8070	19068	32293	1.93	4.3E-01	U178252.1	EST_HUMAN	SV40-110538-070500-191-c08 H10838 Homo sapiens cDNA
8668	19519	33214	1.93	4.3E-01	U178252.1	EST_HUMAN	SV40-110538-070500-191-c08 H10838 Homo sapiens cDNA
7049	20071		0.86	4.3E-01	U303076.1	NT	Salmonella enterica serovar typhimurium (SSC186) gene, peritrichal cdc
7682	20922		0.83	4.3E-01	U303076.1	NT	Salmonella enterica serovar typhimurium (SSC186) gene, peritrichal cdc
8116	21053		1.63	4.3E-01	U303076.1	NT	Salmonella enterica serovar typhimurium (SSC186) gene, peritrichal cdc
8710	21737		2.56	4.3E-01	U187045.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
9510	22014		1.04	4.3E-01	U187045.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
10084	23011		1.88	4.3E-01	U187045.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
10896	23511	37005	0.85	4.3E-01	AW170559.1	EST_HUMAN	h67441.01 Y1 NC_CGAP_GUT Homo sapiens cDNA clone IMAGE:2968554 5'
10879	23709	37301	0.48	4.3E-01	U65262.1	EST_HUMAN	h67441.01 Y1 NC_CGAP_GUT Homo sapiens cDNA clone IMAGE:2968554 5'
11277	20178	33603	1.35	4.3E-01	AF075922.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
11539	24480	38031	1.77	4.3E-01	AW693958.1	EST_HUMAN	Equus caballus microsatellite, LEX207
11539	24480	38032	1.77	4.3E-01	AW693958.1	EST_HUMAN	Equus caballus microsatellite, LEX207
13035	25592		2.24	4.3E-01	U303022.1	NT	Streptomyces coelicolor WH1 gene
13051	15945	27365	1.77	4.2E-01	U303102	SWISSPROT	CELL DIVISION PROTEIN FISH (FISHOLOG PRECURSOR)
3623	16805	29860	1.43	4.2E-01	AE003947.1	NT	Xenopus laevis, c-metrasin 1 gene, upstream flanking region
3651	16804	29869	1.04	4.2E-01	AE003947.1	NT	Xenopus laevis, c-metrasin 1 gene, upstream flanking region
3724	18324		1.22	4.2E-01	AF180203.1	EST_HUMAN	QV1-H10538-070500-191-c08 H10838 Homo sapiens cDNA clone IMAGE:187644 3'
3883	18833	29943	0.89	4.2E-01	AW635927.1	EST_HUMAN	QV1-H10538-070500-191-c08 H10838 Homo sapiens cDNA clone IMAGE:187644 3'
4007	17046	29953	1.72	4.2E-01	U30488	SWISSPROT	SOX-6 PROTEIN
4726	17748		4.8	4.2E-01	U30488	EST_HUMAN	h69001.01 NC_CGAP_P170 Homo sapiens cDNA clone IMAGE:387777 similar to gp.M33500 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN)

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Table 4
Single Exon Probes Expressed in Bone Marrow

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9445	22409	35646	1.45	4.1E-01	6755521	NT	Mus musculus signaling intermediate in T cell pathway-exclusively conserved (Shpac-reading), mRNA
9923	22807		0.58	4.1E-01	AF105897.1	NT	Vesicle glycoprotein 5 (Vg5) gene, complete cds; mitochondrial gene for
10626	23548		1.18	4.1E-01	AL139076.2	NT	Chlamydia pneumoniae (Cpn) complete genome, segment 336
10776	23548	37164	1.1	4.1E-01	AF049879.1	EST_HUMAN	AT645976.1 (Cpna) cDNA, 3' end, G138V12.3
10873	22793	37284	0.51	4.1E-01	AF18854	SWISSPROT	PROTEIN SERINE PROTEINASE DO-LIKE PRECURSOR (89 KDA) (MILINOGENIC PROTEIN) (SK49)
10873	22793	37285	0.51	4.1E-01	AF18854	SWISSPROT	PROTEIN SERINE PROTEINASE DO-LIKE PRECURSOR (89 KDA) (MILINOGENIC PROTEIN) (SK49)
10943	23903		2.1	4.1E-01	BF349382.1	EST_HUMAN	CH247107.2 (Cpna) cDNA, 3' end, G138V12.3
11188	24144	37677	39.55	4.1E-01	U03700.1	NT	ZMPK33 gene for 18 kDa zinc protein
12751	28931		3	4.1E-01	U03700.1	NT	Mus musculus DNA for amyloid precursor protein, complete cds
142	15533		0.55	4.0E-01	AF047123.1	EST_HUMAN	Mus musculus DNA for amyloid precursor protein, complete cds
1040	14085	27036	0.71	4.0E-01	8404658	NT	RC210201.1 (Cpna) cDNA, 3' end, G138V12.3
1342	14377	27348	1.77	4.0E-01	AF230478.1	NT	Grasshopper (Diptera) complete genome
1481	14514		5.11	4.0E-01	6979268	NT	Lactaria tubellus mitochondrion, complete genome
2022	10683	28054	1.12	4.0E-01	U03833.1	NT	Ascaris lumbricoides m2c2 gene
2022	10683	28055	1.12	4.0E-01	U03833.1	NT	Ascaris lumbricoides m2c2 gene
2167	15183	28203	1.09	4.0E-01	AE010381.1	NT	Deinococcus radiodurans RT section 68 of 228 of the complete chromosome 1
2167	15183	28204	1.09	4.0E-01	AE010381.1	NT	Deinococcus radiodurans RT section 68 of 228 of the complete chromosome 1
2616	13246	25710	1.29	4.0E-01	6678460	NT	Mus musculus ubiquitin-protein ligase 3 component 1-recognition (Ubr1), mRNA
2679	10037	28259	1.34	4.0E-01	AL163380.2	NT	Home sapiens chromosome 21 segment 1821C080
2878	10037	28259	1.34	4.0E-01	AL163380.2	NT	Home sapiens chromosome 21 segment 1821C080
3709	16752	29668	2.32	4.0E-01	AF058903.1	NT	Streptococcus pneumoniae 7YC (MIC), Y10 (VID), penicillin-binding protein 2c (pbp2c), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide transferase (murA) genes, complete cds
3840	16890	29753	3.28	4.0E-01	AJ277811.1	NT	Osteo aryl perifer 1 (OS) gene for T cell receptor delta chain (TRD-2), exon 1
3840	16890	29754	3.28	4.0E-01	AJ277811.1	NT	Osteo aryl perifer 1 (OS) gene for T cell receptor delta chain (TRD-2), exon 1
4855	17872		9.36	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5 (CHOROPLAST)
6015	10098	32269	1.14	4.0E-01	AF070501.1	EST_HUMAN	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5 (CHOROPLAST)
6226	13300	32553	0.51	4.0E-01	BF24741.1	EST_HUMAN	EST183867 IMAGE: testaculture, WACR, Homo sapiens (Homo sapiens)
6578	19538	32904	0.92	4.0E-01	P27295	SWISSPROT	STRUCTURAL POLYPEPTIDE (P130) CONTAINS: CONT PROTEIN C, SPIKE GLYCOPROTEINS E3, E2 AND E1, 9 KD P27103
8345	21314	34729	0.8	4.0E-01	AB016625.1	NT	Home sapiens OXN1 gene, complete cds
9360	22235	35753	0.81	4.0E-01	AA332385.1	EST_HUMAN	EST 72086: Cerebellum 1 Homo sapiens cDNA 5' end similar to EST containing Alu repeat

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11895	24776		2	4.0E-41	BF003265.1	EST_HUMAN	661568235 NIH_VGC_38 Homo sapiens cDNA clone IMAGE:3026092 5'
12030	24908		1.75	4.0E-41	L70590.1	NT	Synchochiste sp. PCC 9413 lipase gene, complete cds
12440	24930		3.03	4.0E-41	AL163902.2	NT	Homo sapiens chromosome 21 segment HS21C100
12440	24930		1.3	4.0E-41	P26049	SWISSPROT	HYPOPHOSPHATE 487 KD PROTEIN IN GN2-ST13 INTERGENIC REGION
1339	24933		1.83	3.9E-41	AF120318.1	NT	Corilla gorilla carboxy-ester lipase (CEL) gene, complete cds
2850	15447	26970	3.32	3.9E-41	BC533919.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2718	15710	26728	4.20	3.9E-41	BC2032.1	NT	H. sapiens B-myo gene
3113	15710	26727	4.20	3.9E-41	BC2032.1	NT	H. sapiens B-myo gene
3113	15710	26980	4.59	3.9E-41	AL122866.1	NT	Shiga toxin 2 (Stx2) gene, 3' UTR, cys3, gene, and cys3
4108	17140	30035	1.25	3.9E-41	BF626811.1	EST_HUMAN	765401.ct.NCL_GGAP_B7.61 Homo sapiens cDNA clone IMAGE:3359169 3'
5027	19041	30624	1.74	3.9E-41	BE728607.1	EST_HUMAN	80183548F NIH_VGC_29 Homo sapiens cDNA clone IMAGE:363298 3'
6042	19124	32329	5.95	3.9E-41	BF200048.1	EST_HUMAN	80182635F NIH_VGC_53 Homo sapiens cDNA clone IMAGE:402035 5'
6411	19479	32728	0.89	3.9E-41	U62695.2	NT	Homo sapiens zeta fibrin protein 92 (ZFP92), expressed-XcDSTS protein (XC2609F), and blycan (BLYN) genes, complete cds, and plasma membrane sodium ATPase isoform 3 (PNA3) gene, partial cds
8288	21295	34684	0.8	3.9E-41	U78415.1	NT	Homo sapiens prepro discoidin I (DPF1) gene, complete cds
9213	22179	35910	0.73	3.9E-41	AW117701.1	EST_HUMAN	CMS-CT0105-178892-004-008 C10105 Homo sapiens cDNA
9222	22188		0.89	3.9E-41	BF248934.1	EST_HUMAN	602016944F1 NCL_GGAP_B7.67 Homo sapiens cDNA clone IMAGE:4153322 5'
9590	22542	36003	1.41	3.9E-41	AW195888.1	EST_HUMAN	904821 KIAA0713 PROTEIN ;
9903	22855	36318	1.83	3.9E-41	AB37337.1	EST_HUMAN	W78462.ct.NCL_GGAP_B7.62 Homo sapiens cDNA clone IMAGE:2467658 3' similar to TR-064821
10237	23162	39550	2.89	3.9E-41	M11879.1	NT	SW-RPXS_HUMAN P-48382 BINDING REGULATORY FACTOR ;
10395	23290		0.46	3.9E-41	11465820	NT	Human fibrinogen 27 gene, exons 10 and 11, and L1 and A1 repeats
10527	23449	38947	0.82	3.9E-41	D56722.1	NT	Porphyria purpurea mitochondrion, complete genome
10693	23685	37397	0.48	3.9E-41	M19446.1	NT	Nicotiana glauca mRNA for TATA binding protein (TBP), complete cds
12219	25088		4.98	3.9E-41	AF304354.1	NT	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
12344	25142		2.01	3.9E-41	Q61670	SWISSPROT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12344	25142		1.49	3.9E-41	11433333	NT	HOMEOBOX PROTEIN HLX1
12344	25142		9.02	3.9E-41	7019489	NT	Homo sapiens hypodermal protein FU10888 (FU10888), mRNA
131	25294		0.3	3.9E-41	AB222520.1	NT	Homo sapiens protein kinase PKNbeta (PKNbeta), mRNA
131	25294		1.9	3.9E-41	BC030876.1	NT	Xba1 muscular pain-1 mRNA for perlecanin m domain, complete cds
1898	15011		1.26	3.9E-41	AF101948.1	NT	Xba1a subclone, section 16 of 228 of the complete genome
24065	15499	26493	1.26	3.9E-41	AF101948.1	NT	Chromatinin b12gase acetyltransferase (ace-1) gene, complete cds
2677	15578	26697	2.20	3.9E-41	AF214171.1	NT	Arabidopsis thaliana positive C-myo-like transcription factor (MYSR3) mRNA, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similarity (Tao) Ht BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
14988	14989	27992	8.4	3.0E-01 P476227.1	NT	Man muscular ribosomal protein S19 (Rps19) gene, complete cds	
2309	14990	27992	3.58	3.0E-01 P476227.1	NT	P. fenguin (F3804) gene for ecotin	
2463	14991	28510	1.28	3.0E-01 Q34263.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds	
2463	14992	28511	1.28	3.0E-01 Q34263.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds	
2463	14993	28511	1.28	3.0E-01 Q34263.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds	
2465	14998	28524	1.93	3.0E-01 AW812033.1	EST_HUMAN	RG5-210777-181098-01-407 ST0171 Homo sapiens cDNA	
						PROTEIN-ISOASPARTATE O-METHYLTRANSFERASE (METHYL-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL METHYLTRANSFERASE)	
2638	15027	26660	1.23	3.0E-01 P24226	SWISSPROT	Disaccharyl isomaltase sugar transporter 3 (sugt) mRNA, complete cds	
2638	15027	26660	1.23	3.0E-01 P24226	SWISSPROT	Disaccharyl isomaltase sugar transporter 3 (sugt) mRNA, complete cds	
3433	15028	26453	5.86	3.0E-01 X76758.1	NT	H.sapiens serothin transporter gene, exon 9 and 10	
3433	15029	26453	2.01	3.0E-01 X76758.1	NT	H.sapiens serothin transporter gene, exon 9 and 10	
3433	15030	26454	2.01	3.0E-01 X76758.1	NT	H.sapiens serothin transporter gene, exon 9 and 10	
4438	14762	30351	1.14	3.0E-01 BE107528.1	EST_HUMAN	HT107045-10000-014-0172 HT1045 Homo sapiens cDNA	
4787	17605	30697	1.72	3.0E-01 Y11528.1	NT	Z.mays mRNA for czech kinase II alpha subunit	
5045	18136	30957	2.61	3.0E-01 AW337693.1	EST_HUMAN	hcdp204.1 NC1 CGAP L201 Homo sapiens cDNA, clone IMAGE:3972568.3	
5136	18145	31025	0.91	3.0E-01 AF037699.1	NT	hcdp204.1 NC1 CGAP L201 Homo sapiens cDNA, clone IMAGE:3972568.3	
5274	18280	31143	0.91	3.0E-01 AF037699.1	NT	hcdp204.1 NC1 CGAP L201 Homo sapiens cDNA, clone IMAGE:3972568.3	
5274	18280	31143	0.91	3.0E-01 AF037699.1	NT	hcdp204.1 NC1 CGAP L201 Homo sapiens cDNA, clone IMAGE:3972568.3	
5274	18280	31144	0.91	3.0E-01 AF037699.1	NT	hcdp204.1 NC1 CGAP L201 Homo sapiens cDNA, clone IMAGE:3972568.3	
5456	18548	31469	0.71	3.0E-01 J400595.1	NT	Gallus gallus Homodomain Protein HX024.3 mRNA, complete cds	
6205	19279	32512	1.1	3.0E-01 P14431	SWISSPROT	Gallus gallus Homodomain Protein HX024.3 mRNA, complete cds	
6205	19281	32512	1.1	3.0E-01 P14431	SWISSPROT	Gallus gallus Homodomain Protein HX024.3 mRNA, complete cds	
7355	20325	32512	3.83	3.0E-01 R04056.1	EST_HUMAN	Gallus gallus Homodomain Protein HX024.3 mRNA, complete cds	
7355	20325	32512	3.83	3.0E-01 R04056.1	EST_HUMAN	Gallus gallus Homodomain Protein HX024.3 mRNA, complete cds	
7900	20405	33826	1.86	3.0E-01 AN02174.1	EST_HUMAN	Gallus gallus Homodomain Protein HX024.3 mRNA, complete cds	
8596	21534	34954	0.56	3.0E-01 P08167	SWISSPROT	Gallus gallus Homodomain Protein HX024.3 mRNA, complete cds	
8623	21590	35078	14.03	3.0E-01 AL161886.2	SWISSPROT	Gallus gallus Homodomain Protein HX024.3 mRNA, complete cds	
						SCD-SPONIN	
						Antibiotic resistance DNA chromosome 4, contig fragment No. 79	
9330	22295	35724	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
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9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds	
9330	22295	35725	0.53	3.0E-01 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3)	

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Table 4
Single Exon Probes Expressed in Bone Marrow

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon ID NO:	ORF-SEQ ID NO:	Expression Signal	Mod Similar (Top) Hit BLAST E Value	Top Hit-Accession No.	Top Hit Database Source	Top Hit-Descriptor
4622	17359	30831	0.7	3.5E-01	N181203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-14 similar to R07878.7 Z0498
4669	17894	30874	8.46	3.5E-01	N181343.1	NT	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-14 similar to R07878.7 Z0498
5407	18510	31957	0.64	3.5E-01	G06987	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5407	18510	31958	0.64	3.5E-01	G06987	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5529	18725	31980	1.36	3.5E-01	I42045.1	NT	Human mRNA N180103.08
5345	19434		0.77	3.5E-01	AW65916.1	EST_HUMAN	Human mRNA N180103.08
6548	19609	32871	0.62	3.5E-01	AA431633.1	EST_HUMAN	Human mRNA N180103.08
5593	19653	32925	0.88	3.5E-01	U37160.1	NT	Human mRNA N180103.08
5621	19875	33764	0.92	3.5E-01	G23535	SWISSPROT	Human mRNA N180103.08
7257	19962	34115	3.85	3.5E-01	G23535	SWISSPROT	Human mRNA N180103.08
7788	20742	34115	0.81	3.5E-01	G23535	SWISSPROT	Human mRNA N180103.08
7788	20742	34116	0.81	3.5E-01	G23535	SWISSPROT	Human mRNA N180103.08
8023	20960	34556	2.37	3.5E-01	N00891.1	NT	Human mRNA N180103.08
8405	21373		0.67	3.5E-01	BF538971.1	EST_HUMAN	Human mRNA N180103.08
8405	21373	34764	0.67	3.5E-01	BF538971.1	EST_HUMAN	Human mRNA N180103.08
8405	21373	34764	0.67	3.5E-01	BF538971.1	EST_HUMAN	Human mRNA N180103.08
8279	22245	35874	1.14	3.5E-01	4507610	NT	Human mRNA N180103.08
10093	23019	36464	8.94	3.5E-01	G002294	SWISSPROT	Human mRNA N180103.08
10246	23171	36960	5.51	3.5E-01	Z29825.1	NT	Human mRNA N180103.08
10326	23250	37279	1.01	3.5E-01	BE174794.1	EST_HUMAN	Human mRNA N180103.08
11086	24047	37569	2.48	3.5E-01	X67034.1	NT	Human mRNA N180103.08
11382	24311	37839	1.88	3.5E-01	AJ243176.1	NT	Human mRNA N180103.08
11382	24311	37839	1.88	3.5E-01	AJ243176.1	NT	Human mRNA N180103.08
11919	24820	38397	1.87	3.5E-01	NT7597.1	EST_HUMAN	Human mRNA N180103.08
11940	24820		1.71	3.5E-01	M8285.1	NT	Human mRNA N180103.08
11991	24888	38463	1.6	3.5E-01	L05145.1	NT	Human mRNA N180103.08
12269	25991		1.8	3.5E-01	AF297468.1	NT	Human mRNA N180103.08
12341	26191		1.31	3.5E-01	X67665.1	NT	Human mRNA N180103.08
12801	28240		2.96	3.5E-01	AE007774.1	NT	Human mRNA N180103.08
13065	28642	37430	3.37	3.5E-01	H68541.1	EST_HUMAN	Human mRNA N180103.08
13085	28642	37431	3.37	3.5E-01	H68541.1	EST_HUMAN	Human mRNA N180103.08

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORE SEQ DNC:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13106	25627		1.57	3.4E-01	4798297	NT	Homo sapiens vert-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuroglobinoma derived oncogene homolog) (EBB82), mRNA
708	13770		1.97	3.4E-01	ALJ24056.1	NT	Homo sapiens perflin Nmyc (xon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from Cx cervical carcinoma cell line
977	14028	26982	0.98	3.4E-01	Y09788.2	NT	Pseudomonas fluorescens cofA, cofB genes, cfr22 and partial inaA gene
1529	14384	27332	2.79	3.4E-01	Y00854.1	NT	Arabidopsis thaliana nifA gene for NifA protein (positive regulatory element)
2810	15477	28441	2.01	3.4E-01	D59098.1	NT	Synchytrium sp. PCO8008 complete genome, 11/27: 1311295-1430418
3074	15872	28862	0.86	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C0510
3074	16072	28863	0.85	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C0510
3175	16320	29146	6.63	3.4E-01	U03905.1	NT	Genis familiens rat photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3354	16405	29326	0.94	3.4E-01	AF33682.1	NT	Homo sapiens pulmonary surfactant protein D promoter region and exon 1
3542	16586	29512	3.42	3.4E-01	AF100835.1	NT	Methylophilus sp. strain SST1 putative Gipe (gpe5), Dnak (Dnak), and putative DnaJ (DnaJ) genes, complete cds
3804	16844		1.78	3.4E-01	BE448010.1	EST_HUMAN	78kDa3.4 NCI CGAP_Oy18 Homo sapiens cDNA clone IMAGE:357223 3' similar to TR-QBU15
4082	17116		1.48	3.4E-01	AA584198.1	EST_HUMAN	ncr1510.1 NCI CGAP_Pivd Homo sapiens cDNA clone IMAGE:100347 3'
4674	17695	30592	1.72	3.4E-01	BE569912.1	EST_HUMAN	NR4-ET0403-232026-202-01: BT0403 Homo sapiens cDNA
4889	18004		4.71	3.4E-01	AI240973.1	EST_HUMAN	g95603.x1 NCI CGAP_K168 Homo sapiens cDNA clone IMAGE:1897208 3' similar to cecidins A11 repulsive element
5768	18690	32040	2.74	3.4E-01	AL161694.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment Nc_30
6509	18905		5.14	3.4E-01	AA08313.1	EST_HUMAN	pm12011 st1 Stralagene INT neuron (m637283) Homo sapiens cDNA clone IMAGE:447221 3'
6122	19200		1.74	3.4E-01	L02971.1	NT	Ectovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6146	19221	32451	0.8	3.4E-01	BE748912.1	EST_HUMAN	EC0187181 NCI_NCC_35 Homo sapiens cDNA clone IMAGE:383826 3'
6229	19303	32519	1.91	3.4E-01	AW204906.1	EST_HUMAN	UHF-BH-mel-K2-U1 NCI CGAP_Su3b Homo sapiens cDNA clone IMAGE:271952 3'
6326	19451	32674	1.78	3.4E-01	AL120544.1	EST_HUMAN	DKF-2761249.t1 T61 (synonym: hnm2) Homo sapiens cDNA clone IMAGE:2761249 5'
6907	19669		1.19	3.4E-01	N95225.1	EST_HUMAN	ab5812.21 Soares, Jozal, Jing, NHL (9W) Homo sapiens cDNA clone IMAGE:307342 3'
7135	20111	35424	1.14	3.4E-01	AI469882.1	EST_HUMAN	hms965.x1 NCI CGAP_Brc25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gp33/431 LAMININ RECEPTOR (HUMAN)
7201	19699	35263	0.91	3.4E-01	BF78702.1	EST_HUMAN	9020833BF1 NCI_NCC_35 Homo sapiens cDNA clone IMAGE:4249366 5'
8233	21207		0.94	3.4E-01	AE000493.1	NT	E. coli K12 MG1655 section 383 of 400 of the complete genome
8973	21507	34995	0.83	3.4E-01	Y11460.1	NT	Homo sapiens TCRBV29 gene, allele A.1, partial
8821	21789		1.8	3.4E-01	AA337063.1	EST_HUMAN	EST141768 Endometrial Tumor Homo sapiens cDNA 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9206	21876	35301	0.64	3.4E-01	U04890.1	NT	Citellus gratus cholesteryl 7 alpha-hydroxylase gene, complete cds
9204	22170	35300	1.89	3.4E-01	9033924	NT	Bovine enterovirus strain 4230, complete genome
9547	22629	35976	4.43	3.4E-01	P25013	SWISSPROT	INTERGRIN BETA3 PRECURSOR
9547	22629	35976	4.43	3.4E-01	P25013	SWISSPROT	INTERGRIN BETA3 PRECURSOR
9776	22717	34627	0.49	3.4E-01	A0017510.1	NT	Elysiptus lycallus mRNA for RGC-aminase, complete cds
9901	21124	34627	0.03	3.4E-01	U18492.1	NT	Saccharomyces cerevisiae MafK1 (MAF1) gene, complete cds
9901	21124	34628	0.03	3.4E-01	U18492.1	NT	Saccharomyces cerevisiae MafK1 (MAF1) gene, complete cds
9835	22791	36243	0.43	3.4E-01	AF163857.1	NT	Discopinae (Discopinae) CYP receptor CYP2C1 mRNA, complete cds
10054	22981	36440	1.09	3.4E-01	U06763.1	NT	Opuntia basilaris transposon-like SCOF-1 (scsf-1) mRNA, complete cds
10248	23174	36594	2.14	3.4E-01	AJ225084.1	NT	Human FGA gene, exon 18, 17 and 18
10843	23783		0.98	3.4E-01	AE044566.1	NT	Viridochlorella thermotolerans, section 4 of 251, of the complete chromosome
11357	24307		3.51	3.4E-01	AE003881.1	NT	Methanobacterium thermophilum from bases 1018444 to 1022212 (section 87 of 148) of the complete genome
11383	24339	37660	4.90	3.4E-01	P09229	SWISSPROT	PROBABLE E4 PROTEIN
11407	24371	37609	1.97	3.4E-01	AF445881.1	NT	Rattus norvegicus cytochrome b (cyt b) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11828	24711	38205	1.98	3.4E-01	AB035607.1	NT	Rattus norvegicus mRNA for s-purinM/C18, complete cds
11828	24738	38323	3.33	3.4E-01	AL161915.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12009	24670	38557	1.8	3.4E-01	AI559903.1	EST - HUMAN	h77p05.x1 NC1_OGAP_U1 Homo sapiens cDNA clone IMAGE2214874 3' similar to contains L1.b1 L1 repetitive element
12149	25038		2.08	3.4E-01	U09004.1	NT	Citrus variegation virus putative replicase gene, partial cds
12201	25035		1.59	3.4E-01	Z21021.1	NT	S. cerevisiae RIB5 gene encoding riboflavin synthase
12485	25231		13.04	3.4E-01	U20336.1	NT	Human autoantigen mRNA, complete cds
12512	25761		3.88	3.4E-01	BE218952.1	EST - HUMAN	hV4204.x1 NC1_OGAP_Lu24 Homo sapiens cDNA clone IMAGE3776127 3' similar to contains P7R13
12597	25805		2.19	3.4E-01	9838301	NT	PTF8 repetitive element
12673	26245	37793	3.46	3.4E-01	AJ1297131.1	NT	Beta vulgaris mitochondrion, complete genome
12673	26245	37793	3.46	3.4E-01	AJ1297131.1	NT	Beta vulgaris SL, MAP, T7, CYP, a, SCL & CYP 3 genes
12872	25538		1.84	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing intercalin X (intercalin-X) gene, partial cds, cytochrome P450 2A1 (P4) and complement component C2 (C2) gene
15	13136	26033	10.37	3.3E-01	X07890.1	NT	Ribulose biphosphate carboxylase (RuBisCO) gene
106	13195	26033	4.34	3.3E-01	X07890.1	NT	Ribulose biphosphate carboxylase (RuBisCO) gene
448	13521	26454	1.3	3.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
684	137001	26821	2.26	3.3E-01	7982485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1205	14244	27203	3.26	3.3E-01	Q12448	SWISSPROT	PROLINE-RICH PROTEIN LAR17
1310	14348	27202	2.44	3.3E-01	BF598860.1	EST_HUMAN	60218401.011 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:430281 3'
1510	14442	27191	1.35	3.3E-01	6759889	NT	Mus musculus aftrinigen 5' (Dnig5), mRNA
1610	14781	27190	1.13	3.3E-01	AA332734.1	EST_HUMAN	EST 19722 Embryo, 3 week 1 Homo sapiens cDNA 5' and
2040	15002		1.01	3.3E-01	AF031148.1	NT	Menyococcus capsulatus strain 84th outer membrane protein Mcd8 (mcd8) gene, complete cds
2414	15421		4.46	3.3E-01	4657834	NT	Homo sapiens uridine monophosphate synthetase (urate phosphoribosyl transferase and orodidine-5'- decarboxylase) (UMP5) mRNA
2600	16018	28945	1.76	3.3E-01	AJ31805.1	NT	Bacillus thuringiensis serovar 421 complete genome
3026	16066		0.8	3.3E-01	AJ31805.1	NT	ENTERIC HT-1 ALPHA CHAIN PRECURSOR (L-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 3) (D SUBUNIT) (CLMP P3)
3068	16125	28938	0.81	3.3E-01	AJ007932.2	NT	Streptococcus pneumoniae serotype 9V capsular polysaccharide genes
3506	16533	28479	1.27	3.3E-01	AJ011292.1	NT	Homo sapiens MTX11.1 gene, complete cds
3622	16662	28769	2.18	3.3E-01	Q46445	SWISSPROT	EXODEXYRIBONUCLEASE 1 (BETA CHAIN)
3832	16972	20773	0.8	3.3E-01	P22902	SWISSPROT	GENOUX POLYPROTEIN CONTAINS N-TERMINAL PROTEIN (P1), HELPER COMPONENT
3969	17026	20939	1.54	3.3E-01	AL161088.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4026	17064	28665	2.02	3.3E-01	AF200448.1	NT	Hypoxylon flagiforme chitin synthase gene, partial cds
4395	17423		1.51	3.3E-01	Q31662.1	NT	Rattus norvegicus DNA for neogutacin, partial cds
4715	17735		1.41	3.3E-01	AJ539114.1	EST_HUMAN	197812.1x1 NCL CGAP_L18 Homo sapiens cDNA clone IMAGE:226407 3' similar to gp-357522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4875	17862	30761	1.33	3.3E-01	Q64003.1	NT	Synthetic yeast sp. POC8803 complete genome, 2227, 2765793-2865765
5397	18500	31377	2.48	3.3E-01	Q58818.1	NT	R-norvegicus mRNA for 3UTR of ubiquitin-like protein
5597	18500	31378	2.48	3.3E-01	Q58818.1	NT	R-norvegicus mRNA for 3UTR of ubiquitin-like protein
5664	18759	31628	0.55	3.3E-01	P36955	SWISSPROT	DYNAMIN
5664	18759	31629	0.55	3.3E-01	P36955	SWISSPROT	DYNAMIN
5884	18873	32160	0.61	3.3E-01	BF213873.1	EST_HUMAN	601848909.F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 3'
6098	19137	32447	1.75	3.3E-01	BE016650.1	EST_HUMAN	601472768.T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3875763 3'
6098	19137	32448	1.75	3.3E-01	BE016650.1	EST_HUMAN	601472768.T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3875763 3'
6154	19229	32459	0.82	3.3E-01	Q59597	SWISSPROT	CIRCUMPOROXOZITIC PROTEIN (CS)
6600	20165	33038	0.63	3.3E-01	AJ042433.1	NT	Fluorobacter litoralis gyrB gene for DNA gyrase B subunit, partial cds
6840	20165	33039	0.63	3.3E-01	AJ042433.1	NT	Fluorobacter litoralis gyrB gene for DNA gyrase B subunit, partial cds
7073	20095	33044	4.16	3.3E-01	AJ828131.1	EST_HUMAN	1944001.X1 NCL CGAP_X1011 Homo sapiens cDNA clone IMAGE:2265909 3' similar to contains AU repetitive element/contains element L1 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	Exon SEQ ID NO.	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7073	20095	33405	4.16	3.3E-01	AB251931.1	EST_HUMAN	Y67071 at NC1_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2285600 3' similar to contains AU repetitive element containing element 1.1 repetitive element.
8052	20696	34395	1.91	3.3E-01	N85146.1	EST_HUMAN	J2404F Human fetal heart Lambda ZAP Express Homo sapiens cDNA clone J2408 5' similar to TEGT
8058	21674	35000	22.93	3.3E-01	B5383594.1	EST_HUMAN	652143372F1 NH1 MGC -48 Homo sapiens cDNA clone IMAGE:307180 5'
9050	22948	35468	0.95	3.3E-01	B5210322.1	EST_HUMAN	651873281F1 NH1 MGC -54 Homo sapiens cDNA clone IMAGE:3097180 5'
9498	22433	35871	0.85	3.3E-01	Q32205	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9733	22761	36215	0.98	3.3E-01	B5382949.1	EST_HUMAN	CM3-ET0041-18050-187-410 E10041 Homo sapiens cDNA
9733	22761	36215	0.98	3.3E-01	B5382949.1	EST_HUMAN	CM3-ET0041-18050-187-410 E10041 Homo sapiens cDNA
9848	23032	36318	2.91	3.3E-01	N08968.1	EST_HUMAN	2467001.51 Sorensen fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:297549 3'
10330	23274	36186	2.91	3.3E-01	B5376745.1	EST_HUMAN	RC4-TN0077-25000-011-p04 TN0077 Homo sapiens cDNA
10330	23274	36186	2.12	3.3E-01	U10444.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGPC) gene, exons 1-3, complete cds
10706	24038	37661	2.65	3.3E-01	X33953.1	NT	D. mauritiana Adh gene
10706	24038	37661	2.65	3.3E-01	X33953.1	NT	D. mauritiana Adh gene
11365	24113	37592	2.16	3.3E-01	B5382499.1	EST_HUMAN	h51022F1 NC1_CGAP_Brd4 Homo sapiens cDNA clone IMAGE:4213385 5'
11565	24503	38052	6.16	3.3E-01	BE210351.1	EST_HUMAN	h51022F1 NC1_CGAP_Lu2 Homo sapiens cDNA clone IMAGE:3176978 3'
11673	24639	38218	3.19	3.3E-01	P47983	SWISSPROT	GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (LECTIN LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-26) (CBP30)
12027	24003	38218	3.43	3.3E-01	AA06622.1	EST_HUMAN	h671025.1 NC1_CGAP_G081 Homo sapiens cDNA clone IMAGE:538950 3'
12044	13135	26033	1.97	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL301 root gene
12246	23075	36170	1.84	3.3E-01	6596318	NT	Homo sapiens aldehyde dehydrogenase 1 (ADH1) mRNA
12658	23500	36170	4.62	3.3E-01	AP000002.1	NT	Proteococcus hutchinsonii OT3 genome DNA, 287001-54000 nt, position (27)
13113	23532	31621	1.59	3.3E-01	B5372620.1	EST_HUMAN	601146730F1 NH1 MGC -18 Homo sapiens cDNA clone IMAGE:316206 3'
457	13530		2.08	3.3E-01	AF018281.1	NT	Rattus norvegicus E1F domain binding protein E1F1B mRNA, complete cds
719	13761		0.76	3.3E-01	AF161581.1	NT	Arabidopsis thaliana RNA chromosome 4, coding region, contig 1
1166	14207	27161	10.8	3.3E-01	AF047813.1	NT	Human p53 gene, 17042-17042 nt, complete cds
1287	14322	27855	1.77	3.3E-01	250202.1	NT	Human p53 gene, 17042-17042 nt, complete cds
1391	14425	27594	5.68	3.3E-01	Q48624	SWISSPROT	LACTOSE FERMENASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1639	14671		0.9	3.3E-01	AF209730.1	NT	Arabidopsis thaliana chloroplast 16S rRNA, complete cds
1769	14818	27803	1.15	3.3E-01	X33641.1	EST_HUMAN	h51022F1 NC1_CGAP_Lu2 Homo sapiens cDNA
1789	14828	27815	5.47	3.3E-01	AW57104.1	EST_HUMAN	EST1658204 IMAGE ressequenced, IMAGE3 Homo sapiens cDNA
1799	14828	27815	5.47	3.3E-01	AW57104.1	EST_HUMAN	EST1658204 IMAGE ressequenced, IMAGE3 Homo sapiens cDNA

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Probe Seq ID NO.	Exon Seq ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1890	14988	27692	1.03	3.2E-01	AL111085.1	NT	Bovine chondrocyte strain 14 cDNA library under conditions of nitrogen deprivation
2168	15182	28205	2.33	3.2E-01	BF203817.1	EST_HUMAN	501168801F1NH_1MGC_17 Homo sapiens cDNA clone IMAGE:411812 5'
2468	15540		2.3	3.2E-01	7110079	NT	Mus musculus Promoter11 homeobox (Ptxcd1), mRNA
2720	15714	28732	0.95	3.2E-01	AF565565.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3622	16635		0.9	3.2E-01	D10872.1	NT	Human hNAT allied 3-2 gene for arylamine N-acetyltransferase
4367	17284	30273	0.93	3.2E-01	4159193	NT	Homo sapiens synaptotagmin (SYN) mRNA
4422	17449	30340	1.82	3.2E-01	M149318.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4526	17551	30439	1.31	3.2E-01	Q1298	SWISSPROT	Proteinase, complete cds
4767	17797		8.32	3.2E-01	BF560817.1	EST_HUMAN	603281079F1NH_1MGC_37 Homo sapiens cDNA clone IMAGE:4248805 5'
4915	17932	30823	0.99	3.2E-01	Q27081	SWISSPROT	CYTADHERENCE RECEPTOR PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) ACCESSORY PROTEIN 3 (P39)
5250	18238	31127	0.96	3.2E-01	A700847.1	NT	Homo sapiens integrin alpha 5 (ITGA5) cDNA clone IMAGE:2485195 3' similar to contains Alu
5290	18286		4.18	3.2E-01	A1980472.1	EST_HUMAN	hva290x.1 NC1 COAP GCSY homologous to cDNA clone IMAGE:2485195 3' similar to contains Alu
5344	18449	31320	2.71	3.2E-01	BE173864.1	EST_HUMAN	resistive element/contains element P7877 homologous to cDNA
6048	18149	32351	1.36	3.2E-01	L27221.1	NT	Gliadin intracellular pyruvate/flavonoid oxidoreductase and binding genes
6495	19502	32763	0.88	3.2E-01	AF018464.1	NT	Fugu (fish) gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete cds
6749	19503	33054	0.91	3.2E-01	A718037.1	EST_HUMAN	AV178037 FRTA Homo sapiens cDNA clone FRTAABH07 5'
6807	19549		1.03	3.2E-01	AB002959.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
6189	21139	34565	0.44	3.2E-01	A1277661.1	NT	Human sapiens partial LMOT1 gene for LM domain only 1 protein, exon 1
8512	21480	34584	1.43	3.2E-01	A160206.1	NT	Rat ISO-alpha1 natural killer factor gene, complete cds
8609	21577	34695	0.46	3.2E-01	A1231001.1	NT	Rattus norvegicus repeat, msp NOS-D12Wcat
8710	21678	35103	16.12	3.2E-01	A02595.1	NT	H sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8713	21685	35108	17.12	3.2E-01	BF11833.1	EST_HUMAN	5011697107F1NH_1MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8835	21712		1.94	3.2E-01	AL101574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8945	21722	35201	1.13	3.2E-01	BF246771.1	EST_HUMAN	501165500F1NH_1MGC_57 Homo sapiens cDNA clone IMAGE:4076627 5'
8945	21812	35232	2.13	3.2E-01	BF246771.1	EST_HUMAN	501165500F1NH_1MGC_57 Homo sapiens cDNA clone IMAGE:4076627 5'
8919	21885	35303	0.63	3.2E-01	A120261.1	NT	Oryzopsis caroliniana R1 section 132 of 229 of the complete chromosome 1
9019	21985	35403	0.63	3.2E-01	A120261.1	NT	Oryzopsis caroliniana R1 section 132 of 229 of the complete chromosome 1
9019	21985	35403	0.63	3.2E-01	A120261.1	NT	Oryzopsis caroliniana R1 section 132 of 229 of the complete chromosome 1

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9422	22387	35828	0.46	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9452	22386		2.28	3.2E-01	M89511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9505	22468	33511		0.45	AF041820.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9505	22468	33912		0.45	AF041820.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10333	23377	39732	3.37	3.2E-01	U14614.1	NT	Bacillus thuringiensis plasmid p33-2, <i>exp</i> and <i>orf</i> genes, complete cds, and unknown genes
10559	23481	39976	0.5	3.2E-01	BE330220.1	EST_HUMAN	h46805.x1 NC1 CGAP, LU24 Homo sapiens cDNA clone IMAGE:3181569.3
10674	23562		3.71	3.2E-01	AB011399.1	NT	Homo sapiens gene for <i>AT-6</i> , complete cds
11028	23992	37519	3.03	3.2E-01	T06813.1	EST_HUMAN	ES104102 Fetal brain, Strategene (cutoff9200) Homo sapiens cDNA clone HEBD221
12265	25900		3.67	3.2E-01	U07288.1	NT	Disophthal melanogaster fibrinogen A (Lam-A) mRNA, complete cds
12674	25943		1.39	3.2E-01	BE686948.1	EST_HUMAN	801678307 NIH-MGC 71 Homo sapiens cDNA clone IMAGE:3906532.5
12804	25431		4.84	3.2E-01	OB33217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12850	25719		1.48	3.2E-01	AF176255.1	NT	Bos taurus insulin 1,4,6-trisphosphate receptor type 1 mRNA, complete cds
12936	25516		1.57	3.2E-01	U13974.1	NT	Homo sapiens deoxyribonuclease desminase gene, complete cds
13001	25925	31393	1.33	3.2E-01	BE385776.1	EST_HUMAN	h46805.x1 NC1 CGAP, OV23 Homo sapiens cDNA clone IMAGE:3218954.3 similar to contains MER10.11
13108	25628	31946	1.38	3.2E-01	A74511.1	EST_HUMAN	MER10.11 negative element
2579	15675	26959	3.02	3.1E-01	R18951.1	EST_HUMAN	h46805.x1 Scores feed liver spleen N1F.53 Homo sapiens cDNA clone IMAGE:125051.5 similar to
2708	15828	28717	4.64	3.1E-01	T06813.1	NT	h46805.x1 NC1 CGAP, LU24 Homo sapiens cDNA clone IMAGE:3906532.5
2708	15828	28718	4.64	3.1E-01	T06813.1	NT	Homo sapiens KIA0074 gene product (KIA0074), mRNA
2659	15929		1.63	3.1E-01	AV162036.1	EST_HUMAN	h46805.x1 Scores N1L_1_G03.51 Homo sapiens cDNA clone IMAGE:2076391.3
3168	15243		4.03	3.1E-01	AB020698.1	NT	Homo sapiens gene for Ssr1731 Kinase KXANIRE, exon 6
3827	19967	29860	0.93	3.1E-01	A74511.1	NT	Mus musculus gene for Ssr1731 Kinase KXANIRE, exon 6
4999	18014	30001	1.25	3.1E-01	AE00384.1	NT	Xyella fastidiosa, section 130 of 229 of the complete genome
5239	18247	31119	0.79	3.1E-01	AF130370.1	NT	Rattus norvegicus MEN1 tumor suppressor (Men1) mRNA, alternative splice product, complete cds
5297	18320	31023	2.99	3.1E-01	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5353	18532	31566	0.78	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5631	18779	31648	0.65	3.1E-01	F44132	SWISSPROT	HYPOPHYSAL PROTEIN H1230
5852	18777	31949	0.87	3.1E-01	Z74883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5853	18788		1.01	3.1E-01	Y13378.1	NT	Mus musculus mRNA for polyoma
5853	18788		1.01	3.1E-01	Y13378.1	NT	Homo sapiens fibronin 2 (FN2) gene, exons 10 through 22
5853	18788		2.3	3.1E-01	AF184122.1	NT	Homo sapiens fibronin 2 (FN2) gene, exons 10 through 22

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8418	25660	32732	0.91	3.1E-01	R64322.1	EST_HUMAN	K4104.1 Scores fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:186367.5
8169	19608	32944	2.69	3.1E-01	AW683546.1	EST_HUMAN	RC3-HR0001.310300-071404 HN0001 Homo sapiens cDNA
6853	19740	33015	0.85	3.1E-01	A284483.1	EST_HUMAN	q39401.x1 NC1_CGAP_C68 Homo sapiens cDNA clone IMAGE:1874689.3
8840	19863	33189	0.88	3.1E-01	X17187.1	NT	H sapiens gene for immunoglobulin kappa light chain variable region J8 and A9
6830	20154	33281	0.7	3.1E-01	AW377354.1	EST_HUMAN	MF2-C10222-281088-005-105 C10222 Homo sapiens cDNA
7162	20634	31238	2.55	3.1E-01	BE73792.1	EST_HUMAN	601309121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3654230.5
7642	20884	34275	0.56	3.1E-01	4895390	NT	Homo sapiens hydrolase synthase 2 (HAS2), mRNA
8038	20975	34371	0.49	3.1E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nai6p) gene, complete cds, and Nai3p gene, exons 2-9 and 11-18
8168	21104	34502	0.54	3.1E-01	AW650166.1	EST_HUMAN	L3-C70215-271099-022E08 C70219 Homo sapiens cDNA
8168	21104	34503	0.54	3.1E-01	AW650166.1	EST_HUMAN	L3-C70215-271099-022E08 C70219 Homo sapiens cDNA
8695	21801	35386	0.83	3.1E-01	R48316.1	EST_HUMAN	Y24801.s1 Scores infant brain TNIB Homo sapiens cDNA clone IMAGE:35639.3
12652	25187	36571	0.32	3.1E-01	6878329	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (PIP5K1c), mRNA
10427	25249	36853	0.1	3.1E-01	BF596639.1	EST_HUMAN	902124743F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:2281611.5
10427	25249	36854	1	3.1E-01	BF596639.1	EST_HUMAN	902124743F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:2281611.5
10488	25410	36607	1.75	3.1E-01	A244001.1	EST_HUMAN	q3141.X1 NC1_CGAP_M88 Homo sapiens cDNA clone IMAGE:1866801.3
10956	25888		0.56	3.1E-01	A5925.1	EST_HUMAN	q47098.X1 Scores fetal liver COX2-HL-CO2-HL PRECORSON (HUMAN)
11188	24142	37576	2.35	3.1E-01	BF216117.1	EST_HUMAN	to c4841038_maf-HEMOGLOBIN GAMMA.A AND GAMMA.G CHAINS (HUMAN)
11884	24748	38528	2.3	3.1E-01	7862261	NT	601863562F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:405814.5
12133	25002	38908	1.68	3.1E-01	AF048693.1	NT	Homo sapiens transcription factor for chondro-lar 7 (FKHL7) gene, complete cds
12133	25002	38909	1.68	3.1E-01	AF048693.1	NT	Homo sapiens transcription factor for chondro-lar 7 (FKHL7) gene, complete cds
12415	25186		1.57	3.1E-01	AF294308.1	NT	Andr61a ovine insulin QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds, mitochondrial gene for mitochondrial product
12451	25210		4.64	3.1E-01	AF041492.1	NT	Stizozetion virusum_40S ribosomal protein S11, mRNA, partial cds
12562	25296		4.19	3.1E-01	AF195053.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12944	25523		3.39	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor IQH1 enhancer 3, JM11 protein, JM5 protein, Tet protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds, and L-type calcium channel α
73	18068	26712	1.78	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
254	13351	26271	8.98	3.0E-01	AJ271735.1	EST_HUMAN	h4531063.x1 NC1_CGAP_X41H1 Homo sapiens cDNA clone IMAGE:274943.3
1227	14265	27222	2.16	3.0E-01	AF050400.1	NT	Ballicoptera phyllula gene encoding arial natriuretic peptide
1508	14841	27512	5.96	3.0E-01	AJ095755.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2146	15182	28178	1.13	3.0E-01	AF227778.1	NT	Rattus norvegicus Cys-histidinol-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3225	16280		1.26	3.0E-01	AB030481.1	NT	Chryseobacterium sp. TLY-1, 1870 gene for polyphosphate kinase, complete cds
3998	17037	29827	1.46	3.0E-01	AW817765.1	EST_HUMAN	PAT-S1026-20, 160,001-601, ST082 Homo sapiens cDNA
4541	17864	30451	1.02	3.0E-01	JA271795.1	NT	Beta sapiens 30, intron/exon junctional region, segment 22
5425	18628	31407	2.17	3.0E-01	AJ006795.1	NT	Human alpha 1(I) procollagen gene encoding alpha 1(I) procollagen
6508	18608	31638	0.98	3.0E-01	AF224698.1	EST_HUMAN	Human alpha 1(I) procollagen, beta A, 105000 (MANBA) gene and ubiquitin-conjugating enzyme E2 3 (UBE2D3) genes, complete cds
6510	18810	31641	0.78	3.0E-01	AF224697.1	NT	Canis lupus familiaris hemagglutinin gene, complete cds
6592	18878	31642	3.81	3.0E-01	BE058715.1	EST_HUMAN	RC3-B10333-180700-111-403 B10333 Homo sapiens cDNA
6592	18878	31642	3.81	3.0E-01	BE058715.1	EST_HUMAN	RC3-B10333-180700-111-403 B10333 Homo sapiens cDNA
6819	19715	31674	4.05	3.0E-01	U01347.1	NT	Mus musculus 129evr Clara cell 10 kd protein (mcc10) gene, complete cds
7005	20131	32348	0.79	3.0E-01	U01347.1	NT	Mouse cyclophilin 15 gene, complete cds
7041	18373	31251	0.95	3.0E-01	AF225047.1	NT	Strongyloides purpuratus 34kD alpha laminin-binding protein mRNA, partial cds
7111	20445	33341	0.95	3.0E-01	AF225047.1	NT	Strongyloides purpuratus 34kD alpha laminin-binding protein mRNA, partial cds
7190	20219	33341	0.95	3.0E-01	AF225047.1	NT	Strongyloides purpuratus 34kD alpha laminin-binding protein mRNA, partial cds
7328	20269	33343	0.82	3.0E-01	AF225047.1	NT	Strongyloides purpuratus 34kD alpha laminin-binding protein mRNA, partial cds
7549	20452	33370	4.66	3.0E-01	AF071810.1	NT	Strongyloides purpuratus 34kD alpha laminin-binding protein mRNA, partial cds
7744	20450	34054	1.33	3.0E-01	AF071810.1	NT	Strongyloides purpuratus 34kD alpha laminin-binding protein mRNA, partial cds
8229	21228	34658	1.28	3.0E-01	AE001755.1	NT	Strongyloides purpuratus 34kD alpha laminin-binding protein mRNA, partial cds
8718	21684		4.13	3.0E-01	9910181	NT	S. cerevisiae GAC1
8819	21788	35210	1.34	3.0E-01	BE060853.1	EST_HUMAN	Human alpha 1(I) procollagen, beta A, 105000 (MANBA) gene and ubiquitin-conjugating enzyme E2 3 (UBE2D3) genes, complete cds
9181	22147	35574	0.74	3.0E-01	AF141976.1	NT	Streptococcus autotrophicus isoprenyl transferase (pbcO) gene, partial cds
9223	22189		0.71	3.0E-01	7861065	NT	Human alpha 1(I) procollagen, beta A, 105000 (MANBA) gene and ubiquitin-conjugating enzyme E2 3 (UBE2D3) genes, complete cds
9573	22335	35886	0.95	3.0E-01	AF220607.1	NT	Antibiotic PC07-20 cyclin-specific DNA methyltransferase (cmtA) gene, complete cds, putative
9582	22859	38320	0.61	3.0E-01	P76389	SWISSPROT	Antibiotic PC07-20 cyclin-specific DNA methyltransferase (cmtA) gene, complete cds, putative
10327	22321	38730	0.73	3.0E-01	BF074912.1	EST_HUMAN	HYPERHE TOAL 59.8 KD PROTEIN IN WZ SV40 TRANSFORMED R338 F
10501	23423	38922	0.47	3.0E-01	AF152598.3	NT	Actinobolus actinomycetorum actin (actA) gene, complete cds, putative
10501	23423	38922	0.47	3.0E-01	AF152598.3	NT	Actinobolus actinomycetorum actin (actA) gene, complete cds, putative
10501	23423	38922	0.47	3.0E-01	AF152598.3	NT	Actinobolus actinomycetorum actin (actA) gene, complete cds, putative
10501	23423	38922	0.47	3.0E-01	AF152598.3	NT	Actinobolus actinomycetorum actin (actA) gene, complete cds, putative

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID No.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10760	23881	37177	0.85	3.0E-01	AW118111.1	EST_HUMAN	h033410.1 Sources, NF- κ B, S1 Homo sapiens cDNA clone IMAGE:26806035 3'
10762	23883	37179	2.14	3.0E-01	AB030231.1	NT	Aspergillus oryzae b3a gene for ER chaperone BIP, complete cds
10763	23884	37201	0.82	3.0E-01	BF383941.1	EST_HUMAN	802140139F NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10764	23703	37203	0.82	3.0E-01	BF383941.1	EST_HUMAN	802140139F NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
12061	24034	38552	5.51	3.0E-01	H101028.1	EST_HUMAN	y544010.1 Sources fetal liver spleen TNF α LS Homo sapiens cDNA clone IMAGE:194107 5'
12062	24034	38552	5.51	3.0E-01	H101028.1	EST_HUMAN	y544010.1 Sources fetal liver spleen TNF α LS Homo sapiens cDNA clone IMAGE:194107 5'
12063	24034	38550	1.57	3.0E-01	AF267531.1	NT	Flattus novogibbus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gadh-2 gene)
12064	24574		2.52	3.0E-01	AB077768	NT	Nus musculus rna5 proto-oncogene and lig2 gene for insulin-like growth factor type 2 and L41ps and A478 pseudogenes
12078	25917		0.92	2.9E-01	AJ240985.1	NT	Acidic serous section 08 of 109 of the complete genome
2039	13058	28077	1.19	2.9E-01	AB020793.1	NT	Y174200000 synovial sarcoma, complete genome
2280	13274	26238	1.2	2.9E-01	AF222718.1	NT	Y174200000 synovial sarcoma, complete genome
3265	16319	29240	1.92	2.9E-01	AW754289.1	EST_HUMAN	Y174200000 synovial sarcoma, complete genome
3265	16319	29241	1.92	2.9E-01	AW754289.1	EST_HUMAN	Y174200000 synovial sarcoma, complete genome
3912	16852	29893	1.03	2.9E-01	AF108361.1	EST_HUMAN	ZINC FINGER PROTEIN H141032 Homo sapiens cDNA clone IMAGE:2402603 3'
3985	16995	29911	0.81	2.9E-01	AF108472.1	EST_HUMAN	ZINC FINGER PROTEIN H141032 Homo sapiens cDNA clone IMAGE:2402603 3'
4112	17145		0.77	2.9E-01	AW002602.1	EST_HUMAN	Y174200000 synovial sarcoma, complete genome
4511	17538	30420	1.24	2.9E-01	AA284468.1	EST_HUMAN	Y174200000 synovial sarcoma, complete genome
4710	17731		1.5	2.9E-01	AL183207.2	NT	Y174200000 synovial sarcoma, complete genome
5195	18166		1.25	2.9E-01	AF070890.1	EST_HUMAN	Y174200000 synovial sarcoma, complete genome
5275	18281	31145	3.3	2.9E-01	AJ131017.1	NT	Y174200000 synovial sarcoma, complete genome
5277	18283	31146	1.12	2.9E-01	BE741390.1	EST_HUMAN	Y174200000 synovial sarcoma, complete genome
5330	18438		1.49	2.9E-01	BF37485.1	EST_HUMAN	Y174200000 synovial sarcoma, complete genome
5493	20085	33572	0.76	2.9E-01	AF1921001.1	NT	Y174200000 synovial sarcoma, complete genome
5836	18946	32133	5.1	2.9E-01	X50908.1	NT	B subtilis leucine operon lnc, lncE, lncF, lncG, lncH, lncI, lncJ, lncK, lncL, lncM, lncN, lncO, lncP, lncQ, lncR, lncS, lncT, lncU, lncV, lncW, lncX, lncY, lncZ, lncAA, lncAB, lncAC, lncAD, lncAE, lncAF, lncAG, lncAH, lncAI, lncAJ, lncAK, lncAL, lncAM, lncAN, lncAO, lncAP, lncAQ, lncAR, lncAS, lncAT, lncAU, lncAV, lncAW, lncAX, lncAY, lncAZ, lncBA, lncBB, lncBC, lncBD, lncBE, lncBF, lncBG, lncBH, lncBI, lncBJ, lncBK, lncBL, lncBM, lncBN, lncBO, lncBP, lncBQ, lncBR, lncBS, lncBT, lncBU, lncBV, lncBW, lncBX, lncBY, lncBZ, lncCA, lncCB, lncCC, lncCD, lncCE, lncCF, lncCG, lncCH, lncCI, lncCJ, lncCK, lncCL, lncCM, lncCN, lncCO, lncCP, lncCQ, lncCR, lncCS, lncCT, lncCU, lncCV, lncCW, lncCX, lncCY, lncCZ, lncDA, lncDB, lncDC, lncDD, lncDE, lncDF, lncDG, lncDH, lncDI, lncDJ, lncDK, lncDL, lncDM, lncDN, lncDO, lncDP, lncDQ, lncDR, lncDS, lncDT, lncDU, lncDV, lncDW, lncDX, lncDY, lncDZ, lncEA, lncEB, lncEC, lncED, lncEE, lncEF, lncEG, lncEH, lncEI, lncEJ, lncEK, lncEL, lncEM, lncEN, lncEO, lncEP, lncEQ, lncER, lncES, lncET, lncEU, lncEV, lncEW, lncEX, lncEY, lncEZ, lncFA, lncFB, lncFC, lncFD, lncFE, lncFF, lncFG, lncFH, lncFI, lncFJ, lncFK, lncFL, lncFM, lncFN, lncFO, lncFP, lncFQ, lncFR, lncFS, lncFT, lncFU, lncFV, lncFW, lncFX, lncFY, lncFZ, lncGA, lncGB, lncGC, lncGD, lncGE, lncGF, lncGG, lncGH, lncGI, lncGJ, lncGK, lncGL, lncGM, lncGN, lncGO, lncGP, lncGQ, lncGR, lncGS, lncGT, lncGU, lncGV, lncGW, lncGX, lncGY, lncGZ, lncHA, lncHB, lncHC, lncHD, lncHE, lncHF, lncHG, lncHH, lncHI, lncHJ, lncHK, lncHL, lncHM, lncHN, lncHO, lncHP, lncHQ, lncHR, lncHS, lncHT, lncHU, lncHV, lncHW, lncHX, lncHY, lncHZ, lncIA, lncIB, lncIC, lncID, lncIE, lncIF, lncIG, lncIH, lncII, lncIJ, lncIK, lncIL, lncIM, lncIN, lncIO, lncIP, lncIQ, lncIR, lncIS, lncIT, lncIU, lncIV, lncIW, lncIX, lncIY, lncIZ, lncJA, lncJB, lncJC, lncJD, lncJE, lncJF, lncJG, lncJH, lncJI, lncJJ, lncJK, lncJL, lncJM, lncJN, lncJO, lncJP, lncJQ, lncJR, lncJS, lncJT, lncJU, lncJV, lncJW, lncJX, lncJY, lncJZ, lncKA, lncKB, lncKC, lncKD, lncKE, lncKF, lncKG, lncKH, lncKI, lncKJ, lncKK, lncKL, lncKM, lncKN, lncKO, lncKP, lncKQ, lncKR, lncKS, lncKT, lncKU, lncKV, lncKW, lncKX, lncKY, lncKZ, lncLA, lncLB, lncLC, lncLD, lncLE, lncLF, lncLG, lncLH, lncLI, lncLJ, lncLK, lncLL, lncLM, lncLN, lncLO, lncLP, lncLQ, lncLR, lncLS, lncLT, lncLU, lncLV, lncLW, lncLX, lncLY, lncLZ, lncMA, lncMB, lncMC, lncMD, lncME, lncMF, lncMG, lncMH, lncMI, lncMJ, lncMK, lncML, lncMN, lncMO, lncMP, lncMQ, lncMR, lncMS, lncMT, lncMU, lncMV, lncMW, lncMX, lncMY, lncMZ, lncNA, lncNB, lncNC, lncND, lncNE, lncNF, lncNG, lncNH, lncNI, lncNJ, lncNK, lncNL, lncNM, lncNO, lncNP, lncNQ, lncNR, lncNS, lncNT, lncNU, lncNV, lncNW, lncNX, lncNY, lncNZ, lncOA, lncOB, lncOC, lncOD, lncOE, lncOF, lncOG, lncOH, lncOI, lncOJ, lncOK, lncOL, lncOM, lncON, lncOO, lncOP, lncOQ, lncOR, lncOS, lncOT, lncOU, lncOV, lncOW, lncOX, lncOY, lncOZ, lncPA, lncPB, lncPC, lncPD, lncPE, lncPF, lncPG, lncPH, lncPI, lncPJ, lncPK, lncPL, lncPM, lncPN, lncPO, lncPP, lncPQ, lncPR, lncPS, lncPT, lncPU, lncPV, lncPW, lncPX, lncPY, lncPZ, lncQA, lncQB, lncQC, lncQD, lncQE, lncQF, lncQG, lncQH, lncQI, lncQJ, lncQK, lncQL, lncQM, lncQN, lncQO, lncQP, lncQQ, lncQR, lncQS, lncQT, lncQU, lncQV, lncQW, lncQX, lncQY, lncQZ, lncRA, lncRB, lncRC, lncRD, lncRE, lncRF, lncRG, lncRH, lncRI, lncRJ, lncRK, lncRL, lncRM, lncRN, lncRO, lncRP, lncRQ, lncRR, lncRS, lncRT, lncRU, lncRV, lncRW, lncRX, lncRY, lncRZ, lncSA, lncSB, lncSC, lncSD, lncSE, lncSF, lncSG, lncSH, lncSI, lncSJ, lncSK, lncSL, lncSM, lncSN, lncSO, lncSP, lncSQ, lncSR, lncSS, lncST, lncSU, lncSV, lncSW, lncSX, lncSY, lncSZ, lncTA, lncTB, lncTC, lncTD, lncTE, lncTF, lncTG, lncTH, lncTI, lncTJ, lncTK, lncTL, lncTM, lncTN, lncTO, lncTP, lncTQ, lncTR, lncTS, lncTT, lncTU, lncTV, lncTW, lncTX, lncTY, lncTZ, lncUA, lncUB, lncUC, lncUD, lncUE, lncUF, lncUG, lncUH, lncUI, lncUJ, lncUK, lncUL, lncUM, lncUN, lncUO, lncUP, lncUQ, lncUR, lncUS, lncUT, lncUU, lncUV, lncUW, lncUX, lncUY, lncUZ, lncVA, lncVB, lncVC, lncVD, lncVE, lncVF, lncVG, lncVH, lncVI, lncVJ, lncVK, lncVL, lncVM, lncVN, lncVO, lncVP, lncVQ, lncVR, lncVS, lncVT, lncVU, lncVV, lncVW, lncVX, lncVY, lncVZ, lncWA, lncWB, lncWC, lncWD, lncWE, lncWF, lncWG, lncWH, lncWI, lncWJ, lncWK, lncWL, lncWM, lncWN, lncWO, lncWP, lncWQ, lncWR, lncWS, lncWT, lncWU, lncWV, lncWW, lncWX, lncWY, lncWZ, lncXA, lncXB, lncXC, lncXD, lncXE, lncXF, lncXG, lncXH, lncXI, lncXJ, lncXK, lncXL, lncXM, lncXN, lncXO, lncXP, lncXQ, lncXR, lncXS, lncXT, lncXU, lncXV, lncXW, lncXX, lncXY, lncXZ, lncYA, lncYB, lncYC, lncYD, lncYE, lncYF, lncYG, lncYH, lncYI, lncYJ, lncYK, lncYL, lncYM, lncYN, lncYO, lncYP, lncYQ, lncYR, lncYS, lncYT, lncYU, lncYV, lncYW, lncYX, lncYY, lncYZ, lncZA, lncZB, lncZC, lncZD, lncZE, lncZF, lncZG, lncZH, lncZI, lncZJ, lncZK, lncZL, lncZM, lncZN, lncZO, lncZP, lncZQ, lncZR, lncZS, lncZT, lncZU, lncZV, lncZW, lncZX, lncZY, lncZZ

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	OFF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
13028	25573	31895	1.35	2.8E-01	U09837.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
570	13940		2.2	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
575	13944		1.41	2.8E-01	U28145.1	NT	Quail dwarf locus movement protein, complete cds; owl protein, complete cds
1085	14129	27083	3.9	2.8E-01	AF168950.1	NT	Quail dwarf locus movement factor Mof (c-mos) gene, partial cds
1282	14317	27270	1.06	2.8E-01	BE313442.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
1283	14317	27260	1.06	2.8E-01	BE313442.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
1285	14330	27291	2.85	2.8E-01	D96550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1740	14770	27758	2.22	2.8E-01	AW68020.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
2028	15048	28052	2.08	2.8E-01	AL047402.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
2141	15158	28174	1.81	2.8E-01	AW511165.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
2475	15483	28507	2.18	2.8E-01	AE000484.1	NT	Escherichia coli K12 MG1655 section 384 of 400 of the complete genome
2476	15483	28508	2.18	2.8E-01	AE000484.1	NT	Escherichia coli K12 MG1655 section 384 of 400 of the complete genome
2554	15538		3.07	2.8E-01	AL151955.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 65
2574	15671	28680	1.35	2.8E-01	AB222975.1	NT	Arabidopsis thaliana DNA for topoisomerase, complete cds
2602	16040		1.48	2.8E-01	AF133450.1	NT	Arabidopsis thaliana DNA for topoisomerase, complete cds
2602	16040		1.48	2.8E-01	AF133450.1	NT	Arabidopsis thaliana DNA for topoisomerase, complete cds
3083	18041	28962	2.57	2.8E-01	U14037.1	NT	Human mRNA for transcription factor AREB8, complete cds
3390	18439	29565	1.16	2.8E-01	AF000094.1	NT	Human mRNA for transcription factor AREB8, complete cds
4021	17059	29660	1.12	2.8E-01	AE001165.1	NT	Human mRNA for transcription factor AREB8, complete cds
4120	17181		0.97	2.8E-01	AE004461.1	NT	Human mRNA for transcription factor AREB8, complete cds
4226	17295		2.41	2.8E-01	AD009898.1	EST_HUMAN	Human mRNA for transcription factor AREB8, complete cds
4498	17513	30401	2.62	2.8E-01	U13161.1	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4822	17839	30737	0.92	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB8, complete cds
4822	17839	30739	0.92	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB8, complete cds
4896	17893	30771	2.71	2.8E-01	AF030154.1	NT	Human mRNA for transcription factor AREB8, complete cds
4907	17914	30804	1.37	2.8E-01	BF523186.1	EST_HUMAN	Human mRNA for transcription factor AREB8, complete cds
4920	17937	30829	1.69	2.8E-01	A1272889.1	EST_HUMAN	Human mRNA for transcription factor AREB8, complete cds
5384	29537	31822	23.73	2.8E-01	AA546997.1	EST_HUMAN	Human mRNA for transcription factor AREB8, complete cds
6697	18782	31954	2.52	2.8E-01	AB0116625.1	NT	Human mRNA for transcription factor AREB8, complete cds
5915	19001		1.94	2.8E-01	AA095958.1	EST_HUMAN	Human mRNA for transcription factor AREB8, complete cds
6028	19111	32315	0.87	2.8E-01	AA765298.1	EST_HUMAN	Human mRNA for transcription factor AREB8, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mod Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12684	25351		23.64	2.8E-01	D83226.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12688	25420	31798	3.00	2.9E-01	BE178699.1	EST_HUMAN	PM4-1170602-23040-001-e07 HT0650 Homo sapiens cDNA
12691	25439	31742	1.37	2.8E-01	BE902116.1	EST_HUMAN	PM16730207 NH MG-21 Homo sapiens cDNA clone IMAGE:385994 5'
12699	25579		3.15	2.8E-01	11433629	NT	Homo sapiens CD45-binding protein kinase beta (CDK-189) mRNA
13067	26373		1.76	2.8E-01	AW025400.1	EST_HUMAN	w086053-1 NC1 CGAP-7638 Homo sapiens cDNA clone IMAGE:362768 3'
4771	13348	26477	2.85	2.7E-01	Y17324.1	NT	RefSeq noncoding cDNA (ncRNA)
615	13860	26598	9.43	2.7E-01	AA650061.1	EST_HUMAN	Z68810.61 Scores: local BLAST_Hs_Hs Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
12691	14301	27252	2.18	2.7E-01	AB004006.1	NT	Ipomoea purpurea transposable element TIR100 gene for transposase, complete cds
1625	14658		2.21	2.7E-01	X79815.1	NT	z221010.1 Scores: local BLAST_Hs_Hs Homo sapiens cDNA clone IMAGE:341443 5'
11425	14772	27937	2.88	2.7E-01	W96087.1	EST_HUMAN	GAG POLYPROTEIN CONTAINS: INNER COAT PROTEIN P12, CORE PROTEIN P16, CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10
1791	14820		2.49	2.7E-01	P08341	SWISSPROT	RefSeq noncoding vesicular monoamine transporter type 2, promoter region and exon 1
2143	15363		2.28	2.7E-01	AF347575.1	NT	Feline immunodeficiency virus env gene, isolated HT098P17 (M85), partial
2375	15363	28405	9.35	2.7E-01	130688.1	NT	h48311.12 NCL CGAP-7625 Homo sapiens cDNA clone IMAGE:3046839 3' similar to contains element 1
2461	15465	28468	3.07	2.7E-01	A1810858.1	EST_HUMAN	Human protein inhibitor 1 (Sp14) mRNA, complete cds
2693	15968	28801	1	2.7E-01	AF253278.1	NT	Human protein inhibitor 1 (Sp14) mRNA, complete cds
2697	16055		0.81	2.7E-01	BF038264.1	EST_HUMAN	GM111097-0400203-088-028 HT0955 Homo sapiens cDNA
4038	17070	29076	1.74	2.7E-01	A0282015.1	EST_HUMAN	w092411.1 NC1 C2432-1 G3T1 Homo sapiens cDNA, clone IMAGE:2462838 3'
4053	17090	29085	0.76	2.7E-01	AF218214.1	NT	Oncofetal bursall alpha-subunit 6 (AE6) gene, partial cds
4053	17090	29086	0.76	2.7E-01	AF218214.1	NT	Oncofetal bursall alpha-subunit 6 (AE6) gene, partial cds
4061	17097	29091	2.33	2.7E-01	AF27589.1	NT	Homo sapiens D3George syndrome critical region, noncoding end
4828	17646	30837	0.76	2.7E-01	U75516.1	NT	Tritium seedbank (W2568) gene, complete cds
5079	18080		4.11	2.7E-01	AW686131.1	EST_HUMAN	R1C110286-230200-016-403 GT0286 Homo sapiens cDNA
5339	18444	31197	2.13	2.7E-01	P17277	SWISSPROT	Human myoblasts mitochondrial c10 gene for cytochrome 1, partial cds
5567	18624		1.11	2.7E-01	AB033171.1	NT	Latent transforming growth factor beta binding protein 1 (TF-beta1-BP-1) (transforming growth factor beta-1 masking protein, large subunit)
6476	19541	32787	0.51	2.7E-01	Q00918	SWISSPROT	Latent transforming growth factor beta binding protein 1 (TF-beta1-BP-1) (transforming growth factor beta-1 masking protein, large subunit)
6476	19541	32788	0.51	2.7E-01	Q00918	SWISSPROT	Latent transforming growth factor beta binding protein 1 (TF-beta1-BP-1) (transforming growth factor beta-1 masking protein, large subunit)
6765	19819	33100	1.00	2.7E-01	AED01094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

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Probe SEQ ID NC	Exon SEQ ID NC	ORF SEQ ID NO	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6755	19819	33101	1.06	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6756	20170	33164	2.1	2.7E-01	Q61954	SWISSPROT	FIBRILLIN 1 PRECURSOR
7263	16688	33011	0.64	2.7E-01	AG64070.1	EST_HUMAN	UG6808LX1 NC1 CGAP CLL1 Homo sapiens cDNA clone IMAGE:2079103 3'
7590	20942	33001	0.8	2.7E-01	Q11079	SWISSPROT	HYPOHECTAL 20.9 KD PROTEIN B0693.3 IN CHROMOSOME X
7811	20760	34135	0.85	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7811	20760	34136	0.85	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7811	20760	34136	0.85	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7952	20893	34285	1.9	2.7E-01	AF248954.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7952	20893	34285	1.9	2.7E-01	AF248954.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8012	20950	34343	0.86	2.7E-01	AA351121.1	EST_HUMAN	EST 18740 Infant brain Homo sapiens cDNA 3' and similar to similar to hypothetical protein H
8012	20950	34344	0.86	2.7E-01	AA351121.1	EST_HUMAN	EST 18740 Infant brain Homo sapiens cDNA 3' and similar to similar to hypothetical protein H
8084	21021	34421	0.83	2.7E-01	L07081.1	NT	Cryoblagus cuticular UDP-glucosyltransferase (UG 2B 3) mRNA, complete cds
8185	21185	34576	0.86	2.7E-01	A401347.1	EST_HUMAN	ae03071 rat Soares retina N26-RH Homo sapiens cDNA clone IMAGE:300587 3' similar to contains Alu repetitive element.
8300	21329	34661	0.82	2.7E-01	AF148203.1	NT	Carassius auratus pulchellus adenylate cyclase activating polypeptide type 1 (receptor precursor mRNA, complete cds)
8475	21444	34661	0.83	2.7E-01	AF148203.1	EST_HUMAN	hMT-SN0692-105504-002-009 SN0692 Homo sapiens cDNA
8527	21485	34665	0.82	2.7E-01	AF168503.1	EST_HUMAN	hMT008 at Soares infant brain N108 Homo sapiens cDNA clone IMAGE:23311 3'
8654	21602	35283	0.74	2.7E-01	AL161562.2	NT	A. tubidipennis Italian DNA chromosome 4 contig fragment No. 52
8712	22078	35955	0.82	2.7E-01	Q17074	SWISSPROT	MAJOR VALLT PROTEIN (MP) (LUNG RESISTANCE-RELATED PROTEIN)
8902	22347	35719	0.81	2.7E-01	Q17074	NT	Staphylococcus aureus transposon Tn054
8989	22531	35665	1.08	2.7E-01	Q08609	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRS)
9588	22531	35665	1.08	2.7E-01	Q08609	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRS)
9651	22644	35665	1.17	2.7E-01	P07928	SWISSPROT	FINMERAE W PROTEIN
10146	23045	36562	0.94	2.7E-01	D06990.1	NT	Rattus norvegicus DNA for perlecanin assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10491	23383	36853	0.85	2.7E-01	AF091848.1	NT	Oryzopsis latifolia adenylylase cDNA, partial cds
10491	23383	36853	0.85	2.7E-01	AF091848.1	NT	Oryzopsis latifolia adenylylase cDNA, partial cds
10711	23533	37029	1.06	2.7E-01	AF156535.1	NT	Male musculus transcription factor NF-ATc1 (NF-A1) mRNA, complete cds
10711	23533	37029	1.06	2.7E-01	AF156535.1	NT	Male musculus transcription factor NF-ATc1 (NF-A1) mRNA, complete cds
10911	23533	37030	1.06	2.7E-01	AF156536.1	NT	Homo sapiens xenodermis pigmentum complementation group C (XPC) gene, Intron 9
11183	24121	37648	4.87	2.7E-01	AF170943.1	EST_HUMAN	Homo sapiens xenodermis pigmentum complementation group C (XPC) gene, Intron 9
11183	24121	37648	4.87	2.7E-01	AF170943.1	EST_HUMAN	AV705943 ADB Homo sapiens cDNA clone ADBC0005 5'
11183	24121	37649	4.87	2.7E-01	AF170943.1	EST_HUMAN	AV705943 ADB Homo sapiens cDNA clone ADBC0005 5'

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11171	24728	37659	2.31	2.7E-01	AJ132269.1	NT	Homo sapiens caveolin-1/2 locus, CAV1p1, D78522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12056	24839		2.08	2.7E-01	BE1141036.1	EST_HUMAN	MRP11/TOB1/201099-02-010 HT0097 Homo sapiens cDNA
12060	24861		1.52	2.7E-01	Q14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C48H05C
12069	25244	31802	1.39	2.7E-01	AL162281.2	NT	Homo sapiens chromosome 21 segment HS21C081
12757	25755		1.46	2.7E-01	AB000782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12851	25460		1.63	2.7E-01	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN R44
12848	25526		3.16	2.7E-01	AF217491.1	NT	Homo sapiens fragile 160 kDa redoxin (FOR) gene, exon 6
470	13541	25470	1.97	2.6E-01	P78411	SWISSPROT	IRQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
481	13554		1.51	2.6E-01	D10496.1	NT	Bot taurus mRNA for mb-1, complete cds
1364	14428	27397	1.60	2.6E-01	B638067.1	EST_HUMAN	BT015083P1 NIH_JGC_71 Homo sapiens cDNA clone IMAGE3972345 5'
1431	14463	27441	1.39	2.6E-01	AB013260.1	NT	Glycine max pseudogene for B4 30K
1672	14633	27851	6.4	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment Nc. 2
1672	14633	27852	8.4	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment Nc. 2
2104	15121		7.46	2.6E-01	AY735152.1	EST_HUMAN	RIBOSOMAL PROTEIN L7A (HUMAN); gb:U4689_ods1 Mouse surfeit locus protein 3 protein gene (MOUSE)
2460	15464		0.99	2.6E-01	U298X1	NT	D. rerio rtd, gene
2553	15555		8.34	2.6E-01	BE2540.1	EST_HUMAN	BT172019P1 NIH_JGC_9 Homo sapiens cDNA clone IMAGE2990049 5'
3108	16105		1.02	2.6E-01	AB074591.1	EST_HUMAN	EST T38033 IMAGE sequences, MAGM Homo sapiens cDNA
3594	16939	26559	1.02	2.6E-01	M2242.1	NT	Baculovirus 72 DNA (epitome-N) methyltransferase (dam) gene, complete cds
3657	16700	25516	2.11	2.6E-01	AF220118.1	NT	Homo sapiens acylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3982	17022	26932	0.71	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii rps18a gene for Ribosome P RNA subunit
3982	17022	26933	0.71	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii rps18a gene for Ribosome P RNA subunit
4181	17212	30100	17.99	2.6E-01	BE060596.1	EST_HUMAN	OV-1/BT009450-001-132-003 BT0030 Homo sapiens cDNA
4384	17412	30296	1.39	2.6E-01	AF176303.1	NT	Entherococcus faecalis strain N97-330 vno glycoprotein resistance gene cluster, complete cds; and unknown gene
4522	17547	30434	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4522	17547	30435	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4579	17601	30487	1.47	2.6E-01	AA457617.1	EST_HUMAN	sa05007.1 Strizagenes fida retina R37202-Homo sapiens cDNA clone IMAGE-83477 5'
4671	17698	30565	2.31	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3) mRNA, complete cds
4745	17765	30659	1.46	2.6E-01	AF442703.1	NT	Ophiostoma nidiosus mannanase-like protein (mNk) gene, complete cds; chloroplast gene for chloroplast product

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (70%) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9042	22008	35426	4.00	2.6E-01	BE60339.1	EST_HUMAN	RC5-E10082-31080-021-F10 E10082 Homo sapiens cDNA
9614	22009	35428	4.00	2.6E-01	BE60339.1	EST_HUMAN	RC5-E10082-31080-021-F10 E10082 Homo sapiens cDNA
9822	22671	36128	0.99	2.6E-01	X17604.1	NT	S. cerevisiae INV. gene for invertase (EC 3.2.1.26)
10096	23022		0.93	2.6E-01	AF087121.1	NT	Leontine canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10227	23162	36041	1.08	2.6E-01	AF97369	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10227	23162	36042	1.08	2.6E-01	AF97369	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10550	23472		0.61	2.6E-01	Q33295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10575	23795		0.91	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10678	23895		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11694	24730		32.27	2.6E-01	X31763.1	NT	Human lambda5-immunoglobulin constant region complex (germline)
12464	25693		2.77	2.6E-01	10190855	NT	Mus musculus jerry (jry), mRNA
12464	25693		3.33	2.6E-01	BE983491.1	EST_HUMAN	6015105251 NIH MGC_71 Homo sapiens cDNA clone IMAGE3912617.5'
12523	25297	31906	4.42	2.6E-01	AF130895.1	NT	Homo sapiens NucleoXpress gamma subunit (NXTD2) gene, complete cds, alternatively spliced
12846	25456		2.01	2.6E-01	Q98423.1	NT	Cmna codaya mRNA for acetylcholine kinase, complete cds
12874	25535		1.74	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
13010	25952		3.07	2.6E-01	AF4785.1	SWISSPROT	HYPOPHOSPHATE PROTEIN MG039
241	13340	20268	2.33	2.5E-01	4842286	NT	Homo sapiens ATP synthase, H ⁺ -transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	13340	20268	1.07	2.5E-01	4842286	NT	Homo sapiens ATP synthase, H ⁺ -transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
259	13352		4.83	2.5E-01	M25501.1	NT	Staphylococcus epidermidis cytoplasmic acid gene, complete cds
833	13800	26844	1.87	2.5E-01	U00864.1	NT	Mus musculus C9orf36a phosphatase 3-phosphatase dehydrogenase (Gpd3L) gene, complete cds
1128	14167	27119	9.8	2.5E-01	T06937.1	EST_HUMAN	2611607.r1 Staphylococcus aureus (832720) Homo sapiens cDNA clone IMAGE117488.5'
1922	14564	27526	1.55	2.5E-01	AL115624.1	NT	Bos taurus alpha-actin 14 cDNA library under conditions of nitrogen deprivation
1741	14771		5.06	2.5E-01	48854506	NT	Homo sapiens hypoxanthine phosphoribosyl transferase, nuclear gene, complete cds
1800	15880	27020	0.94	2.5E-01	BE606994.1	EST_HUMAN	PM4-CT9400-310700-005-008 CT9400 Homo sapiens cDNA
1800	15880	27921	0.94	2.5E-01	BE606994.1	EST_HUMAN	PM4-CT9400-310700-005-008 CT9400 Homo sapiens cDNA
2417	15424		13.96	2.5E-01	AE003975.1	NT	Acetivibrio salicinarum section 7 of 109 of the complete genome
2603	16006		1.06	2.5E-01	AA251987.1	EST_HUMAN	2611612.r1 NC_CG81 Homo sapiens cDNA clone IMAGE384862.5'
2644	15841	28065	0.94	2.5E-01	X09510.1	NT	B. subtilis mRNA for D-aspartate oxidase
3423	16471		2.83	2.5E-01	AW673471.1	EST_HUMAN	EST1954644 IMAGE384862.5' resequencing, MAGM Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3548	16591	28516	0.87	2.5E-01	AF233876.1	NT	Danio rerio papilio YY precursor gene, complete cds
3590	16906	29526	7.94	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3591	16906	29526	1.15	2.5E-01	AF174483.1	EST_HUMAN	wt11607.x1 Soares NSF_F8 JW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3284760 3
3591	16906	29526	1.15	2.5E-01	AF174483.1	EST_HUMAN	wt11607.x1 Soares NSF_F8 JW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3284760 3
4058	17130	29604	1.76	2.5E-01	F32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4349	17373		0.99	2.5E-01	Q03314	SWISSPROT	PRIS PROTEIN
4780	17600		1.34	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (Mh)
4780	17606	30598	4.71	2.5E-01	AF007788.1	NT	Chromolaena litoralis diaphane associated protein 2 (DAP2) mRNA, complete cds
4821	17538	30736	2.32	2.5E-01	AE004416.1	NT	Mus musculus chromosome 1, section 13 of 93 of the contig subchromosomes
4840	17837		3.69	2.5E-01	AL230113.1	NT	Mus musculus smooth y gene, full length 4 segment containing 5' UTR and gag portion of MEERVL (murine)
4870	17887	30775	0.84	2.5E-01	BE006703.1	EST_HUMAN	h92711.4 Soares NLF_1_GBC_S1 Homo sapiens cDNA clone IMAGE:3022600 5
5085	18096	30972	0.84	2.5E-01	AF875988.1	EST_HUMAN	WIP-Y1FRA_284.D.022858
5343	18251		0.96	2.5E-01	AA768390.1	EST_HUMAN	cellular 1 NOL_C28AP_C081 Homo sapiens cDNA clone IMAGE:1316020 3 similar to contains AU repetitive element
5395	18323	31380	13.56	2.5E-01	SS3390.1	NT	T3 receptor-associating collectin-1 (human, fetal liver, mRNA, 2830 nt)
6070	19151	32353	0.64	2.5E-01	AJ006346.1	NT	Homo sapiens KVLQ11 gene
6071	19152		0.87	2.5E-01	AL163072.2	NT	Homo sapiens chromosome 21 segment HS210007
6525	19566	32847	0.48	2.5E-01	P22129	SWISSPROT	PROTEIN KINASE VP815
6760	19833	33118	0.86	2.5E-01	AJ251973.1	NT	Homo sapiens partial atserin-1 gene
7245	19980	33277	0.8	2.5E-01	8394138	NT	Rattus norvegicus rbn 3 (RABIN3), mRNA
7515	20357	33896	0.79	2.5E-01	U13892.1	NT	Feline calicivirus CB168 RNA helicase/cytosine protease/RNA-dependent RNA polymerase precursor and capsid protein precursor, genes, complete cds, and unknown gene
7804	20955		1.13	2.5E-01	AF134119.1	NT	Mus musculus SKO1 (Skd1) gene, complete cds
7892	20798	34174	0.68	2.5E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7996	20941	34223	3.88	2.5E-01	AL163082.2	NT	Homo sapiens chromosome 21 segment HS210082
8177	21147	34555	2.72	2.5E-01	BF109040.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS210082
8186	21156	34557	0.62	2.5E-01	BF090712.1	EST_HUMAN	60168339R2 NH_MGC_66 Homo sapiens cDNA clone IMAGE:362818 3
8996	21536	34596	2.02	2.5E-01	BF038956.1	EST_HUMAN	60146228F1 NH_MGC_66 Homo sapiens cDNA clone IMAGE:3692800 5
8740	21708	35151	0.67	2.5E-01	P04492	SWISSPROT	EB1 PROTEIN, SMALL TANTIGEN (EB1 19K)
8983	21948	35373	3.37	2.5E-01	H63238.1	EST_HUMAN	Y84607.1 Soares fetal liver spiken TNF.L3 Homo sapiens cDNA clone IMAGE:202601 5
9227	22160	35623	0.81	2.5E-01	IM69268.1	NT	Mus musculus testis-specific protein (TPX-1) gene, exon 10
9874	22827	36280	16.45	2.5E-01	U89051.2	NT	Homo sapiens matrix metalloproteinase MMP-13 gene, promoter region

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Single Exon Probes Expressed in

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Med Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3163	16210	20134	1.71	2.4E-01	X74209.1	NT	H.sapiens AGT gene, Fat fragment of intron 4
3875	16718	26632	1	2.4E-01	AF169793.1	NT	Podopora aeneina HETC protein (Hs-c) gene, complete cds
3773	16815	20724	0.95	2.4E-01	AE000312.1	NT	Etcherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4002	17069	28724	0.97	2.4E-01	D26960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4974	17689		0.98	2.4E-01	AL181589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
5089	18009	30976	0.95	2.4E-01	D00844.1	NT	Hepatitis C virus genomic RNA, for polyprotein, complete cds
5537	18634	31974	0.77	2.4E-01	A0265707.1	EST_HUMAN	wc35908.x1 NCI_Q6AP_Gas4 Homo sapiens cDNA clone IMAGE:2457123 3'
5537	18634	31974	0.77	2.4E-01	D00871.1	NT	Glycine max mRNA for mitotic cyclin B1-type, complete cds
5562	18659	31605	0.69	2.4E-01	D00871.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5736	18832	32011	0.32	2.4E-01	AF091216.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5766	18858	32012	0.65	2.4E-01	M083377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5901	22549		1.03	2.4E-01	AJ153586.2	NT	Brachyotus floridae mRNA for calcium-binding protein (CBP) gene, 5' end
5908	19032	32779	2.06	2.4E-01	BF562338.1	EST_HUMAN	Q0810 SP-LINO FACTOR, ARGININE/SERINE RICH 4, contains element TARI TARI 1 repetitive element
6098	19177	32995	2.07	2.4E-01	AF035546.1	NT	Oryzophila polyomavirus p85a M2P kinase gene, complete cds
6209	19283	32515	2.02	2.4E-01	AF035546.1	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6204	19337	32570	0.84	2.4E-01	AF173397.1	EST_HUMAN	AV733787 cda Homo sapiens cDNA clone cdaAD411 5'
6523	19586	32544	0.69	2.4E-01	AF036072.1	EST_HUMAN	AF040241.1 Scores, testis, N11 Homo sapiens cDNA clone IMAGE:272833 3'
6685	19742	33010	1.72	2.4E-01	A069989.1	EST_HUMAN	wc18511.x1 NCI_Q6AP_Gas4 Homo sapiens cDNA clone IMAGE:2457123 3'
7217	19852	33279	0.61	2.4E-01	BF163883.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7598	20529	33668	2.93	2.4E-01	A30011.1	NT	Mus musculus tyrosine aminotransferase gene, complete cds
7748	20701	34066	0.65	2.4E-01	A04732.1	EST_HUMAN	Bos taurus pumyl cyclase-activating protein 2 (guac2) mRNA, complete cds
7644	20933		0.81	2.4E-01	U00013.1	NT	Y55511.1 Scores, multiple sclerosis, 2NBM-MSP Homo sapiens cDNA clone IMAGE:277460 5'
7696	20935	34320	0.97	2.4E-01	AF22844.1	NT	Rattus norvegicus Sprague-Dawley heme oxygenase-2 non-reducing isoform gene, complete cds
8416	21385	34762	0.81	2.4E-01	AF07265.1	NT	Mus musculus Dlxm4 protein (Dlxm4d4) mRNA, complete cds
8416	21385	34763	0.81	2.4E-01	A07265.1	NT	Mus musculus psh gene and promoter
8652	21690	35063	1.5	2.4E-01	AJ012956.1	NT	12ethymura thermophilic microtubule gene encoding ribosomal protein L3, exon 1-2
8948	21912	35337	0.98	2.4E-01	BF542794.1	EST_HUMAN	65187679F NIH_MGC_39 Homo sapiens cDNA clone IMAGE:410039 5'
9011	21687		0.97	2.4E-01	BF578276.1	EST_HUMAN	60269168F NIH_MGC_38 Homo sapiens cDNA clone IMAGE:410038 5'
9487	22451	35861	0.51	2.4E-01	AL13907.2	NT	Campylobacter jejuni NCCTC11168 complete genome, segment 4/6

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top-Hit Database Source	Top Hit Description
9467	22461	35882	0.51	2.4E-01	AL138077.2	NT	Campylobacter jejuni NC1011168 complete genome, segment 4/6
9621	22742	38783	7.83	2.4E-01	AB93451.1	EST_HUMAN	nt434024.1 Soares, NF1_7_GBC_S1 Homo sapiens cDNA clone IMAGE2330908 3' similar to contains NER22b71TAR1 repetitive element.
10062	22869	35437	0.57	2.4E-01	AF222687.1	NT	Drosophila melanogaster SGPB gene, complete cds
10062	22869	35438	0.57	2.4E-01	AF222687.1	NT	Drosophila melanogaster SGPB gene, complete cds
10695	23728	37227	1.69	2.4E-01	CD08692	SWISSPROT	COLLAGEN ALPHA1(X) CHAIN PRECURSOR
11119	24078	37603	2.86	2.4E-01	AL181464.2	NT	Human alpha 1(X) chain precursor
11155	24141	37675	1.77	2.4E-01	AF030168.1	NT	Human alpha 1(X) chain precursor
11534	24478		1.52	2.4E-01	Z71647.1	NT	Human alpha 1(X) chain precursor
12096	24607	38584	4.88	2.4E-01	P08900	SWISSPROT	PROLINE RICH GLYCOPOLYMER-RELATED PROTEIN PRECURSOR
12100	25015	38617	2.5	2.4E-01	AF217461.1	NT	Homo sapiens fragile 180 cDNA
12294	25749		1.03	2.4E-01	AF042413.1	NT	Human alpha 1(X) chain precursor
12391	25150		2.1	2.4E-01	AJ278187.1	NT	Human alpha 1(X) chain precursor
12375	25734		2.27	2.4E-01	V01507.1	NT	Human alpha 1(X) chain precursor
12782	25945		1.31	2.4E-01	BF226976.1	EST_HUMAN	Human alpha 1(X) chain precursor
13008	25559		8.49	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C061
399	13464	26384	0.89	2.3E-01	S76958.1	NT	aromatase cDNA
638	13704		5.65	2.3E-01	U39713.1	NT	aromatase cDNA
668	13733	26550	21.34	2.3E-01	U67596.1	NT	aromatase cDNA
604	13887	26837	4.19	2.3E-01	BE311893.1	EST_HUMAN	Human alpha 1(X) chain precursor
1511	14649	27514	1.33	2.3E-01	6877930	NT	Human alpha 1(X) chain precursor
1588	14801		1.02	2.3E-01	U22837.2	NT	Human alpha 1(X) chain precursor
1608	14840	27617	1.21	2.3E-01	AJ26480.1	NT	Human alpha 1(X) chain precursor
1636	14868	27644	2.92	2.3E-01	U10867.1	NT	Human alpha 1(X) chain precursor
2001	15079		1.33	2.3E-01	U235583.1	NT	Human alpha 1(X) chain precursor
2432	15437	28478	2.76	2.3E-01	BE297718.1	EST_HUMAN	Homo sapiens partial intron 3 of the wild type AF4JFEL gene
2630	15857	28671	1.27	2.3E-01	U11316.1	NT	Human alpha 1(X) chain precursor
2635	14422	27591	2.34	2.3E-01	AB015033.1	NT	Human alpha 1(X) chain precursor
2074	18032	26955	1.25	2.3E-01	AA61978.1	EST_HUMAN	Human alpha 1(X) chain precursor
3100	15161		7.15	2.3E-01	U21732.1	EST_HUMAN	Human alpha 1(X) chain precursor
3393	16432	28460	1.28	2.3E-01	U68586.1	EST_HUMAN	Human alpha 1(X) chain precursor

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Exon Signal	Best Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3854	1664	26798	1.05	2.3E-01	S8292.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rat, Morris hepatoma cell line, Genbank, 2522, 17c, Homo sapiens KIA0450] mRNA
3955	1695		5.02	2.3E-01	7652133	NT	Homo sapiens KIA0450 gene product (KIA0450), mRNA
4212	17241		0.82	2.3E-01	032397	NT	Rat fetal reticulocyte factor (ANF) gene, 5' end
4377	17405	30285	0.34	2.3E-01	S82292.1	EST_HUMAN	X17911.1 Swans placenta N22AP Homo sapiens cDNA clone IMAGE146017.5
4428	17453	30285	0.34	2.3E-01	78788.1	NT	Mus musculus reelin (Rein-1) gene, promoter region
4428	17453	30285	1.07	2.3E-01	020890.1	NT	Synochrysalis sp. POC5863 complete genome, 127, 1-133569
4515	17540	30286	1.9	2.3E-01	AF022533.1	NT	Homo sapiens mitogen-activated protein kinase 238c (PRK413) mRNA, complete cds
4584	17626	30302	7.42	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (nuclear protein 15) (NP15) mRNA
5587	18097	30373	0.65	2.3E-01	AB034000.1	NT	Mus musculus ulp1 mRNA, complete cds
5200	18209	31083	0.91	2.3E-01	U91238.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RorA1 gene, and sodium phosphate transporter (NPT3) gene, complete cds
8377	18481	31356	2.19	2.3E-01	AB040043.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5503	18603	31532	2.51	2.3E-01	BF068381.1	EST_HUMAN	743056x1 NO_024P OV18 Homo sapiens cDNA clone IMAGE3476659 3' similar to SW: GAG_SNAHV
5608	18704	31861	4.56	2.3E-01	X65957.1	NT	P03300 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] ;
5733	18827		1.01	2.3E-01	38712.1	NT	C. familiaris reml gene
6845	18855	32719	0.81	2.3E-01	S90371.1	NT	Vitellinoma cornu small subunit ribosomal RNA gene
6051	19132	32540	2.02	2.3E-01	A708840.1	EST_HUMAN	285 rRNA, Leuconostoc carnosum, Genbank, 2860 nt
6051	19132	32541	2.02	2.3E-01	A708840.1	EST_HUMAN	ae27612.1 Bantled axon HPLRB Homo sapiens cDNA clone IMAGE2318446 3' similar to gb:X1328
6812	19668	33154	0.76	2.3E-01	AF196098.1	NT	CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
							ae27612.1 Bantled axon HPLRB Homo sapiens cDNA clone IMAGE2318446 3' similar to gb:X1328
							CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
							ae27612.1 Bantled axon HPLRB Homo sapiens cDNA clone IMAGE2318446 3' similar to gb:X1328
							CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
							Cryptogenic ciliary cytoplasmic oxidase subunit VII (cox16b2) mRNA, complete cds; nuclear gene for mitochondrial product
							ae27612.1 Bantled axon HPLRB Homo sapiens cDNA clone IMAGE2318446 3' similar to gb:X1328
							Repetitive element
7061	20063	33591	5.28	2.3E-01	A718148.1	EST_HUMAN	Homo sapiens cytochrome oxidase subunit VII (cox16b2) mRNA
7318	20286	33632	0.69	2.3E-01	9628323	NT	Scapharca corallinae 16S rRNA, complete cds
7505	20470	33850	0.78	2.3E-01	AF000227.1	NT	Scapharca corallinae 16S rRNA, complete cds
7646	20608	33872	2.65	2.3E-01	A7173388.1	EST_HUMAN	Glial fibrillary acidic protein (GFAP) precursor RNA, partial cds
7649	20608	33874	10.72	2.3E-01	A7173388.1	EST_HUMAN	Glial fibrillary acidic protein (GFAP) precursor RNA, partial cds
7649	20608	33875	10.72	2.3E-01	A7173388.1	EST_HUMAN	Glial fibrillary acidic protein (GFAP) precursor RNA, partial cds
7668	20810		3.39	2.3E-01	0754779	NT	Mus musculus myosin XV (Myo15) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12494	26937	31312	11.07	2.3E-01	BE86246.1	EST_HUMAN	601507202P1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:585868 5'
12544	26267		2.36	2.3E-01	BF60319.1	EST_HUMAN	602144508F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:428711 5'
12591	26295		3.71	2.3E-01	LA00919.1	NT	Rattus norvegicus mRNA for acid gland for chemical
12600	29348		2.12	2.3E-01	LA0946.1	NT	Pleurodesis cell libraries for protein P4033 (P4033) mRNA, complete cds
12626	26511		1.48	2.3E-01	BF479811.1	EST_HUMAN	ncs3912.x1 Tupaia, solid, nerve Homo sapiens cDNA clone IMAGE:358560 3' similar to coriaria element
90	13205	26130	0.99	2.2E-01	AF062190.1	EST_HUMAN	oz74n0x1 Soares, fetal liver, spleen, NIH/5, S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
1587	16010	27576	2.33	2.2E-01	AF167803.1	NT	TRC13040 C13040 A11-BINDING CASSETTE PROTEIN.
2100	14717	28139	2.2	2.2E-01	U34600.1	NT	Homo sapiens PRKAR1A gene, pseudogenes
2412	16419	28445	8.18	2.2E-01	BF877383.1	EST_HUMAN	Fresh-walled NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4265868 5'
2593	16594	28511	2.54	2.2E-01	BE812383.1	EST_HUMAN	602144508F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869190 5'
2593	16594	28512	4.85	2.2E-01	BE812383.1	EST_HUMAN	602144508F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869190 5'
2593	16592	28988	4.85	2.2E-01	BE155635.1	EST_HUMAN	PRK24-T0363-261289-003-412 HT0353 Homo sapiens cDNA
2593	15562	28989	4.85	2.2E-01	BE155635.1	EST_HUMAN	PRK24-T0363-261289-003-412 HT0353 Homo sapiens cDNA
2932	15900		1.29	2.2E-01	AF208293.1	NT	Homo sapiens FRAXB common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3403	16452		2.28	2.2E-01	AF16782.1	NT	Xenopus laevis DNA chromosome 4, conf1 fragment No. 62
3627	18867		0.05	2.2E-01	AF16782.1	NT	Xenopus laevis DNA chromosome 4, conf1 fragment No. 62
4240	17269		1.2	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4247	17276	30158	5.96	2.2E-01	AF165142.1	NT	Mus musculus mixed lineage kinase 3 (MLK3) and two pore domain K+ channel subunit (Kcnk16) genes, complete cds
4252	17321	30159	2.33	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mkk1) mRNA, complete cds
4252	17321	30200	2.33	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mkk1) mRNA, complete cds
4253	17321	30204	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4253	17341	30295	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4259	17432	30270	23.17	2.2E-01	AW35108.1	EST_HUMAN	RC1-C10248-141189-221-g04 CT0249 Homo sapiens cDNA
4993	17860	30773	1.38	2.2E-01	D00094.1	NT	Human beta-2-microglobulin mRNA (AC01899) pseudogene
4998	17865	30773	1.87	2.2E-01	AA21216.1	EST_HUMAN	z957c05.t1 Streptococcus edm (AC01899) pseudogene
5092	18092		1.34	2.2E-01	L13299.1	NT	Mus musculus vicillin gene, exon 3
5160	18165	31048	1.22	2.2E-01	BE141035.1	EST_HUMAN	MRH-H10067-201099-002-510 HT0067 Homo sapiens cDNA
5181	18190	31009	1.51	2.2E-01	H05148.1	EST_HUMAN	YR208.H1 Soares fetal liver spleen NIH/5 Homo sapiens cDNA clone IMAGE:280601 5' similar to
5265	18271		1.06	2.2E-01	AF169206.2	NT	gb214119.1 mat CD59 GLYCOPROTEIN PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21C006

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5838	19528	33112	2.18	2.2E-01	5803002	NT	Homo sapiens diaphanous (Discophila, homodig) 2 (DIAPH2), transcript variant 156, mRNA
5949	19529	33113	3.59	2.2E-01	D94000.1	NT	Synochroptis sp. POCO850 complete genome, 1927, 2392725-2539569
6114	19192	32415	0.81	2.2E-01	U67097.1	NT	Gallus gallus 1-box containing protein (Ch-1b) mRNA, complete cds
6854	19917	33211	0.81	2.2E-01	U67097.1	NT	Gallus gallus 1-box containing protein (Ch-1b) mRNA, complete cds
6994	20189	33514	0.7	2.2E-01	AB035490.1	NT	Homo sapiens gene for Ucln1, complete cds
6994	20189	33514	0.68	2.2E-01	AA490106.1	EST	AB029638.1 Stragene field refra 937202 Homo sapiens cDNA clone IMAGE 839568 3'
7222	20244	33578	0.68	2.2E-01	AA490106.1	EST	AB029638.1 Stragene field refra 937202 Homo sapiens cDNA clone IMAGE 839568 3'
7222	20244	33578	7.78	2.2E-01	AV756238.1	EST	AV756238.1 Homo sapiens cDNA clone BAF4008 5'
7396	20307	33950	1.43	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pssA) and ABC transporter ATP-binding protein (tbpA) genes, complete cds, and unknown genes
7396	20307	33951	1.43	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pssA) and ABC transporter ATP-binding protein (tbpA) genes, complete cds, and unknown genes
7503	20474	33834	2.11	2.2E-01	M24136.1	NT	Human glycophorin 3 gene, exon 1
7503	20474	33835	2.11	2.2E-01	M24136.1	NT	Human glycophorin 3 gene, exon 1
7728	20594	34046	0.99	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M228 section 45 of 63 of the complete genome
7866	20935	34207	0.8	2.2E-01	AF097697.1	NT	Homo sapiens homeobox B1 (HOXB1) gene, partial cds, and homeobox B6 (HOXB6), homeobox B6 (HOXB6), homeobox B7 (HOXB7), and homeobox B5 (HOXB5) genes, complete cds
8000	20959	34332	0.8	2.2E-01	AF097697.1	NT	Homo sapiens homeobox B1 (HOXB1) gene, partial cds, and homeobox B6 (HOXB6), homeobox B6 (HOXB6), homeobox B7 (HOXB7), and homeobox B5 (HOXB5) genes, complete cds
8354	21323	34693	2.81	2.2E-01	AF155143.1	NT	Spodoptera frugiperda 3A3-MT, sense, promoter region
8425	21394	34693	1	2.2E-01	Z6933.1	NT	Zell aplk and wplk genes
8605	21882	35284	0.49	2.2E-01	AI132918.1	NT	Pin topophytes McP2 gene 3 UTR
9234	22200	35620	0.51	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9234	22200	35620	0.51	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9247	22213	35945	4.12	2.2E-01	AE007153.1	NT	Thermoplasma maritima section 26 of 138 of the complete genome
9237	22293	35960	0.47	2.2E-01	U09964.1	NT	Mus musculus ICR Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-5) gene, complete cds
9376	22341	35972	3.89	2.2E-01	AW855039.1	EST	PM5-CTG105-241 289-209-007 CTG105 Homo sapiens cDNA
9470	22434	35972	1.4	2.2E-01	8390247	NT	Mus musculus diaphanous (Discophila, homodig) 2 (DIAPH2) (D94000.1) mRNA
9470	22434	35972	1.4	2.2E-01	BF078354.1	EST	MR1-TN0045-11090-008-002 TN0045 Homo sapiens cDNA
9444	22568	36037	1.3	2.2E-01	W02588.1	EST	2a6081.1 Somers-rich protein 2NHHM Homo sapiens cDNA clone IMAGE 231591 5'
9444	22568	36037	1.3	2.2E-01	W02588.1	EST	2a6081.1 Somers-rich protein 2NHHM Homo sapiens cDNA clone IMAGE 231591 5'
9692	22819	36274	15.89	2.2E-01	P48934	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (L-BA-BASSOASSO TRANSCRIPT 2)
9707	22950	36116	0.66	2.2E-01	AJ009639.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (Mkp3)
9718	22746	36197	0.78	2.2E-01	7857429	NT	Mus musculus caldesmon specific factor 2 (OSF-2), mRNA
9731	22759	36212	4.38	2.2E-01	M68843.1	NT	Brechenyano ratio spandymn beta and gamma chains (Epd) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9679	22906	39371	0.5	2.2E-01	Q00680	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG3) (CNG3)
10174	23099	39579	3.74	2.2E-01	AF167941.1	NT	Fusaria myceliata chloroplast-localized small heat shock protein (CPHSP2) mRNA, complete cds; nuclear gene for chloroplast product
10313	23237	39719	1.76	2.2E-01	BF205007.1	EST_HUMAN	3078037247.11H3_1005_19 Homo sapiens cDNA clone IMAGE:1100189 5'
10337	23458	39959	1	2.2E-01	9625971	NT	Human histoplasma 5' complete cDNA
10397	23619	37113	0.52	2.2E-01	T59472.1	EST_HUMAN	363365.11 Shigella sonnei (9637371) Homo sapiens cDNA clone IMAGE:78555 5'
10697	23619	37114	0.52	2.2E-01	T59472.1	EST_HUMAN	363365.11 Shigella sonnei (9637371) Homo sapiens cDNA clone IMAGE:78555 5'
10735	23657	37150	0.51	2.2E-01	AJ508284.1	NT	Pseudomonas sp. 3078037247.11H3_1005_19 Homo sapiens cDNA clone IMAGE:78555 5'
10810	23731	37274	0.88	2.2E-01	AF011001.1	NT	Human histoplasma 5' complete cDNA
10856	23778	37274	0.67	2.2E-01	AF011001.1	NT	Human histoplasma 5' complete cDNA
10856	23778	37274	0.67	2.2E-01	AF011001.1	NT	Human histoplasma 5' complete cDNA
11751	23639	38215	3.77	2.2E-01	U01918.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11789	23644	37459	3.41	2.2E-01	7706215	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
12017	25960		2.32	2.2E-01	U03871.2	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
12026	25179		3.88	2.2E-01	AF18643.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
12513	17462	30370	6.62	2.2E-01	AF18643.1	EST_HUMAN	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
12514	25246		1.7	2.2E-01	AF18643.1	EST_HUMAN	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
13111	25946		1.36	2.2E-01	AF18643.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
972	14024	26978	1.56	2.1E-01	AA595289.1	EST_HUMAN	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
975	14026	26980	1.06	2.1E-01	AF18643.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11296	14169		2.39	2.1E-01	AF022314.2	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
1203	14242	27160	0.89	2.1E-01	AF022314.2	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
1203	14242	27200	0.89	2.1E-01	AF022314.2	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
1512	14544	27616	1.05	2.1E-01	AJ249995.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
1929	14983	27649	1.94	2.1E-01	AA008624.1	EST_HUMAN	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
21065	15181	29201	3.26	2.1E-01	BF959073.1	EST_HUMAN	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
24369	19005	29510	2.19	2.1E-01	U078968.1	EST_HUMAN	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome

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Probe Seq ID NO.	ORF Seq ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9871 22934	39277	2.77	2.1E-01	X07978.1	NT	A. bellina mRNA for ARtemisin protein
9975 22963	39387	1.26	2.1E-01	AB036530.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10822 23814	37109	1.13	2.1E-01	Z27087.1	NT	Beta vulgaris mRNA for elongation factor 1 beta
10726 23847	37140	2.89	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE DELTA (DGLYCERDE KINASE) (DOK-DELTA) (DAG KINASE DELTA)
10731 23693	37146	0.93	2.1E-01	BF54254.1	EST_HUMAN	(80 KD) DIACYLGLYCEROL KINASE 8021314271 NIH_MGC_31 Homo sapiens cDNA clone IMAGE:370831 5'
11009 23974	37498	3.99	2.1E-01	AF254296.1	NT	Arctic limulepous isolate NG 140H dehydrogenase subunit 2 (ND2) gene, complete cds, mitochondrial gene for mitochondrial product
11800 24771	38476	2.15	2.1E-01	1103847	EST_HUMAN	Homo sapiens paracatops polyomavirus 2 (PPV2), mRNA
11903 24786	38378	1.61	2.1E-01	BE180423.1	EST_HUMAN	RC3H11022-3043030-1 P011110522 Homo sapiens cDNA
12137 25022	37602	1.38	2.1E-01	X57624.1	NT	Oncoprotein tyrosine kinase for ALA-BL DNA, repeat region
12860 25339	37601	1.94	2.1E-01	AF217480.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase (FOR) gene, exons 8, 9, and partial cds
12860 25800	37601	1.8	2.1E-01	132588.1	NT	Homo sapiens p53R2 gene
12914 25493	37601	1.2	2.1E-01	132588.1	EST_HUMAN	8014077251 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3918578 5'
13045 25998	31682	1.62	2.1E-01	BE57230.1	EST_HUMAN	74584221 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3918578 5'
201 13502	26231	1.32	2.0E-01	AB017435.1	NT	Gallus gallus mRNA for avian, complete cds
535 13608	26231	1.62	2.0E-01	AB017435.1	NT	Homo sapiens CG1-18 protein, (LOC51008), mRNA
700 13762	26231	1.25	2.0E-01	U77985.1	NT	O. carinatus geminina light heavy chain V-H pseudogene, allotype VH42
811 13869	26231	1.25	2.0E-01	U77985.1	NT	Mus musculus Major Histocompatibility Locus class II region
1013 14081	27012	0.72	2.0E-01	AF002055.1	NT	Synchytrium sp. PC08003 complete genome, 7127, 7614-9-220915
1127 14170	27121	1.02	2.0E-01	AL183213.2	NT	Homo sapiens chromosome 21 segment H321C013
1259 14294	27238	1.43	2.0E-01	1132865.5	NT	Homo sapiens act1 gene
1311 14347	27319	2.04	2.0E-01	AW38467.1	EST_HUMAN	PM1-HT0422-201289-002-006 H10422 Homo sapiens cDNA
1454 14437	27490	1.39	2.0E-01	AL343697.1	NT	Flum pox virus strain M, complete genome, isolate PS
1463 14456	27490	15.27	2.0E-01	4503408	NT	Homo sapiens dyadectrin, alpha (DTNA), mRNA
1463 14456	27490	15.27	2.0E-01	AF007074.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0905
1500 14892	27665	1.62	2.0E-01	AF260700.1	NT	Homo sapiens sodium iodide symporter mRNA, partial cds
1706 14738	27118	1.39	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (brady1) gene, complete cds
1730 14760	27118	2.09	2.0E-01	AF111770.3	NT	Homo sapiens 14q32 Jigged2 gene, complete cds
1772 14801	27118	3.8	2.0E-01	U67525.1	NT	Melanconococcus jenningsii section 67 of 150 of the complete genome
1807 14931	27228	0.94	2.0E-01	BE071330.1	EST_HUMAN	801494471 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:385330 5'
1807 14931	27227	0.94	2.0E-01	BE071330.1	EST_HUMAN	801494471 NIH_MGC_30 Homo sapiens cDNA clone IMAGE:385330 5'
2345 14934	27227	1.85	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3499	18546	26472	0.74	2.0E-01	P46807	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN AT1HB-10) (HD-ZIP PROTEIN AT1HB-10)
3552	19827	26774	0.82	2.0E-01	AW328058.1	EST_HUMAN	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
3620	19783	26774	0.79	2.0E-01	P46844	SWISSPROT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
3655	19895	26769	1.14	2.0E-01	AI183204.2	SWISSPROT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
3977	17017	28631	0.7	2.0E-01	Z45906.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
4597	17818		10.26	2.0E-01	BE226165.1	EST_HUMAN	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
5078	18088	30669	7.66	2.0E-01	8922080	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
5144	18153	31033	0.97	2.0E-01	I19216.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
5209	18302	31163	0.93	2.0E-01	BE338491.1	EST_HUMAN	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
5620	18619	31593	2.31	2.0E-01	X58900.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
5831	18921	32104	1.89	2.0E-01		NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
5940	18029	32220	0.69	2.0E-01	U15300.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
6178	19259	32460	5.47	2.0E-01	U15300.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
6298	18370		0.79	2.0E-01	N75907.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
6417	18484	32735	0.59	2.0E-01	P02467	SWISSPROT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
6669	19620	32895	3.06	2.0E-01	X10303.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
6679	19739	33012	4.25	2.0E-01	AW350955.1	EST_HUMAN	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
7512	20477	33838	1.27	2.0E-01	AF250371.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
7679	20037	33969	0.72	2.0E-01	P54422	SWISSPROT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
8054	20991	34389	0.51	2.0E-01	V00726.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
8285	21254		6.17	2.0E-01	AF028026.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
8542	21510		3.1	2.0E-01	X91151.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
9074	22040		0.43	2.0E-01	BE52247.1	EST_HUMAN	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
9706	22656	38115	1.99	2.0E-01	U82511.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
9745	22696	38141	0.76	2.0E-01	U71122.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
9914	22738		6.23	2.0E-01	AE001278.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
10033	23028	38506	0.52	2.0E-01	I11420	SWISSPROT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
10033	23028	38507	0.52	2.0E-01	I11420	SWISSPROT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
10231	23173		1.94	2.0E-01	AF146992.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
10401	23263	38607	1.94	2.0E-01	AF146992.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
10401	23263	38608	1.94	2.0E-01	AF146992.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element
10528	23450	38648	0.54	2.0E-01	AF157814.1	NT	W18002.N1.GC.GP.-HNB Homo sapiens cDNA, clone IMAGE:2740395 3' similar to contains element

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Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10528	23460	35040	0.64	2.0E-01	AF17614.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10576	23467		0.78	2.0E-01	X76938.1	NT	D melanogaster DNA mobile element (hoppe)
10770	23591	37188	0.97	2.0E-01	X79121.1	NT	R. norvegicus mRNA for transferrin, complete cds
11186	24145	37678	2.24	2.0E-01	D85008.1	NT	Salvadora mullus mRNA for transferrin, complete cds
11186	24145	37679	2.24	2.0E-01	D85008.1	NT	Salvadora mullus liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12841	25325		1.42	2.0E-01	AF220687.2	NT	Homo sapiens mRNase-Lm isoform (mRNA), complete cds
12828	25779		1.66	2.0E-01	AF302773.1	NT	Homo sapiens MAGI2 messenger, MAGI2 Homo sapiens cDNA
12837	25781	31000	1.34	2.0E-01	AF678287.1	EST_HUMAN	EST1387405 MAGI2 messenger, MAGI2 Homo sapiens cDNA
12875	25508	31707	4.12	2.0E-01	A02382.1	EST_HUMAN	corb1aL1.1 Homo sapiens cDNA clone IMAGE: 640510.3
12888	25483		2.88	2.0E-01	AF078164.2	NT	Homo sapiens Kufs-binding protein (KUB3) mRNA, partial cds
1170	13221		9.9	1.0E-01	754978	NT	Homo sapiens Aryl hydrocarbon receptor repressor (AHR), mRNA
352	13441	26396	0.08	1.0E-01	AF04353.1	NT	Mus musculus pale ear (66) gene, wild type alleles, 3' region, partial cds
657	13723	29547	2.68	1.0E-01	U32381.2	NT	Homo sapiens p33 gene, wild type alleles, 3' region, partial cds
657	13723	29548	2.68	1.0E-01	U32381.2	NT	Homo sapiens p33 gene, wild type alleles, 3' region, partial cds
655	13730	29555	0.69	1.0E-01	BC073051.1	EST_HUMAN	Human lymphoid protein kinase C-activating protein mRNA, complete cds
655	13730	29555	0.69	1.0E-01	BC073051.1	EST_HUMAN	Human lymphoid protein kinase C-activating protein mRNA, complete cds
908	14039		0.89	1.0E-01	7205180	NT	Mus musculus Interleukin 2 receptor, gamma chain (IL2rg), mRNA
1100	17130	27101	8.8	1.0E-01	A435883.1	EST_HUMAN	EST167784 Fall lung II Homo sapiens cDNA 5' end
142	14456	27170	2.9	1.0E-01	AF091382.1	NT	Sorghum bicolor 22 kDa tyrosin cluster
2030	19358	26423	3.22	1.0E-01	AF18423.1	NT	Pleurodom virus reovirus binding protein-2 (Rbp-2) gene, complete cds
2034	19592	28912	3.47	1.0E-01	A02382.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase (hprt), mRNA
2346	19006		4.89	1.0E-01	U06006.1	NT	Gallus gallus ovalbumin (V) gene, complete cds
3406	19435	26078	4	1.0E-01	D13167.1	NT	Mouse gene for immunoglobulin diversity region D1
3422	19539	26464	5.36	1.0E-01	AF16407.1	EST_HUMAN	Y42101.1 Soares fetal liver spleen (NFES) Homo sapiens cDNA clone IMAGE: 72947.5
3817	19897	26763	0.97	1.0E-01	AF24017.1	NT	Rattus norvegicus erythrocyte diacylglycerol kinase, complete cds
3848	19898	26761	2.26	1.0E-01	U30769	SWISSPROT	FAIR-RULE PROTEIN ODO-PAIRED
4018	17037	22856	3.91	1.0E-01	AB009784.1	NT	Rattus norvegicus erythrocyte diacylglycerol kinase, complete cds
4110	17144	30038	1.42	1.0E-01	AF074106.1	EST_HUMAN	Schistosoma haematobium pombis DNA for cytoplasmic dynein heavy chain, complete cds
4259	17289	30169	1.34	1.0E-01	BE834943.1	EST_HUMAN	OM3-CT0315-271186-045-511 CT0315 Homo sapiens cDNA
4499	17521	35048	0.83	1.0E-01	AF181463.2	NT	NRT-FN010-280700-007-404 FN010 Homo sapiens cDNA
5047	19090		1.15	1.0E-01	AF223942.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5231	18239		1.01	1.0E-01	A061190.1	EST_HUMAN	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds t65937.2AT NC_004868 Homo sapiens cDNA clone IMAGE: 2239886.3 similar to gp321974 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);

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Probe SEQ ID NO.	Ent Seq ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5095	18780		5.2	1.9E-01 AW130149.1	EST_HUMAN	EST_HUMAN	K28a07.21 NCL CGAP_UH Homo sapiens cDNA clone IMAGE2619444 3' similar to gb:M73779 RETINOIC
5728	18822	32002	8.11	1.9E-01 AF127037.1	NT	EST_HUMAN	ACD RECEPTOR ALPHA-1 (HUMAN);
5809	19026	32219	0.71	1.9E-01 AF091216.1	NT	EST_HUMAN	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE) gene, exon 1a
5887	19072		2.16	1.9E-01 AL113118.1	EST_HUMAN	EST_HUMAN	Homo sapiens protein (Wt) gene, complete cds
6461	19526	32776	0.95	1.9E-01 AL113118.1	EST_HUMAN	EST_HUMAN	Human cDNA clone NT249-4001328 5'
6527	19590		0.88	1.9E-01 AF170299.1	EST_HUMAN	EST_HUMAN	AF0982.2 NCL CGAP_C3 Homo sapiens cDNA clone IMAGE2284089 3'
7164	18395	31240	1.46	1.9E-01 AW146432.1	EST_HUMAN	EST_HUMAN	AF0982.2 NCL CGAP_C3 Homo sapiens cDNA clone IMAGE2616030 3' similar to gb:X03559 ATP
7189	20217	33547	0.95	1.9E-01 AF034620.1	NT	EST_HUMAN	SYNTHASE BETA CHAIN, M1 TOCHRONAL PRECURSOR (HUMAN);
7193	20217	33548	0.95	1.9E-01 AF034620.1	NT	EST_HUMAN	repetitive element;
7474	20440	33769	0.85	1.9E-01 U73848.1	NT	EST_HUMAN	g9a12.41 SacA1 Homo sapiens cDNA clone IMAGE31603 3' similar to contains MER13
7709	20696	34033	0.75	1.9E-01 U93688.1	NT	EST_HUMAN	Homo sapiens tubby like protein 1 (TULP1) gene, exon 9-11
7734	20698	34053	1.35	1.9E-01 U93692.1	NT	EST_HUMAN	Homo sapiens tubby like protein 1 (TULP1) gene, exon 9-11
7784	20737	34109	2.54	1.9E-01 AF072724.1	NT	EST_HUMAN	Drosophila melanogaster larval shock syndrome toxin-1 (ss), enteronin (ent), and magrase (m) genes, complete cds
8318	21287	34701	1.41	1.9E-01 AL161957.2	NT	EST_HUMAN	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP) gene, complete cds
9034	22800	35421	12.86	1.9E-01 AB033024.1	NT	EST_HUMAN	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
9297	22293	35932	1.32	1.9E-01 M14568.1	NT	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
9297	22293	35932	1.32	1.9E-01 M14568.1	NT	EST_HUMAN	Homo sapiens mRNA for KIAA1189 protein, partial cds
10234	23159	36647	0.87	1.9E-01 AA912468.1	EST_HUMAN	EST_HUMAN	Marasipal cat beta-globin gene mRNA, partial cds
10602	23524	37019	0.72	1.9E-01 BE630033.1	EST_HUMAN	EST_HUMAN	Marasipal cat beta-globin gene mRNA, partial cds
10602	23524	37020	0.72	1.9E-01 BE630033.1	EST_HUMAN	EST_HUMAN	d95910.1 NCL CGAP_PNS1 Homo sapiens cDNA clone IMAGE1337500 3' similar to contains Alu
11008	24088	37586	1.87	1.9E-01 AF23301.1	NT	EST_HUMAN	repetitive element;
11831	24714	38298	1.47	1.9E-01 M22253.1	NT	EST_HUMAN	RCCE-E10082-060700-022-A02 E10082 Homo sapiens cDNA
12033	24859	38504	3.94	1.9E-01 AJ243113.1	NT	EST_HUMAN	RCCE-E10082-060700-022-A02 E10082 Homo sapiens cDNA
12049	24822	38519	1.53	1.9E-01 U07344.1	NT	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12875	25540		1.92	1.9E-01 AF069596.1	NT	EST_HUMAN	Rattus norvegicus sodium channel 1 mRNA, complete cds
34	13134	26555	2.18	1.9E-01 U75200.1	NT	EST_HUMAN	Rattus norvegicus partial E-H72 receptor gene, exons 2 to 5
260	19637	24281	1.39	1.9E-01 AB022090.1	NT	EST_HUMAN	Influenza A/Guangdong/34/72 nucleoprotein (seg 5) gene, 5' end
							Rattus norvegicus nuclear serine/threonine protein kinase mRNA, complete cds
							Mus musculus p116Rip mRNA, complete cds
							Mus musculus Ctg gene for chaperonin containing TOP-1 gamma subunit, partial cds

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Probe SEQ ID NO.	Exp SEQ ID NO.	QRT-SEQ ID NO.	Expression Signal	Most Similar BLAST E-VALUE	Top Hit Accession No.	Top Hit Database Source
370	13436	26386	1.91	1.8E-01	45026303	NT
983	14034	26566	0.89	1.8E-01	AF152722.1	EST_HUMAN
1093	14138	27037	1.08	1.8E-01	AF039893.1	EST_HUMAN
1293	14328	27290	9.43	1.8E-01	AL117183.1	NT
1603	14358	27507	1.17	1.8E-01	U07634.2	EST_HUMAN
1603	14358	27507	1.17	1.8E-01	U07634.2	EST_HUMAN
1603	14358	27508	1.37	1.8E-01	44560366	NT
1864	14869		1.37	1.8E-01		
1862	14907		1.47	1.8E-01	AF173708.1	EST_HUMAN
1930	14954	27650	1.66	1.8E-01	AB051897.1	NT
2702	16068		3.94	1.8E-01	AF0455728.1	EST_HUMAN
2608	16067		1.95	1.8E-01	AF146499.1	NT
3141	16162	28806	0.85	1.8E-01	AF1462300.1	EST_HUMAN
3141	16162	29108	1.35	1.8E-01	AF14695718.1	EST_HUMAN
3379	16426	29354	0.82	1.8E-01	BF1635821	EST_HUMAN
3337	16680	29564	1.66	1.8E-01	H03039.1	EST_HUMAN
3337	16680	29595	1.69	1.8E-01	H03309.1	EST_HUMAN
4360	17387		0.75	1.8E-01	AF072854.1	NT
4566	17608	30503	5.42	1.2E-01	AF155562.2	NT
4806	17623	30718	2.5	1.8E-01	AB0051897.1	NT
5031	18053	30941	1.11	1.8E-01	X79794.1	NT
5031	18053	30941	1.11	1.8E-01	AF041270.1	EST_HUMAN
5031	18053	30970	1.96	1.8E-01	AF172382.1	EST_HUMAN
5031	18053	30970	0.63	1.8E-01	AF172382.1	EST_HUMAN
5214	18146	31018	2.66	1.8E-01	AF161258.1	NT
5214	18146	31018	0.73	1.8E-01	U07540.1	NT
5214	18223		31.49	1.8E-01	BE062326.1	EST_HUMAN
5967	18476	31493	0.64	1.8E-01	AF161594.2	EST_HUMAN
5967	18502		1.97	1.8E-01		

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6526	16569	32348	0.9	1.7E-01	U370978.1	EST_HUMAN	la2c11.x1 Soares_fetal_lung_NbHc.19W Homo sapiens cDNA clone IMAGE:204482.3'
6526	16569	32349	0.9	1.7E-01	U370978.1	EST_HUMAN	la2c11.x1 Soares_fetal_lung_NbHc.19W Homo sapiens cDNA clone IMAGE:204482.3'
7031	18382	31250	0.78	1.7E-01	BE300286.1	EST_HUMAN	650944067.1 NH_MGC_17 Homo sapiens cDNA clone IMAGE:2860246.3'
7031	18382	31250	0.78	1.7E-01	AF036522.3	NT	Muscuticatus saralis oviductin precursor (OVI) gene, complete cds
7033	20383	31250	0.79	1.7E-01	U36910.1	NT	Homo sapiens rHE gene
7140	20397	33748	1.56	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, SaluA-VT2 prophage inserted region
7140	20397	33748	1.56	1.7E-01	AF000422.1	NT	Escherichia coli O157:H7 genomic DNA, SaluA-VT2 prophage inserted region
7516	20480	33841	8.65	1.7E-01	BE34719.1	EST_HUMAN	601590225.1 NH_MGC_21 Homo sapiens cDNA clone IMAGE:3494964.3'
7721	20970	34543	1.42	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL66 (HPLD PROTEIN)
7739	26688	34557	0.71	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8194	21164	34573	1.24	1.7E-01	AF00073.1	NT	Homo sapiens hominigeninase 1, 2-diolylase gene, complete cds
8296	21265	34576	0.62	1.7E-01	AF15069.1	NT	Pseudomonas putida long-chain-acyl-CoA ligase (lactD) gene, complete cds
8620	21968	35004	7.37	1.7E-01	7706428	EST_HUMAN	Homo sapiens cleavage and polyadenylation specificity factor 3, 72AD subunit (CPEF3), mRNA
8620	21968	35005	7.37	1.7E-01	7706428	EST_HUMAN	Homo sapiens cleavage and polyadenylation specificity factor 3, 72AD subunit (CPEF3), mRNA
9045	22011	35433	0.6	1.7E-01	AW92873.1	NT	RC2390002.2:70200-01-r10 BNO32, Homo sapiens cDNA
9078	22045	35468	3.22	1.7E-01	U00384.1	NT	Rat (RHR strain) SXT gene
9166	22162	35590	0.61	1.7E-01	AF271413.1	NT	Homo sapiens neurogranin 3, isoform 3, complete cds, alternatively spliced
9166	22162	35591	0.61	1.7E-01	AF271413.1	NT	Homo sapiens neurogranin 3, isoform 3, complete cds, alternatively spliced
9349	22314	35739	0.44	1.7E-01	AF77002.1	EST_HUMAN	X65027.1131 NH_MGC_18 Homo sapiens cDNA clone IMAGE:144242.5'
9523	22466	35833	0.43	1.7E-01	BE35342.1	EST_HUMAN	6011118275.1 NH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184.5'
9523	22466	35834	0.43	1.7E-01	BE35342.1	EST_HUMAN	6011118275.1 NH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184.5'
10046	22875	36337	8.16	1.7E-01	AP01508.1	NT	823133, Haplodipus genomic DNA, vector 2/14
10056	22983	36451	0.47	1.7E-01	AW977458.1	EST_HUMAN	EST188554 IMAGE reassurance, MAGO Homo sapiens cDNA
10056	22983	36451	0.47	1.7E-01	AW977458.1	EST_HUMAN	EST188554 IMAGE reassurance, MAGO Homo sapiens cDNA
10073	23000	36470	1.83	1.7E-01	U16258.1	NT	Human class IV alcohol dehydrogenase (ADH17) gene, exon 3
10148	23074	36545	0.98	1.7E-01	U24005.1	NT	Human immunodeficiency virus type 1 (HIV-1) env gene (partial)
10148	23074	36545	0.98	1.7E-01	U24005.1	NT	Human immunodeficiency virus type 1 (HIV-1) env gene (partial)
10157	23092	36570	2.43	1.7E-01	U331149.1	NT	Grasshopper metapneumonia virus type 1 (GPV) env gene (partial)
10593	23515	36570	2.43	1.7E-01	AF163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10729	23680	37176	1.24	1.7E-01	11427203	NT	Homo sapiens scute carrier family 7, Calicott amino acid transporter, y+ system, member 2 (SLC7A2), mRNA
10761	23682	37178	1.61	1.7E-01	AA627972.1	EST_HUMAN	nc90607.1 NCI COMP_C69 Homo sapiens cDNA clone IMAGE:1148392.3' similar to gbL25081
10966	23895	37330	0.42	1.7E-01	AF161542.2	NT	TRANSFORMING PROTEIN RHOC (RHOC)
11040	24004	37330	8.17	1.7E-01	BE350935.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Spinder (Tpe) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5069	18079	30660	1.16	1.E-01/AJ187071.1	EST_HUMAN	EST_HUMAN	348308 v1.NH_MGC_10 Homo sapiens cDNA clone IMAGE:349623 5' similar to gb:U18715
5461	19503	31475	0.57	1.E-01/AJ160381.1	NT	NT	TRYPHOPHYANIN-TRNA SYNTHETASE (HUMAN). gb:U69897 M.musculus (MOUSE). Plasmidom Maciparin (strain D26) variant-specific surface protein (var-1) gene, complete cds
5800	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5801	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5802	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5803	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5804	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5805	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5806	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5807	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5808	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5809	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5810	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5811	19596	31668	2.82	1.EE-01/AW197496.1	EST_HUMAN	EST_HUMAN	sm3031.1.H1.C21.GF6_G03 Homo sapiens cDNA clone IMAGE:266969 3' similar to TR:O79894/O79894 XPHOTONICAL 127.6 KD PROTEIN :
5812	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5813	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5814	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5815	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5816	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5817	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5818	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5819	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5820	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5821	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5822	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5823	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5824	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5825	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5826	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	801837297.NIH_MGC_18 Homo sapiens cDNA clone IMAGE:404383 3'
5827	19219	32449	0.97	1.EE-01/BF182564.1	EST_HUMAN	EST_HUMAN	

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Exon Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11017	23682	37609	2.56	1.6E-01	AW50583.1	EST_HUMAN	13-CT022-11196-028-001 CT0220 Homo sapiens cDNA
11121	24082	37607	1.82	1.6E-01	Z28073.1	NT	S.cerevisiae chromosome XI reading frame ORF YML073w
11122	24082	37608	1.92	1.6E-01	Z28073.1	NT	S.cerevisiae chromosome XI reading frame ORF YML073w
11334	24392	37820	1.5	1.6E-01	AF108964.1	EST_HUMAN	U0146790F11P1_MGC_19 Homo sapiens cDNA clone IMAGE3181183.5
11451	24394		3.84	1.6E-01	BE20094.1	EST_HUMAN	Plasmidom filipium calcium-dependent protein kinase3 (cpk3), gene, complete cds
11740	24529		1.75	1.6E-01	AF108964.1	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit [Ap1b1], mRNA
12151	25006	38204	6.79	1.6E-01	6071652	NT	Mus musculus protein kinase, cGMP-dependent, type II (Pkg2), mRNA
12275	25009	38179	1.76	1.6E-01	6071648	NT	Mus musculus protein kinase, cGMP-dependent, type II (Pkg2), mRNA
12606	25097		1.82	1.6E-01	AW10946.1	EST_HUMAN	RV17688B GLC Homo sapiens cDNA clone G16EM97.5
12697	25271		22.15	1.6E-01	AB04310.1	EST_HUMAN	RC1170074-20203-014-001.1 L170374 Homo sapiens cDNA
12856	25463		2.73	1.6E-01	AK021498.1	NT	Cucumis sativus KS mRNA for anti-leucine synthase, complete cds
12945	25524		2.95	1.6E-01	AF287344.1	NT	Fitchia hybrid culture Q9 9208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12871	25537	37176	2.24	1.6E-01	6066822	NT	Rattus norvegicus chondroitin sulfate proteoglycan 6 (neuronglycan 6) (Capp6), mRNA
12876	25543		1.93	1.6E-01	BE267894.1	EST_HUMAN	81123456F11P1_MGC_6 Homo sapiens cDNA clone IMAGE3345938
2461	13345	28270	1.73	1.5E-01	BE710087.1	EST_HUMAN	U3370819-04070-197-E05 HT0819 Homo sapiens cDNA
2468	13345	28271	1.73	1.5E-01	BE710087.1	EST_HUMAN	U3370819-04070-197-E05 HT0819 Homo sapiens cDNA
2681	18113		1.24	1.5E-01	AF116861.1	EST_HUMAN	AV171068 DCA Homo sapiens cDNA clone DCA04068.5
2682	18113		1.31	1.5E-01	JL163243.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS210384
2683	18113		1.31	1.5E-01	JL163243.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS210384
2689	18113		1.31	1.5E-01	AF030735.1	NT	Oryzopsis euryloides L1 for EGS22 myelin heavy chain, 3'UTR
2698	18113	27069	1.07	1.5E-01	AF030735.1	NT	Oryzopsis euryloides L1 for EGS22 myelin heavy chain, 3'UTR
10996	14103	27063	1.27	1.5E-01	Z23653.1	NT	Rattus norvegicus malic acid dehydrogenase 1 (MDH1), mRNA
11115	14103		1.07	1.5E-01	Z23653.1	NT	Rattus norvegicus malic acid dehydrogenase 1 (MDH1), mRNA
12801	14315	27276	3.58	1.5E-01	Z23653.1	NT	Rattus norvegicus malic acid dehydrogenase 1 (MDH1), mRNA
12801	14315	27277	3.58	1.5E-01	AF117540.1	NT	Rattus norvegicus malic acid dehydrogenase 1 (MDH1), mRNA
1478	14611	27447	1.64	1.5E-01	AF144483.1	EST_HUMAN	U14-B16-356-001F11P1_MGC_19 Homo sapiens cDNA clone IMAGE2733641.3
1623	14847	27943	1.95	1.5E-01	AF144483.1	EST_HUMAN	U14-B16-356-001F11P1_MGC_19 Homo sapiens cDNA clone IMAGE2733641.3
1722	15717	28736	1.47	1.5E-01	BE563811.1	EST_HUMAN	9029326F11P1_MGC_19 Homo sapiens cDNA clone IMAGE3276937.5
2024	15952		0.76	1.5E-01	AF572516.1	EST_HUMAN	905602.2 NT1 CGAP F11 Homo sapiens cDNA clone IMAGE3276937.5
3048	18019	29019	1.71	1.3E-01	MF81141.1	NT	San taurin factor v1 variant 2 (factor V1 mRNA, complete cds)
3383	18413	29336	6.95	1.5E-01	AA93049.1	EST_HUMAN	908905.4 NT1 CGAP G04 Homo sapiens cDNA clone IMAGE1371337.3 similar to gb-M11433
3381	18430	29357	0.74	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN1, CELLULAR (HUMAN);
3381	18430	29358	0.74	1.5E-01	Z23104.1	NT	L. tagellensis mRNA for G protein-coupled receptor
3381	18430	29358	0.74	1.5E-01	Z23104.1	NT	L. tagellensis mRNA for G protein-coupled receptor

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database, Source	Top Hit Descriptor
3440	18487	29405	0.97	1.5E-01	AW61237.1	EST_HUMAN	h22922x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:2609539 3' similar to contains element MER16 repetitive element:
3768	18810	29719	2.22	1.5E-01	U0894.1	NT	Mus musculus C/EBP β Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-3) gene, complete cds
3762	18823	29731	0.8	1.5E-01	7108398	NT	protein, mRNA
3795	18835	29740	0.86	1.5E-01	U07882.1	NT	XYNA1, Thymine nucleoside diphosphate, 4182 base pairs
3841	18920	29829	2.25	1.5E-01	AW66593.1	EST_HUMAN	HT1080.X1 Soares, NT_1, GRC, S1 Homo sapiens cDNA clone IMAGE:2661411 3'
3858	18926	29846	0.71	1.5E-01	AJ003105.1	NT	Populus trichocarpa cv. 'Trichocarpa 1883' gene
3896	18936	29847	0.71	1.5E-01	AJ003105.1	NT	Populus trichocarpa cv. 'Trichocarpa 1883' gene
4030	17115	30011	2.63	1.5E-01	AW396658.1	EST_HUMAN	h22922x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:2609539 3' similar to contains element MER16 repetitive element:
4213	17242	30127	9.83	1.5E-01	AL102384.2	NT	h22922x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:2609539 3' similar to contains element MER16 repetitive element:
4513	17538	30422	0.81	1.5E-01	BE179253.1	EST_HUMAN	601 833685F1 NIH, MGC, 7 Homo sapiens cDNA clone IMAGE:3938348 5'
4513	17538	30423	0.81	1.5E-01	BE179253.1	EST_HUMAN	601 833685F1 NIH, MGC, 7 Homo sapiens cDNA clone IMAGE:3938348 5'
4765	17776	30672	1.86	1.5E-01	BE179253.1	EST_HUMAN	601 833685F1 NIH, MGC, 7 Homo sapiens cDNA clone IMAGE:3938348 5'
4783	15717	28735	2.86	1.5E-01	BE179253.1	EST_HUMAN	601 833685F1 NIH, MGC, 7 Homo sapiens cDNA clone IMAGE:3938348 5'
4800	17947	30747	1	1.5E-01	BE172963.1	EST_HUMAN	CAC-HT10565-280202-245-310 HT10563 Homo sapiens cDNA
4830	17947	30748	1.2	1.5E-01	BE172963.1	EST_HUMAN	CAC-HT10565-280202-245-310 HT10563 Homo sapiens cDNA
5034	18048	31025	1.02	1.5E-01	AL101560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5134	18243	31025	1.02	1.5E-01	AL101560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5327	18434	31186	2.46	1.5E-01	P07596	SWISSPROT	THROMBOSPONDIN 1 (THROMBOSPONDIN 1)
5397	18482	31331	1.03	1.5E-01	AF268952.1	NT	Caenorhabditis elegans L1 b2a chain (labeled) gene, complete cds
5401	18504		5.5	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5516	18712	31870	4.35	1.5E-01	AW650754.1	EST_HUMAN	IL3-CT10219-100200-064-F10 CT10219 Homo sapiens cDNA
5559	18755	31922	7.17	1.5E-01	U08016.1	NT	Mus musculus transforming growth factor alpha (TGF α) mRNA, complete cds
5559	18755	31922	7.17	1.5E-01	U08016.1	NT	Mus musculus transforming growth factor alpha (TGF α) mRNA, complete cds
6012	19095	32265	0.76	1.5E-01	4508910	NT	Homo sapiens sodium channel, voltage-gated, type IV, brain polypeptide (SCN4A) mRNA
6120	19198	32422	1.74	1.5E-01	6763959	NT	Mus musculus DNA methylase 2 (Dnmt2) mRNA
6120	19198	32423	1.74	1.5E-01	6763959	NT	Mus musculus DNA methylase 2 (Dnmt2) mRNA
6120	19198	32423	1.74	1.5E-01	6763959	NT	Mus musculus DNA methylase 2 (Dnmt2) mRNA
6161	19266	32467	1.96	1.5E-01	AJ276503.1	NT	Mus musculus genomic fragment, 237 nt, cDNA clone IMAGE:3833981 5'
6319	18900	32830	3.25	1.5E-01	BE172958.1	EST_HUMAN	601 833685F1 NIH, MGC, 7 Homo sapiens cDNA clone IMAGE:3938348 5'
6376	18443		1.89	1.5E-01	4506399	NT	Homo sapiens POU3-1 (Pou3 domain) (POU3A) mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6478	19543	32791	1.7	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6681	29384	32985	1.8	1.5E-01	A0201039.1	NT	Archaeoglobus fulgidus section 08 of 172 of the complete genome
6681	19738	33013	4.63	1.5E-01	11417298	NT	Human sapiens chromosome 5 open reading frame 3 (CBORF3), mRNA
6692	19746	33028	1.8	1.5E-01	P45608	SWISSPROT	GLUTAMATE-CYSTEINE LIASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
8740	19766	33075	2.35	1.5E-01	Q29462	SWISSPROT	AMELOGENIN
8842	18995	33189	0.85	1.5E-01	AJ71780.1	EST_HUMAN	hw3570.31 NCI CGAP, GC58 Homo sapiens cDNA clone IMAGE:1241971.3'
8871	19924	33220	1.8	1.5E-01	P30743	SWISSPROT	HYPOTHETICAL 517 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7171	18462	31427	5.15	1.5E-01	AW97595.1	EST_HUMAN	EST1382378 IMAGE resources, MARG Homo sapiens cDNA
7214	25879		0.71	1.5E-01	A4811548.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
7434	25879		1.01	1.5E-01	A6710384.1	NT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
7521	20581	33946	1.69	1.5E-01	A6710384.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
7640	20763	34189	0.96	1.5E-01	AF290275.1	NT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
7640	20763	34170	0.96	1.5E-01	AF290275.1	NT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
7687	20822	34177	1.84	1.5E-01	AW50811.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
7687	20822	34178	1.84	1.5E-01	AW50811.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
8014	20352	34346	0.71	1.5E-01	U46590.1	NT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
8303	21362	34799	1.21	1.5E-01	P21303	SWISSPROT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
8662	21360	34950	0.97	1.5E-01	AA970317.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
8665	21623		1.01	1.5E-01	BE847798.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
8743	21713		13.33	1.5E-01	P16900.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
8776	21743	35165	1.99	1.5E-01	U27835.1	NT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
8940	21906	35330	1.79	1.5E-01	D84476.1	NT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
8982	21928		0.74	1.5E-01	P43446	SWISSPROT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
9190	22156	35595	1.31	1.5E-01	4501972	NT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
9460	22424	35862	3.05	1.5E-01	NT4225.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
9548	22511	35960	1.03	1.5E-01	BF955485.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
9555	22617		2.75	1.5E-01	AV759418.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
9760	22701		0.87	1.5E-01	AUT30007.1	EST_HUMAN	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element
9908	21331	34334	8.92	1.5E-01	U00458.1	NT	hpa30231 NCI CGAP, GC81 Homo sapiens cDNA clone IMAGE:1337019.3' similar to contains element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit E- BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3914	10924	28695	0.93	1.4E-01	R06232.1	EST_HUMAN	y974603.1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:14487.9
3914	10924	28695	0.93	1.4E-01	R06232.1	EST_HUMAN	y974603.1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:14487.9
4202	17263	30120	11.04	1.4E-01	A1690904.1	EST_HUMAN	x55602.21 NCBI CGAP_LUG4 Homo sapiens cDNA clone IMAGE:2273570.3
4202	17263	30121	11.04	1.4E-01	A1690904.1	EST_HUMAN	x55602.21 NCBI CGAP_LUG4 Homo sapiens cDNA clone IMAGE:2273570.3
4255	17294	30173	3.96	1.4E-01	AZ001710.1	NT	Thermoplasma maritima strain 22 of 138 of the complete genome
							460041.01 Soares fetal liver; sequeNcE INFLS.S1 Homo sapiens cDNA clone IMAGE:453973.3 similar to pXJ1057_mel1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN)containing Alu repetitive element
4440	17486		0.71	1.4E-01	AAT76237.1	EST_HUMAN	Homo sapiens phosphodiesterase 4A, cAMP-specific (dundee (Drosophila))homolog phosphodiesterase E2)
4703	17724	30616	0.92	1.4E-01	AAT63861	NT	PDE4EA, mRNA
4907	17924	30817	0.89	1.4E-01	A1686569.1	EST_HUMAN	A1686569 GFC Homo sapiens cDNA clone GDCU039.5
5379	18483	31358	4.72	1.4E-01	T00677.1	EST_HUMAN	yf16112.1 Stragelung lung (8637210) Homo sapiens cDNA clone IMAGE:17812.3
5402	18535	31391	4.95	1.4E-01	A0044568.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5420	18505	31362	4.09	1.4E-01	A0044555.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6430	19498	32749	2.8	1.4E-01	BZ32699.1	EST_HUMAN	h67620.1 NCBI CGAP_K4T1 Homo sapiens cDNA clone IMAGE:313359.3
6629	19697	32965	6.11	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBAI Homo sapiens cDNA clone HEMBA1000769.5
6628	19687	32966	6.11	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBAI Homo sapiens cDNA clone HEMBA1000769.5
5723	19709	33056	3.48	1.4E-01	A16082796.1	EST_HUMAN	z67162.11 Soares INF_1_GBC.S1 Homo sapiens cDNA clone IMAGE:3633788.1
6737	19793		1.26	1.4E-01	BE260593.1	EST_HUMAN	KY761006.1 Homo sapiens cDNA clone IMAGE:3633788.1
6769	19813	33093	2.02	1.4E-01	BF378533.1	EST_HUMAN	KY761006.1 Homo sapiens cDNA clone IMAGE:3633788.1
7833	20034		0.74	1.4E-01	AF18668.1	EST_HUMAN	DY2761040.0.781 (jonesy: hem2) Homo sapiens cDNA clone DKFZ67261.0610.5
7915	20075		0.97	1.4E-01	A0157931.1	EST_HUMAN	UH-Hd46-a2-05021.1 NCBI CGAP_S501 Homo sapiens cDNA clone IMAGE:2710289.3
7941	20076	33995	1.61	1.4E-01	F06746.1	EST_HUMAN	PC3C1001 normalized infant brain cDNA Homo sapiens cDNA clone c-1601
							wM412X1.NCBI CGAP_CL01 Homo sapiens cDNA clone IMAGE:246262.3 similar to SWICE1_HUMAN
							p4668 CASPASE-4 PRECURSOR, 1 kb
7984	20362		0.61	1.4E-01	A1702927.1	EST_HUMAN	h69620.31 Homo sapiens cDNA clone IMAGE:246262.3 similar to SWICE1_HUMAN
8027	20433	34039	0.82	1.4E-01	A00505.1	EST_HUMAN	CG10471.1 Swiss NMIMR_C14 Homo sapiens cDNA clone IMAGE:107363.3
8335	20505	34051	1.34	1.4E-01	A00505.1	EST_HUMAN	CG10471.1 Swiss NMIMR_C14 Homo sapiens cDNA clone IMAGE:107363.3
8918	21785		0.24	1.4E-01	A165947.1	EST_HUMAN	A165947 GLC Homo sapiens cDNA clone GLCF5306.3
							RQ3012.2 Soares NSF 6B_WT_P.A.P.S1 Homo sapiens cDNA clone IMAGE:2120111.3 similar to
9195	22102		0.97	1.4E-01	A1436903.1	EST_HUMAN	TCO427010.02710 GAG POLYPROTEIN, 1 kb
9284	22230	33561	4.98	1.4E-01	A4307075.1	EST_HUMAN	EST178162 Colon carcinoma (HCC) cell line Homo sapiens cDNA, 5' end
9346	22231	33735	0.96	1.4E-01	A0022659.1	EST_HUMAN	d69603.1 Y Morion Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487489.5
9476	22442	33619	0.94	1.4E-01	R62746.1	EST_HUMAN	y10905.11 Soares placenta N22HP Homo sapiens cDNA clone IMAGE:133073.5
9478	22442	33684	0.94	1.4E-01	R62746.1	EST_HUMAN	y10905.11 Soares placenta N22HP Homo sapiens cDNA clone IMAGE:133073.5

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
530	13631	28519	2.91	1.3E-01	AB013138.1	NT	Homo sapiens gene for NBS1, complete cds
637	13703	28624	0.76	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
637	13703	28625	0.76	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
845	13931	28625	0.76	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
845	13931	28625	0.76	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
895	13950	28625	1.32	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
1028	14074	27024	1.6	1.3E-01	AF13818.1	NT	Rattus norvegicus A-kinase anchor protein mRNK, complete cds
1129	14172	27213	2.88	1.3E-01	AF13818.1	NT	Rattus norvegicus A-kinase anchor protein mRNK, complete cds
1220	14288	27213	1.51	1.3E-01	AF13818.1	NT	Rattus norvegicus A-kinase anchor protein mRNK, complete cds
1438	14471	27665	0.93	1.3E-01	AF146077.1	EST_HUMAN	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
1876	14987	27665	2.07	1.3E-01	AF146077.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
2180	16195		1.66	1.3E-01	AJ243376.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
2298	16310		0.96	1.3E-01	AW81104.1	EST_HUMAN	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
2399	16397		3.94	1.3E-01	AE011918.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
2502	16503	28510	2.23	1.3E-01	AE011918.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
3485	18511	29432	0.98	1.3E-01	U21572.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
3735	18777	29680	0.91	1.3E-01	AF000001.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
3735	18777	29680	0.91	1.3E-01	AF000001.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
3741	19783	29680	0.89	1.3E-01	AF000001.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
3794	19777	29680	0.67	1.3E-01	AF000001.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
3816	18866	29752	0.74	1.3E-01	697840	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
4014	17053		1.48	1.3E-01	AL161581.2	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
4081	13703	28624	7.11	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
4081	13703	28625	7.11	1.3E-01	AJ277808.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
4163	17184		1.12	1.3E-01	AF020713.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
4185	17216		4.1	1.3E-01	AF056434.1	EST_HUMAN	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
4194	17226	30114	2.47	1.3E-01	AF026805.1	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
4215	17244	30126	20.19	1.3E-01	AF027471.1	EST_HUMAN	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK
4343	17370		1.49	1.3E-01	AL163380.2	NT	Human calicivirus HUNLV/Grlngton/93/UK RNA for capsid protein (ORF2), strain HUNLV/Grlngton/93/UK

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
4895	17830	30414	0.6	1.3E-01	M21972.1	NT	Bovine branched chain alpha-keto acid thiolipoyl transacylase mRNA, complete cds
4904	18338	30470	2.72	1.3E-01	BE727338.1	EST_HUMAN	60112606P1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:280003 5'
4964	17867	30470	2.72	1.3E-01	AA138019.1	EST_HUMAN	AA138019 PLACE1 Homo sapiens cDNA clone PLACE100483 5'
5014	18028	30470	0.93	1.3E-01	BF091680.1	EST_HUMAN	RC4-TN0071-18000-012-cds TN0077 Homo sapiens cDNA
5060	18070	30470	0.93	1.3E-01	BF091680.1	EST_HUMAN	h07005.X1 NCL_CGAP_X4712 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1 bt L1
5368	18801	31379	0.76	1.3E-01	AW46688.1	EST_HUMAN	L1 repetitive element
5438	18838	31446	1.98	1.3E-01	AW84417.1	EST_HUMAN	QYU-UN0088-100-000-188-208 UN0083 Homo sapiens cDNA
5478	18873	31446	0.91	1.3E-01	AF107783.1	NT	Emricale C virus ORF C-10 genome polyprotein RNA polymerase II ER81-02 (RPR2) gene, partial cds
5570	18873	31446	0.91	1.3E-01	AF107783.1	NT	Hepatitis C virus ORF C-10 genome polyprotein RNA polymerase II ER81-02 (RPR2) gene, partial cds
5665	18760	32096	0.68	1.3E-01	AF098840.1	NT	60187499P1 NIH_MGC 34 Homo sapiens cDNA clone IMAGE:4101119 5'
5813	18603	32096	0.85	1.3E-01	BF210920.1	EST_HUMAN	6020393372 NCL_CGAP_Bm57 Homo sapiens cDNA clone IMAGE:417253 5'
6089	19178	32396	0.58	1.3E-01	BF527281.1	EST_HUMAN	6020393372 NCL_CGAP_Bm57 Homo sapiens cDNA clone IMAGE:417253 5'
6099	19178	32397	0.58	1.3E-01	BF527281.1	EST_HUMAN	Schistosoma japonicum gene for alkali, complete cds
6300	19688	32697	1.29	1.3E-01	AB031326.1	NT	C jacchurion 4' full liver spleen TNF.S Homo sapiens cDNA clone IMAGE:232609 5'
6720	19776	33035	2.08	1.3E-01	X68891.1	NT	X68891.1 Homo sapiens cDNA randomly primed auxiliary Homo sapiens cDNA
6940	20164	33487	0.64	1.3E-01	U73423.1	EST_HUMAN	60145697F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:396079 5'
6955	20160	33487	0.82	1.3E-01	U73423.1	EST_HUMAN	60145697F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:396079 5'
7009	20136	33450	1.04	1.3E-01	BE726226.1	EST_HUMAN	602044345F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:4181866 5'
7009	20135	33451	1.04	1.3E-01	BE726226.1	EST_HUMAN	602044345F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:4181866 5'
7171	20234	33451	0.72	1.3E-01	BF526560.1	EST_HUMAN	602044345F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:207075 5'
7471	20449	33451	2.15	1.3E-01	H48954.1	EST_HUMAN	6012606P1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:296005 5'
8292	21261	34069	0.97	1.3E-01	BE27238.1	EST_HUMAN	Homo sapiens PRO0611 protein (PRO0611), mRNA
8306	21275	34069	1.98	1.3E-01	BE27238.1	EST_HUMAN	602187015T1 NIH_MGC 49 Homo sapiens cDNA clone IMAGE:429074 3'
8338	21305	34720	1.18	1.3E-01	BF065232.1	EST_HUMAN	601335325F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:389904 5'
8500	21548	35001	0.96	1.3E-01	BE262268.1	EST_HUMAN	S cerevisiae chromosome IV reading frame ORF_YOL04c
8617	21685	35001	0.6	1.3E-01	Z1102.1	NT	Homo sapiens core histone H2A2 (H2A2), mRNA
8688	21685	35001	4.98	1.3E-01	Z1102.1	NT	Homo sapiens core histone H2A2 (H2A2), mRNA
8728	21687	35001	4.98	1.3E-01	Z1102.1	NT	602187015T1 NIH_MGC 49 Homo sapiens cDNA clone IMAGE:429074 3'
8973	21840	35263	1.95	1.3E-01	BF065232.1	EST_HUMAN	X39411.1 Homo sapiens cDNA clone IMAGE:128284 5' similar to
9000	22336	35964	0.55	1.3E-01	R11172.1	EST_HUMAN	SP-RLB_RAT_P28016 60S RIBOSOMAL PROTEIN
9300	22635	35965	0.55	1.3E-01	R11172.1	EST_HUMAN	Y39411.1 Homo sapiens cDNA clone IMAGE:128284 5' similar to
9574	22638	35967	0.95	1.3E-01	11058003	NT	SP-RLB_RAT_P28016 60S RIBOSOMAL PROTEIN
9574	22638	35968	0.95	1.3E-01	11058003	NT	Plutella xylostella granulovirus, complete genome

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9627	22876	38132	3.9	1.3E-01	AF23128.1	NT	Oryzopsis sativus Hs-K-A1Pase alpha 2c subunit mRNA, complete cds
10129	23095		0.74	1.3E-01	NB8548.1	EST_HUMAN	J78377 Human fetal heart LaminA ZAP Express Homo sapiens cDNA clone J7837 8' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10411	23333		0.89	1.3E-01	830340	NT	Radius nonreducing peptidyl arginine deaminase, type IV (Pdi), mRNA
10489	23411	35908	0.89	1.3E-01	AW681599.1	EST_HUMAN	WR3-CT0232-201099-001-407 CT0222 Homo sapiens cDNA
10737	23702	37173	1.08	1.3E-01	AL163243.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
10891	23811	37173	0.65	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA, clone HEMBB1002837 5'
10893	23865	37312	0.45	1.3E-01	AU247836.1	EST_HUMAN	2820587.3pRime NH1_MGC.7 Homo sapiens cDNA, clone HEMBB1002837 5'
10893	23862		2.97	1.3E-01	BF330969.1	EST_HUMAN	WR4-8T0398-130700-0108 B10388 Homo sapiens cDNA
10893	23862		3.95	1.3E-01	867149.1	NT	Mus musculus cellin 2, muscle (C2), mRNA
11070	24019	38182	1.77	1.3E-01	AW053361.1	EST_HUMAN	262086.X1 NC1 CGAP C619 Homo sapiens cDNA, clone IMAGE:284444 3'
11070	24008	38183	1.77	1.3E-01	AW053361.1	EST_HUMAN	262086.X1 NC1 CGAP C619 Homo sapiens cDNA, clone IMAGE:284444 3'
11822	24803	38393	2.33	1.3E-01	BE570426.1	EST_HUMAN	262086.X1 NC1 CGAP C619 Homo sapiens cDNA, clone IMAGE:284444 3'
12387	25171	31817	1.83	1.3E-01	BE515445.1	EST_HUMAN	262086.X1 NC1 CGAP C619 Homo sapiens cDNA, clone IMAGE:284444 3'
12385	25260		3.33	1.3E-01	AL142760.1	NT	Gallus gallus egg 1, yolk, 60 Homo sapiens cDNA, clone IMAGE:284444 3'
12692	25337	31766	1.37	1.3E-01	BF57203.1	EST_HUMAN	90207755F1 NH1_MGC.82 Homo sapiens cDNA, clone IMAGE:284444 3'
12685	25475		1.48	1.3E-01	AB026828.1	NT	Ehrythrae fuscellis mRNA for AL245, complete cds
12915	25494		2.52	1.3E-01	AW001114.1	EST_HUMAN	WR4489.X1 Soares, Diethylmale, cDNA, MHCOD Homo sapiens cDNA, clone IMAGE:284444 3'
383	13406	26426	14.65	1.2E-01	AI421744.1	EST_HUMAN	IR3802.X1 NC1 CGAP Brn233 Homo sapiens cDNA, clone IMAGE:284444 3'
424	13119		1.38	1.2E-01	U68912.1	NT	ANNEXIN V (HUMAN)
549	13819		2.78	1.2E-01	AF039442.1	NT	Diclyosialium disodium ORF DG1016 gene, partial cds
1377	14411	27381	2.19	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CQ-45 mRNA, partial cds
1377	14411	27382	2.19	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2M4 Homo sapiens cDNA, clone NT2M400189 3'
1383	14417		4.89	1.2E-01	AV735949.1	EST_HUMAN	AU149146 NT2M4 Homo sapiens cDNA, clone NT2M400189 3'
1388	14421		0.92	1.2E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
1507	14540		1.23	1.2E-01	A4897474.1	EST_HUMAN	s44906.s1 Soares, NF1, T_GBC.31 Homo sapiens cDNA, clone IMAGE:146584 3' similar to TRIC16971
1635	14607	27643	1.92	1.2E-01	Q14934	SWISSPROT	Q16871 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1635	14607	27643	2.99	1.2E-01	A235402.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-AT3)
1635	14607	27656	18.89	1.2E-01	U68211.1	NT	950692.X1 NC1 CGAP Esoc Homo sapiens cDNA, clone IMAGE:180583 3'
1635	14607	27656	18.89	1.2E-01	U68211.1	NT	H.sapiens cDNA for endogenous removal like element
1934	14688		1.79	1.2E-01	AW440038.1	EST_HUMAN	U44-815-ant-s-103-U51 NC1 CGAP Sibs Homo sapiens cDNA, clone IMAGE:273454 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2193	13208	28227	1.65	1.2E-01	BF28460.1	EST_HUMAN	601621167F1 NH_MGC_62 Homo sapiens cDNA clone IMAGE:646224.5'
2294	13306	28326	1.21	1.2E-01	AL183213.2	NT	Homo sapiens chromosome 21 segment HS210215
2605	13596	28814	2.05	1.2E-01	AW690556.1	EST_HUMAN	QY348006-228001.281046 Homo sapiens cDNA
2602	13602	28824	1.61	1.2E-01	BE216988.1	EST_HUMAN	trh60421 NC1 CGAP L224 Homo sapiens cDNA clone IMAGE:3173803.3'
2738	13752	29746	37.89	1.2E-01	A033398.1	EST_HUMAN	trh60741 NC1 CGAP P411 Homo sapiens cDNA clone IMAGE:2228488.3' similar to TRG140448 Q14048 COLLAGEN VI ALPHA2(AC1) TYPE C-TERMINAL DOMAIN [1] contains element PTFB repetitive element
2846	13915	29838	1.4	1.2E-01	U18118.1	NT	Human F1A antibody binding protein (F1A) mRNA, partial cds
2913	13971	29895	2.03	1.2E-01	AT24070.1	EST_HUMAN	605 RIBOSOMAL PROTEIN L30 (HUMAN)
2948	14004	29829	2.32	1.2E-01	AF12470.1	NT	Human cDNA library: binding protein (E1A) mRNA, complete cds
3017	14075	29895	0.73	1.2E-01	AF5892.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3244	14238	29224	0.81	1.2E-01	AW37688.1	EST_HUMAN	QY14B10258-281056-021-005 B10258 Homo sapiens cDNA
3271	14342	29502	0.86	1.2E-01	U187803.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3333	14679	29502	0.86	1.2E-01	X55862.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3420	14638	29503	0.95	1.2E-01	X55862.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3769	14621	30125	0.7	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21) from 2795131 to 3013540
4211	17240	30126	2.16	1.2E-01	Z54355.1	NT	p clark1 mRNA; repeat region (ID 24177)
4211	17240	30126	2.16	1.2E-01	Z54355.1	NT	p clark1 mRNA; repeat region (ID 24177)
4761	17771	30867	0.98	1.2E-01	Z48183.1	NT	L-asculetum mRNA for glyoxalase-I
5168	18128	31036	0.91	1.2E-01	P16456	SWISSPROT	HENOY'SIN PRECURSOR
5160	18159	31039	0.91	1.2E-01	AL183227.2	NT	Homo sapiens chromosome 21 segment HS210227
5160	18159	31039	0.91	1.2E-01	AL183227.2	NT	Homo sapiens chromosome 21 segment HS210227
5164	18173	31052	1	1.2E-01	AL181516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5244	18242	31114	0.81	1.2E-01	BE674902.1	EST_HUMAN	trh60404822 NH_MGC_83 Homo sapiens cDNA clone IMAGE:3980711.3'
5322	18428	31178	0.75	1.2E-01	AA744958.1	EST_HUMAN	trh604044.1 NC1 CGAP G08T Homo sapiens cDNA clone IMAGE:1262690.3'
5373	18478	31351	0.91	1.2E-01	AF228391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 1-4b, and partial cds, alternatively spliced
5383	18487	31391	2.27	1.2E-01	W33035.1	EST_HUMAN	20360221 Saccharomyces cerevisiae, YNUPA Homo sapiens cDNA clone IMAGE:321659.5'
5442	18544	31496	2.15	1.2E-01	Z95269.1	NT	Homo sapiens gene encoding protein with 133 amino acids (C133)
5583	18679	31643	0.95	1.2E-01	Z48234.1	NT	Homo sapiens cDNA clone IMAGE:368561.5'
6324	19394	32936	2.68	1.2E-01	BE520945.1	EST_HUMAN	trh604044.1 NC1 CGAP G08T Homo sapiens cDNA clone IMAGE:368561.5'
6378	19444	32886	1.1	1.2E-01	P10942	SWISSPROT	WATKINS-TYPE P-SPECIFIC POLYPEPTIDE P1

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Ht BLAST E Value	Top Ht Accession No.	Top Ht Database	Top Ht Descriptor
8431	19497	32759	2.19	1.2E-01 AIW84275.1	EST_HUMAN	EST_HUMAN	LOC:CT0031-22:1099-113-604 CT0031 Homo sapiens cDNA
6460	19498	33215	1.36	1.2E-01 JM30925.1	NT	EST_HUMAN	Mouse polyclonal/retroviral RNA, complete cds
6804	19499	33145	0.89	1.2E-01 BF124788.1	EST_HUMAN	EST_HUMAN	602231212F1.NCI, CGAP, BIR67 Homo sapiens cDNA clone IMAGE:148368 f
6996	20100	33517	0.95	1.2E-01 AF269738.1	NT	EST_HUMAN	JC virus antigenome, VP2, VP3, VP1, large T antigen, and small t antigen genes, complete cds
7210	20233	33557	0.67	1.2E-01 H477789.1	EST_HUMAN	EST_HUMAN	pB0004711 Soares fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:193759 f
7210	20233	33568	0.67	1.2E-01 H477789.1	EST_HUMAN	EST_HUMAN	pB0004711 Soares fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:193759 f
7854	20769	34175	0.62	1.2E-01 AJ77741.1	NT	EST_HUMAN	Homo sapiens pituitary tumor enhancer binding factor 3 (alternative transcript) dnap76, dnap76 gamma, dnap76 alpha and ILP3)
8063	21090	34396	0.90	1.2E-01 JF28801.1	EST_HUMAN	EST_HUMAN	802159169F1.NIH, MGCC, B3 Homo sapiens cDNA clone IMAGE:426032 f
8098	21094	34433	0.67	1.2E-01 DF7458.1	NT	EST_HUMAN	Human mRNA for KIAA0282 gene, partial cds
8098	21094	34434	0.67	1.2E-01 DF7458.1	NT	EST_HUMAN	Human mRNA for KIAA0282 gene, partial cds
8224	21163	34721	1.24	1.2E-01 BE07072.1	EST_HUMAN	EST_HUMAN	Pho-B/8731-29030-02-B09 B00137 Homo sapiens cDNA
8295	21284	34678	0.71	1.2E-01 AF13763.1	EST_HUMAN	EST_HUMAN	wB69g33.1 NCI, CGAP, cdc Homo sapiens cDNA clone IMAGE:232800.1 similar to SW-6372_HUMAN
8381	21370	34724	3.76	1.2E-01 Q02359	SWISSPROT	SWISSPROT	Q02359.1 NCI, CGAP, cdc Homo sapiens cDNA clone IMAGE:232800.1 similar to SW-6372_HUMAN
8652	21620	35040	0.61	1.2E-01 A183881.1	EST_HUMAN	EST_HUMAN	NADH:UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX II)
8739	21707		10.95	1.2E-01 AW36962.1	EST_HUMAN	EST_HUMAN	pC040701 Barlsted clone HPR187 Homo sapiens cDNA clone IMAGE:237743 f
8759	21726		3.58	1.2E-01 AF53772.1	NT	EST_HUMAN	pc040701.1 NCI, CGAP, EST Homo sapiens cDNA clone IMAGE:238787.3 similar to gbM13462 LAMIN A (HUMAN)
8759	21765	35197	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1	NT	EST_HUMAN	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sh) gene, partial cds, and transcriptional regulator Cact (cactR) and multiple efflux protein CactB (cactB) genes, complete cds
8759	21765	35198	0.69	1.2E-01 AF53772.1			

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar ("Top Hit") BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11836	24719		1.54	1.2E-01	M81109.1	NT	Rabbit gp330gen-associated protein phosphatase regulatory subunit (R51) mRNA, complete cds
12162	25016		3.66	1.2E-01	AV586033.1	EST_HUMAN	AV586033 GLC Homo sapiens cDNA clone GLOFB12.3
12517	25246		2.78	1.2E-01	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 22
12593	25022	31304	6.17	1.2E-01	Q04612	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-ROX) (CDW138) (CD138 ANTIGEN)
12805	25432		2.66	1.2E-01	X53981.1	NT	Norwegian V946 gene for (CD44) (hyaluronin)
12857	25035	31310	1.98	1.2E-01	BE057418.1	EST_HUMAN	C14-817024.1 H1118393.1 Y10 BT0233 Homo sapiens cDNA
12889	25077	31731	6.62	1.2E-01	AJ256953.1	EST_HUMAN	924092.31 NO-CCOP-Luc Homo sapiens cDNA, clone IMAGE:168840.3
12911	25492		2.81	1.2E-01	L10187.1	NT	Chengdu alpha thymulin alpha 3 adult mRNA, partial cds
12917	25662		9.28	1.2E-01	D06433	SWISSPROT	Protein kinase chromosome 11, section B5 of the complete chromosome
12948	25525	31712	1.78	1.2E-01	AJ324424.1	NT	Protein kinase chromosome 11, section B5 of the complete chromosome
13082	16538		2.08	1.2E-01	E87116.1	EST_HUMAN	Bacterial subtilisin complete genome (section 15 of 21) from 2765131 to 3013540
13098	25523		1.53	1.2E-01	B511493.1	EST_HUMAN	BT18608.1 NCI CGAP B103 Homo sapiens cDNA clone IMAGE:2167083.3
998	13638	28552	1.01	1.7E-01	AJ051053.1	EST_HUMAN	mdm91.1 NCI CGAP C010 Homo sapiens cDNA clone IMAGE:1068520.3 similar to gp203665.7, m1
617	18982	26569	1.84	1.1E-01	AA595058.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1037	14135	27054	1.95	1.1E-01	BF097008.1	EST_HUMAN	G021268471 NH1_MGC_56 Homo sapiens cDNA clone IMAGE:4288771.5
1087	14135		1.48	1.1E-01	AL181560.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 60
1183	18620	27156	4.8	1.1E-01	AW972188.1	EST_HUMAN	ES7384143 IMAGE resequence, IMAGE Homo sapiens cDNA
1234	14320	27255	2.03	1.1E-01	D64004.1	NT	Synectocyte sp. PCS583 complete genome, 2107, 2689797-3002955
1524	14856	27637	2.46	1.1E-01	AL142033.1	EST_HUMAN	AL142033.1 PLACE2 Homo sapiens cDNA clone PLACE2000403.5
2322	15333		2.72	1.1E-01	6756219.1	NT	Mus muscular pro-1 cell antigen receptor alpha (P1ra), mRNA
2545	18526		0.93	1.1E-01	6078678.1	NT	Rattus norvegicus Procollagen II alpha 1 (Co2a1), mRNA
2574	16703		0.93	1.1E-01	AW821806.1	EST_HUMAN	RCO-S10379-310100-032-24 Homo sapiens cDNA
3048	16103	28017	0.95	1.1E-01	FQ226.1	EST_HUMAN	HSC-IRF027 normalized Infant brain cDNA Homo sapiens cDNA clone c1402.3
3432	16403	28396	1.86	1.1E-01	BE393185.1	EST_HUMAN	Mus muscular calcium channel, voltage-dependent, 1 type, alpha 1G subunit (Caen1g), mRNA
3486	16512	28433	1.18	1.1E-01	X52135.1	NT	00105687971 NH1_MGC_44 Homo sapiens cDNA clone IMAGE:3627068.5
3569	16541	28960	1.3	1.1E-01	X52135.1	NT	C. reinhardtii nuclear gene on linkage group XX
3661	16718		0.86	1.1E-01	Y07696.1	NT	A. thaliana gene for trypsinase
3715	16788		0.86	1.1E-01	P97384	SWISSPROT	ANNEXIN XI (CALCITRIOL-INDUCED ANNEKIN XI) (CIP-5)
3722	16788	28676	1.23	1.1E-01	X52708.1	NT	ANNEXIN XI (CALCITRIOL-INDUCED ANNEKIN XI) (CIP-5)
4137	17169	30054	1.14	1.1E-01	AW181942.1	EST_HUMAN	U65 gene gene (205,008,036-07) ST0289 Homo sapiens cDNA
4137	17169	30055	1.14	1.1E-01	AW181942.1	EST_HUMAN	URS-S1030-250100-025-07 ST0289 Homo sapiens cDNA
4281	17310		9.39	1.1E-01	AF157065.1	NT	Drosophila melanogaster Kareschi protein (Klar) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7991	20902	34294	2.99	1.1E-01	AY87884.1	EST - HUMAN	ab31508.s1 Soares_pantylipid_lipase, N44P1 Homo sapiens cDNA clone 124043 3' similar to gb:303483
8111	21048	34444	0.48	1.1E-01	BE78290.1	EST - HUMAN	CHROMOGRANIN A PRECURSOR (CHROMOG) Homo sapiens cDNA clone IMAGE:387229 5'
8301	21270	34682	0.48	1.1E-01	U97482.1	NT	304740355T1 NH_38C5.51 Homo sapiens cDNA clone IMAGE:387229 5'
8550	21518	34639	1.91	1.1E-01	AA463574.1	EST - HUMAN	Melanocortin 4 precursor (MCR4) Homo sapiens cDNA clone IMAGE:943382
8550	21518	34637	1.91	1.1E-01	AA463574.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
8568	21566	34682	1.1	1.1E-01	U97233.1	NT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
8637	21605		1.08	1.1E-01	U97191E.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
8684	21682	35086	1.59	1.1E-01	AL154549.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9170	22138	35552	1.82	1.1E-01	U02482.1	NT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9283	22229	35960	0.98	1.1E-01	U803724.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9302	22377	35750	0.98	1.1E-01	U503096.1	NT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9398	22383	35784	2.37	1.1E-01	AA122183.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9398	22383	35783	2.37	1.1E-01	AA122183.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9490	22434	35864	0.77	1.1E-01	U12272.1	NT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9520	22443	35928	2.1	1.1E-01	U72876.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9545	22509		0.92	1.1E-01	BE003005.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9545	22509		0.96	1.1E-01	BE14205.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
9630	22718		2.05	1.1E-01	BF085146.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
10270	23135		0.88	1.1E-01	AL161543.2	NT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
10476	23338		1.05	1.1E-01	BE315506.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
10596	23468		1.01	1.1E-01	U60560.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
10701	23623	37119	1.05	1.1E-01	U02285.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
11195	10103	20017	1.7	1.1E-01	U02285.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
11287	24218		3.13	1.1E-01	AF169322.1	NT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
11384	24331	37890	3.51	1.1E-01	R22708.1	EST - HUMAN	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
11392	24338	37898	1.54	1.1E-01	6981351	NT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
11542	24483	38035	2.18	1.1E-01	U21910.1	NT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
11542	24483	38035	2.18	1.1E-01	U21910.1	NT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382
11636	24573	38137	3.69	1.1E-01	P17437	SWISSPROT	NP45410.1 NC_C03AP Thy1 Homo sapiens cDNA clone IMAGE:943382

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1280	2504		2.03	1.E-01	AA182183.1	EST_HUMAN	263372.1 Stragapine muscle 937209 Homo sapiens cDNA clone IMAGE:327743.3'
1279	25161		3.69	1.E-01	BE767028.1	EST_HUMAN	RC201112.1 D96004.014403 NT112 Homo sapiens cDNA
1283	27322		2.18	1.E-01	BE374588.1	EST_HUMAN	61160656R.NH.MGC.83 Homo sapiens cDNA clone IMAGE:395604.3'
1280	2580	31699	1.30	1.E-01	BF237783.1	EST_HUMAN	61160656R.NH.MGC.84 Homo sapiens cDNA clone IMAGE:415408.5'
1305	3169		1.32	1.E-01	P14400	SWISSPROT	ELECTROMOTOR NEURON ASSOCIATED PROTEIN 1
1305	14345		2.05	1.E-01	Q6285	SWISSPROT	DEUTERONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1277	14312	27273	1.05	1.E-01	A185459.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
1393	14402	27308	2.25	1.E-01	AL151504.2	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
2497	15500	26526	1.18	1.E-01	AI1451395.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
3524	15570	26403	1.32	1.E-01	BF703390.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
3732	16774	26699	0.68	1.E-01	BF703390.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
3849	16850	26792	2.49	1.E-01	AF220705.1	NT	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
3849	16850	26792	2.49	1.E-01	AF220705.1	NT	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
3849	16850	26792	2.49	1.E-01	AF220705.1	NT	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
4585	17607		0.85	1.E-01	AF736703.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
4741	17781	30955	1.32	1.E-01	U56490.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
4957	17972	30963	2.34	1.E-01	AI1962344.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
6297	18274	31138	0.97	1.E-01	AV172471.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
5273	18279		1.04	1.E-01	AV1763950.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
6304	18497		8.1	1.E-01	U56490.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
5492	18592		0.89	1.E-01	U56490.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
6980	19085		0.87	1.E-01	AK024472.1	NT	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
6140	19216	32445	12.15	1.E-01	AF274975.1	NT	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
6469	19544	32762	0.9	1.E-01	AA451876.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
6463	19548	32797	0.85	1.E-01	AA400335.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
7220	20242		1.82	1.E-01	Q28821.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
8039	20377		2.16	1.E-01	Y74488.1	NT	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
8108	21045	34444	0.85	1.E-01	AJ011400.1	NT	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
8108	21045	34445	0.85	1.E-01	AJ011400.1	NT	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2
8295	21204	34645	0.83	1.E-01	AA361091.1	EST_HUMAN	W68001.1 NCL CGAP.14011 Homo sapiens cDNA clone IMAGE:349877.3' similar to contains MER7.2

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon ID NO:	OSF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6287	21266	34695	0.48	1.0E-01	AF262225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6287	21259	34696	0.43	1.0E-01	AF262225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8069	21474		0.68	1.0E-01	4793305	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8837	21804		0.84	1.0E-01	AW19397.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
9540	22303	35852	1.19	1.0E-01	AF102852.2	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
9542	22303	36241	0.84	1.0E-01	AF102852.2	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
9550	22301		0.84	1.0E-01	U078739.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
9552	22326		2.63	1.0E-01	AF201694.1	NT	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
9552	22326	36259	0.81	1.0E-01	W011935.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
9552	22326	36898	0.81	1.0E-01	AF240154.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
9140	21065		1.63	1.0E-01	BF240154.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
10355	23220	36703	8.1	1.0E-01	AB044798.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
10355	23220	36704	8.1	1.0E-01	AB044798.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
10502	23424		0.95	1.0E-01	AV1957405.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
10507	23429	36926	0.59	1.0E-01	T51652.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
10504	23416	37110	0.95	1.0E-01	BE762762.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
11018	23983		1.65	1.0E-01	AJ1159127.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
11370	24317	37844	2.25	1.0E-01	BF242946.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
11370	24317	37845	2.25	1.0E-01	BF242946.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
11728	24914	38191	3.16	1.0E-01	BE760543.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
12365	25451		4.11	1.0E-01	BE537718.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
12365	25451		2.16	1.0E-01	7662105	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12880	25262		2.89	1.0E-01	X00954.1	NT	Drosophila melanogaster fts gene
12804	25265		1.45	1.0E-01	AA737951.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
12768	25428		4.47	1.0E-01	BE537719.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
12843	25481		1.32	1.0E-01	BE537719.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
12843	25522		6.14	1.0E-01	U06854.1	NT	Quaternary proteinase inhibitor (QPI) gene, complete cds
13016	25891		7.59	1.0E-01	AP001507.1	NT	Bacillus thuringiensis genomic DNA, section 114
13016	25866					NT	Bacillus thuringiensis genomic DNA, section 114
2769	15761	28797	1.74	9.8E-02	AF274038.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II (regulatory subunit) (pale-R1) mRNA
2768	15760	28803	1.71	9.8E-02	BE543554.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
2768	15760	28803	1.71	9.8E-02	BE543554.1	EST_HUMAN	ABO1X1 NC-300000 Homo sapiens cDNA clone IMAGE:337699 3' similar to gpX17208 495
3280	16334	23254	1.48	9.8E-02	AF208510.1	NT	Homo sapiens nuclear interleukin-3 alpha gene, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID	Exon SEQ ID	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3974	17014	26928	0.67	9.E-02	A021837.1	EST_HUMAN	zfx4503.x5 Scores every tumor NHOBT Homo sapiens cDNA clone IMAGE:7408273
4177	17288	30822	1.02	9.E-02	B5E7426.1	EST_HUMAN	TG717C12.NCI CGAP_L24 Homo sapiens cDNA clone IMAGE:327669.3
7044	20969	33373	2.50	9.E-02	B5E71496.1	EST_HUMAN	707102A.HUG11.MGC_71 Homo sapiens cDNA clone IMAGE:330080.4
7103	18394	31239	7.77	9.E-02	D8370.1	NT	Aspergillus terreus ES2D mRNA for plasticidin S diaminease, complete cds
8247	21216	34624	0.65	9.E-02	AW10088.1	EST_HUMAN	pdd306c.v1.NCI CGAP_Ox26 Homo sapiens cDNA clone IMAGE:2569538.3 similar to Alu repetitive element;contains element MIR repeat repetitive element
8247	21216	34624	0.65	9.E-02	AW10088.1	EST_HUMAN	pdd306c.v1.NCI CGAP_Ox26 Homo sapiens cDNA clone IMAGE:2569538.3 similar to contains Au repetitive element;contains element MIR repeat repetitive element
8912	22016	36008	1.23	9.E-02	G795111	EST_HUMAN	Mus musculus phosphatidyl transfer protein (Ptp), mRNA
9605	19355	31516	1.28	9.E-02	G49338.1	NT	O active HMGCoA gene for alpha-amylase
3160	15216	25130	4.50	9.E-02	AF14627.1	NT	Daucus carota leucanthopyridin oxigenases 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4291	17280	30160	6.93	9.E-02	AF257329.1	NT	Leposaphes miculatus beta-tubulin mRNA, complete cds
4291	17280	30160	6.93	9.E-02	AF257329.1	NT	Leposaphes miculatus beta-tubulin mRNA, complete cds
7123	20679	30161	0.94	9.E-02	X34138.1	NT	Human HPTT delta mRNA for protein tyrosine phosphatase delta
9609	22013	36143.1	1.21	9.E-02	U61943.1	NT	Human lamin B1 chain gene, exon 28
11738	23943	37465	1.83	9.E-02	BF37421.1	EST_HUMAN	RF1440763.F37.NCI_MGC_89 Homo sapiens cDNA clone IMAGE:3564287.5
12330	21711	3184	1.84	9.E-02	E830731	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1392	14497	27357	1.75	9.E-02	AB00898.1	NT	Nov abnonsens mRNA for NACP-male enzyme, complete cds
1589	14631	14631	1.33	9.E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (leptodactylis, transmembrane dwarfism) (FGFR3) mRNA
2202	15283	28303	2.78	9.E-02	B5E6889.1	EST_HUMAN	YH147055.SJ26SC.08E_10518 Homo sapiens cDNA
4098	17047	31398	0.88	9.E-02	G09766	SWISSPROT	SELL SYNGRASE A33 ANTIGEN PRECURSOR (ALTOPROTEIN A33)
4098	17047	31398	0.88	9.E-02	G09766	SWISSPROT	Cyclo-oxygenase 1 myelin basic kinase (mbp) and DNA polymerase III delta prime subunit (dnpc) genes, complete cds
8418	18521	31398	0.88	9.E-02	AF096188.1	NT	Condenser crescentalis Phenyldiolase kinase (mbp) and DNA polymerase III delta prime subunit (dnpc) genes, complete cds
8418	18521	31398	0.88	9.E-02	AF096188.1	NT	Condenser crescentalis Phenyldiolase kinase (mbp) and DNA polymerase III delta prime subunit (dnpc) genes, complete cds
8130	10207	32432	1.48	9.E-02	AW964778.1	EST_HUMAN	Bacillus subtilis stable genome (section 16 g 2), from 2897/71 to 32134/10
7617	20492	33943	3.35	9.E-02	D267116.1	NT	Ywt1403.1 Wistar-Kyoto Olfactory Enkephalin Homo sapiens cDNA clone IMAGE:254758.3
8315	21284	34697	1.09	9.E-02	N22798.1	EST_HUMAN	ywt1403.1 Wistar-Kyoto Olfactory Enkephalin Homo sapiens cDNA clone IMAGE:254758.3
8315	21284	34698	1.09	9.E-02	N22798.1	EST_HUMAN	ywt1403.1 Wistar-Kyoto Olfactory Enkephalin Homo sapiens cDNA clone IMAGE:254758.3
9201	22167	35597	1.32	9.E-02	A0193884.1	EST_HUMAN	PEPTIDYL-PROLYL-CIS-TRANS ISOMERASE 4 (HUMAN)
20472	20472	20472	2.01	9.E-02	U58333.1	NT	Mus musculus ligand (lign) mRNA, partial cds
11526	24410	28066	1.27	9.E-02	A000721.1	EST_HUMAN	cat7417.1 Scores_NhmMpu_S1 Homo sapiens cDNA clone IMAGE:1679486.3
2332	19591	28066	1.27	9.E-02	A000721.1	EST_HUMAN	cat7417.1 Scores_NhmMpu_S1 Homo sapiens cDNA clone IMAGE:1679486.3

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Table 4

Single Exon Probes Expressed in Bone Marrow

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11280	20797	34173	2.22	9.4E-02	U7853.1	NT	Human BRCA1, RhoA and cell genes, complete cds, and p53 gene, partial cds
12212	29829		10.73	9.4E-02	U31816.1	NT	Reticular calcium channel alpha-1C subunit (RQB2) mRNA, partial cds
13087	25717	31982	1.37	9.4E-02	U27698.1	NT	Human p49b1.1:1 beta-actin-GABA transporter mRNA, complete cds
3021	16039		1.71	9.3E-02	489259	NT	Human sapiens BAI1-associated protein 3 (BAIP3) mRNA
3011	16039		7.38	9.3E-02	681245	NT	Human sapiens nasopharyngeal epithelium specific protein 1 (NESG1) mRNA
3270	16324	26247	2.01	9.3E-02	BF57511.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
4179	17210	30396	3.73	9.3E-02	BC391943.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
4179	17210	30396	3.73	9.3E-02	BC391943.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
4718	17139	30877	3.73	9.3E-02	AF014574.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
5745	18359		0.66	9.3E-02	AF014574.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
8133	21031	34490	0.59	9.3E-02	AL183210.2	NT	Bacillus thuringiensis serotype 4 DNA, region 114
8591	21459	34976	0.16	9.3E-02	AW496027.1	EST_HUMAN	Homo sapiens chromosome 21 segment 1537C010
9480	22444		0.42	9.3E-02	AL113176.1	NT	EST169 Human Fetal Brain MATCHMAKER cDNA, library/Homo sapiens cDNA
10058	22926	36464	0.32	9.3E-02	BE95283.2	EST_HUMAN	Bacillus cereus strain T4 cDNA, library under conditions of nitrogen deprivation
10551	22473	36967	3.65	9.3E-02	Q16034	SWISSPROT	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
10551	22473	36968	3.65	9.3E-02	Q16034	SWISSPROT	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
10583	23635		3.59	9.3E-02	AW205117.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
12432	25750		2.55	9.3E-02	AJ248550.1	NT	Phorbol-12-myristate-13-acetate-induced protein 1 (P12) gene for DNA, partial cds
12831	25778		9.12	9.3E-02	AW488500.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
13040	28924		2.24	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region, beta-2-microglobulin (beta-2-microglobulin) gene, partial cds, B1p1 (B1p1), sparsely (sparsely), RAGDS-like factor (RUF), K2 (K2), BINGA (BINGA), beta1, 3, galactosyl transferase (beta-1, 3-galactosyl tr-
231	13331	26252	7.81	9.2E-02	U60315.1	NT	Neisseria meningitidis serotype 4, complete genome
231	13331	26253	7.81	9.2E-02	U60315.1	NT	Neisseria meningitidis serotype 4, complete genome
231	13331	26254	7.81	9.2E-02	U60315.1	NT	Neisseria meningitidis serotype 4, complete genome
2236	15250		2.72	9.2E-02	RC4156.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
3194	16249	20167	3.72	9.2E-02	Q28831	SWISSPROT	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
3316	16359	29289	0.89	9.2E-02	AA53434.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
3599	16544		1.27	9.2E-02		NT	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
4266	17295		1.24	9.2E-02	U62048.1	NT	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
4337	17364		0.84	9.2E-02	BC290722.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'
4659	17689	30679	1.4	9.2E-02	X95403.1	NT	Gallus gallus Vax-CX gene
8342	21311	34726	1.87	9.2E-02	U49230.1	EST_HUMAN	h2753589F1.NH_U003_31 Homo sapiens cDNA clone IMAGE:428328 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8517	21485	34869	2.19	9.2E-02	X69236.1	NT	H. vulgaris xylose isomerase gene
12002	24679	39475	1.74	9.2E-02	AF028582.3	NT	Mesocricetus auratus subcutis precursor (OVI) gene, complete cds
13019	25990		1.31	9.2E-02	11698972	NT	Podobasus arenae mitochondrion, complete genome
423	13118	26017	7.62	9.1E-02	X7695.1	NT	O. cuniculus X12 neuron gene
3954	16727		0.96	9.1E-02	AF372569.1	EST_HUMAN	P102310346-191246-001-032 E10349 Homo sapiens cDNA
4510	17335	30419	1.5	9.1E-02	AF161554.2	NT	Antelopeia thallina DNA chromosome 1, complete fragment No. 54
5304	18307		0.98	9.1E-02	U01059.1	NT	Codon intestinalis embryo-specific mRNA, complete cds
5819	18509	32063	1.27	9.1E-02	AF129756.1	NT	Homo sapiens INSIG4 gene, partial cds and CLIC1, DOAH, G6b, G6c, G6d, G6e, G6f, BAT5, G6b, CSK2B, BAT4, G4, Ape M, BAT3, BAT2, AIF-1, IOT, LST-1, LTB, TNF, and LTA genes, complete cds
7528	26000		0.52	9.1E-02	AF020303.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinase gene families
7616	26576	33639	12.92	9.1E-02	AF020356.1	EST_HUMAN	af7a65.V1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7937	26979	24269	0.14	9.1E-02	AF020094.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7977	26916	34007	0.82	9.1E-02	U02073.1	NT	Mus musculus thymopoietin beta mRNA, complete cds
9276	22242	35071	0.82	9.1E-02	U14376.1	NT	Homo sapiens gamma adducin gene, exon 9
10793	23714		1.82	9.1E-02	T02984.1	EST_HUMAN	FB10F10 Fetal brain, Striatum Homo sapiens cDNA clone FB10F10 3' end
10923	23744	37245	1.24	9.1E-02	U74059.1	NT	15619-Cy1 actin (Tf-fucosylates graafian-sea uridine, embryo, Genomic, 5275 nt)
10932	23742	37271	0.8	9.1E-02	U11487.1	NT	A. thaliana RHT1, TCI, G14587-5, G14587-6, and PRL1 genes
12101	25609		3.53	9.1E-02	9633494	NT	Bacteriophage M1, complete genome
12993	25919		2.15	9.1E-02	AA176901.1	EST_HUMAN	z38H12.1? Striatum muscle 937200 Homo sapiens cDNA clone IMAGE:611783 3' similar to
12988	26217		1.62	9.1E-02	AF032095.1	NT	SW-TRT3_HUMAN P45376 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12916	26771		1.78	9.1E-02	AJ291380.1	NT	Rattus norvegicus cell cycle protein p56CDC gene, complete cds
						NT	Homo sapiens partial MUC3B gene for MUC3B mcdn, scores 1-11
						NT	FOLATE RECEPTOR ALPHA PRECURSOR (PR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV-19) (V8 CELL FBP)
746	13907	25747	6.38	9.0E-02	P16326	SWISSPROT	hx68910.1 NC_000470 Homo sapiens cDNA clone IMAGE:3176542 3' similar to contains AU
						NT	invertebrate element
16540	14872	27645	6.7	9.0E-02	BE220482.1	EST_HUMAN	PIV4 p60c95-06 from USA, envelope glycoprotein (env) gene, partial cds
2815	19907	28928	6.5	9.0E-02	AF138522.1	NT	PIV4 p60c95-06 from USA, envelope glycoprotein (env) gene, partial cds
2815	19907	28927	6.5	9.0E-02	AF138522.1	NT	PIV4 p60c95-06 from USA, envelope glycoprotein (env) gene, complete cds
3347	10395	29021	1.11	9.0E-02	AF279135.1	NT	Deoxyribonucleoside triphosphate (dNTP) synthase, putative mouse, liver mRNA, 1474 nt
4326	17395	30243	0.83	9.0E-02	S66757.1	NT	Concated-3'-shunting globin (beta) (beta) concated-3'-shunting globin, liver mRNA, 1474 nt
4326	17395	30244	0.83	9.0E-02	S66757.1	NT	Concated-3'-shunting globin (beta) (beta) concated-3'-shunting globin, liver mRNA, 1474 nt

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12500	25268		1.81	8.5E-02	6690220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hd1), mRNA
12501	25269		1.5	8.5E-02	U25895.1	NT	Human, hippocampus/hippocampus-enriched gene 1 (Hd1), mRNA
1374	14008	27378	1.25	8.5E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3321	18991	29874	1.03	8.5E-02	AA295128.1	EST - HUMAN	EST11838 Ovaria Homo sapiens cDNA 5' end
4065	17101		3.7	8.5E-02	U000208	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 35K KOD SUBUNIT (TAH1135) (TAH1130) (TAH1130)
4207	17209		1.29	8.5E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (GHGA), mRNA
4331	17369		2.3	8.5E-02	4580428	NT	Homo sapiens period gene 6 (period, keratins) (PAX6), isoform b, mRNA
7792	20744		0.95	8.5E-02	D17520.1	NT	Shrew, S. 13.1 Shrew, cDNA (8537204) Homo sapiens cDNA clone IMAGE:5662383
9339	22204	35732	1.32	8.5E-02	AJ151972.1	EST - HUMAN	60118177051 NH: M5C-7 Homo sapiens cDNA clone IMAGE:3335448 5'
11453	24369	37041	3.43	8.5E-02	BE294455.1	EST - HUMAN	60118177051 NH: M5C-7 Homo sapiens cDNA clone IMAGE:3335448 5'
11453	24369	37042	3.43	8.5E-02	BE294455.1	EST - HUMAN	60118177051 NH: M5C-7 Homo sapiens cDNA clone IMAGE:3335448 5'
11503	24531	39088	5.78	8.5E-02	U040726.1	EST - HUMAN	60118177051 NH: M5C-7 Homo sapiens cDNA clone IMAGE:3335448 5'
12441	25204	31627	2.4	8.5E-02	Z11691.1	NT	Saccharomyces cerevisiae XIV reading frame ORF YNL285W
1654	14686	27691	1.55	8.7E-02	AJ07281.1	EST - HUMAN	aa05501.51 Source: NIH/NHLBI, 3T1 Homo sapiens cDNA clone IMAGE:1981161 3'
3707	16750	22655	3.84	8.7E-02	U82955.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and blycane (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3707	16750	22655	3.84	8.7E-02	U82955.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and blycane (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4138	17195	30550	1.2	8.7E-02	AF178503.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5138	18147	31053	1.02	8.7E-02	AE000965.1	NT	Methanobacterium thermoautotrophicum (strain 1776161 to 1189402) (section 101 of 148) of the complete genome
5138	18175	31053	0.97	8.7E-02	8660384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
5138	18175	31053	0.97	8.7E-02	8660384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
5337	18400	31565	6.04	8.7E-02	AA386975.1	EST - HUMAN	z25598a.1 NCI: CGAP: GC51 Homo sapiens cDNA clone IMAGE:70138 3'
5337	18400	31565	6.04	8.7E-02	AA386975.1	EST - HUMAN	z25598a.1 NCI: CGAP: GC51 Homo sapiens cDNA clone IMAGE:70138 3'
7032	20147	33467	0.81	8.7E-02	AJ271855.2	NT	Mus musculus partial Koniq' gene for potassium channel protein, isoform 10-14
7032	20147	33467	0.81	8.7E-02	AJ271855.2	NT	Mus musculus partial Koniq' gene for potassium channel protein, isoform 10-14
7243	19078	33275	0.83	8.7E-02	AF28142.1	NT	Oncorhynchus mykiss TA1 binding protein 1 mRNA, partial cds
8650	21827	33550	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 355 of the complete genome
8650	21827	33550	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 355 of the complete genome
11037	24030	35251	2.15	8.7E-02	U04759.1	NT	Oryzias latipes cytochrome P-450 (CYP4A4) gene, 5' end
11641	24578	38144	1.79	8.7E-02	AJ007763.1	NT	Gluconobacter oxydans 1201-16 and 1201-16a genes

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Max Similar (Clustal W) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12121	24822	35953	1.99	8.7E-02	274090.1	NT	S cerevisiae chromosome IV reading frame ORF YDL012c
12123	24992	35994	1.99	8.7E-02	274090.1	NT	S cerevisiae chromosome IV reading frame ORF YDL012c
12428	25190		1.8	8.7E-02	X71118.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12507	14292	27355	6.2	8.6E-02	AJ271735.1	NT	Human spleen X4 pseudotuberculosis region, segment 2/2
2250	13270	26265	1.95	8.6E-02	BE403867.1	EST_HUMAN	601304201P11NH_MGC_21 Homo sapiens cDNA clone IMAGE3636443 5'
3252	12371	25176	4.41	8.6E-02	U5468.1	NT	Trichomonas vaginalis vesiculobulin (vblu1) gene, complete cds
3698	16701		4.37	8.6E-02	AF153362.1	NT	Drosophila discaloid adenylyl cyclase (acy1) gene, complete cds
3793	19334		0.96	8.6E-02	U29187.1	NT	Mus musculus long nucleobase protein (Pmpb) and phospholipid protein (Pmpd) genes, complete cds
4512	17537	30421	0.97	8.6E-02	U58175.1	NT	Oryzopsis cinnulata glutelin-2 gene, untranscribed exon and 5' flanking region
5170	18178		1.09	8.6E-02	13419.1	NT	Oncomelan virus-like hepatitis C virus, 3' end, bicistral any open homologue, flanking/ochromic c
5278	16282		1.09	8.6E-02	AB011163.1	NT	Human spleen mRNA for G3A359.1 protein, partial cds
6213	19287	32520	4.24	8.6E-02	Y08283.1	NT	Homo sapiens LON1B gene
6510	19574	32938	1.48	8.6E-02	U00446.1	NT	Homo sapiens LON1B gene
6510	19574	32939	1.48	8.6E-02	U00446.1	NT	Homo sapiens LON1B gene
7534	20781	34159	1.01	8.6E-02	P14616	SWISSPROT	Mus musculus insulin receptor-related protein (SRCAP) mRNA
8322	21231	34940	1.33	8.6E-02	5730066	NT	Human spleen Src2-related CBP activator protein (SRCAP) mRNA
8322	21231	34941	1.33	8.6E-02	5730066	NT	Human spleen Src2-related CBP activator protein (SRCAP) mRNA
8405	21374	34782	0.86	8.6E-02	11427438	NT	Human spleen Src2-related CBP activator protein (SRCAP) mRNA
8409	21438		0.81	8.6E-02	U00168.1	NT	Human spleen Src2-related CBP activator protein (SRCAP) mRNA
10094	20020	30495	1.04	8.6E-02	AF111703	NT	Human spleen Src2-related CBP activator protein (SRCAP) mRNA
10131	20957		1.57	8.6E-02	AF165218.1	EST_HUMAN	Human spleen Src2-related CBP activator protein (SRCAP) mRNA
10513	23435	39533	0.97	8.6E-02	AF22804.1	NT	Human spleen Src2-related CBP activator protein (SRCAP) mRNA
11579	24517	39072	2.47	8.6E-02	BF30906.1	EST_HUMAN	Human spleen Src2-related CBP activator protein (SRCAP) mRNA
11579	24517	39073	2.47	8.6E-02	BF30906.1	EST_HUMAN	Human spleen Src2-related CBP activator protein (SRCAP) mRNA
11757	23922	37441	9.23	8.6E-02	AEO01073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11991	24782	39370	1.57	8.6E-02	AF23360.1	NT	Bacillus stearothermophilus BarF methylase (FIM) and BarF restriction endonuclease (FIR) genes, complete cds
2405	15413	28437	2.86	8.6E-02	AEO00952.1	NT	Helicobacter pylori 26992 section 130 of 134 of the complete genome
3792	18846	32028	0.71	8.6E-02	A486491.1	EST_HUMAN	GRB307.1 NCL_GGAP_K08 Homo sapiens cDNA clone IMAGE1192617 3' similar to GRK1144 HLA
5793	19835		1.92	8.6E-02	P09399	SWISSPROT	CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN)
8127	19205	32425	6.34	8.6E-02	AF23385.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds

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Table 4

Singla Exon Probes Expressed in Bone Marrow

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean (Top) HI BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10706	23026		0.5	8.3E-02	AF020409.1	NT	Dichthelium discolorum Doc2a (doc2a) mRNA, complete cds
12444	25924		1.48	8.3E-02	BE594848.1	EST_HUMAN	501644707P NIH_10GC_38 Homo sapiens cDNA clone IMAGE:3026863 5'
1379	14413		7.44	8.2E-02	108170.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
1464	14827	27498	1.77	8.2E-02	AF167077.2	NT	Gallus gallus glutamate transporter (EAAT4) mRNA, complete cds
3089	16147		2.24	8.2E-02	AL162266.2	NT	Homo sapiens chromosome 21 segment HS210006
3815	16856		1.61	8.2E-02	AL161488.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4033	17071	28972	1.22	8.2E-02	AL162266.2	NT	Homo sapiens chromosome 21 segment HS210006
4313	17342	32222	5.83	8.2E-02	P46800	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4313	17342	32222	5.83	8.2E-02	P46800	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4313	17342	32222	5.83	8.2E-02	P46800	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5108	18116	30662	4.13	8.2E-02	J78039.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5108	18128	31004	4.13	8.2E-02	J78039.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5300	18128	31004	0.95	8.2E-02	J78039.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5408	18511	31389	1.47	8.2E-02	AF030030.1	EST_HUMAN	501435878P NIH_10GC_71 Homo sapiens cDNA clone IMAGE:3024523 5'
7221	20243	33577	2.84	8.2E-02	AF030030.1	NT	Boa taurus connective tissue type I procollagen (CT1) gene, complete cds
8005	20944		0.6	8.2E-02	AF145344.1	EST_HUMAN	AV145341 CB Homo sapiens cDNA clone CB1A197 5'
9057	22023		0.45	8.2E-02	J26397.1	NT	Radius norvegicus plasma membrane G2p2-21P5a isoform 3 (PMCA3) gene, 5' flanking region
9124	22030	33516	2.76	8.2E-02	AW87126.1	EST_HUMAN	RC2P10094-031260-011-005 P10094 Homo sapiens cDNA
8693	22835	38346	5.43	8.2E-02	X04197.1	NT	Boa taurus connective tissue type I procollagen (CT1) gene, complete cds
10121	22047	36526	2.38	8.2E-02	BE254318.1	EST_HUMAN	80115053F NIH_10GC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
12450	25209	31831	6.88	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR38, section 73 of 84 of the complete genome
12835	259710		5.74	8.2E-02	AF273966.1	NT	Mus musculus epidermal growth factor receptor (Egf) gene, exons 8 through 28, and complete cds, alternatively spliced
1403	14326	27498	1.05	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5948	16838	32123	1.05	8.1E-02	AEO0-0006.1	NT	Xyella fastidiosa, section 132 of 228 of the complete genome
6516	16978	32836	1.38	8.1E-02	T11532.1	EST_HUMAN	A14847f Heart Homo sapiens cDNA clone A1484
7403	20371		0.81	8.1E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS210079
7835	20782		0.9	8.1E-02	AB026881.1	EST_HUMAN	we8908.x1 NCI_DGAP_L224 Homo sapiens cDNA clone IMAGE:2385603 3'
8883	21681	35072	0.83	8.1E-02	11423974	NT	Homo sapiens hypothetical protein FJ11090 (FJ11090), mRNA
8883	21681	35073	0.83	8.1E-02	11423974	NT	Homo sapiens hypothetical protein FJ11090 (FJ11090), mRNA
10272	23187		1.98	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lentigin precursor, gene, complete cds
11827	24710	38294	1.53	8.1E-02	AL103022.2	NT	Homo sapiens chromosome 21 segment HS210002
6	16830	25026	4.82	8.0E-02	AW864653.1	EST_HUMAN	EST 738672 IMAGE resequences, IMAGE Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Next Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1709	15976	27722	13.83	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidin succinyltransferase, complete cds (exon 1-15)
1709	15976	27723	13.83	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidin succinyltransferase, complete cds (exon 1-15)
1919	14940	27069	4.07	8.0E-02	BE067718.1	EST_HUMAN	PM3-5 T3347-17020-001-308 S10347 Homo sapiens cDNA
2334	15392	26417	1.05	8.0E-02	D56915.1	NT	Synuclein-like sp. P-26803 complete genomic, 17277, 2137256-2567259
2334	15392	26418	1.05	8.0E-02	D56915.1	NT	Synuclein-like sp. P-26803 complete genomic, 17277, 2137256-2567259
2478	15482	27418	4.89	8.0E-02	BF724074.1	EST_HUMAN	Or16539-54F1 TM141003_5 Homo sapiens cDNA clone IMAGE4078019 5'
2631	14137	27086	0.99	8.0E-02	M23446.1	NT	Or16539-54F1 TM141003_5 Homo sapiens cDNA clone IMAGE4078019 5'
2631	14137	27086	0.99	8.0E-02	M23446.1	NT	Or16539-54F1 TM141003_5 Homo sapiens cDNA clone IMAGE4078019 5'
2830	15959	26862	0.76	8.0E-02	AL45357.1	EST_HUMAN	Human cDNA clone, cytochrome P-450, complete cds
3830	16910	28772	0.94	8.0E-02	AL45357.1	EST_HUMAN	Human cDNA clone, cytochrome P-450, complete cds
4810	17827	30724	0.71	8.0E-02	AL45357.1	EST_HUMAN	Human cDNA clone, cytochrome P-450, complete cds
4810	17827	30724	0.71	8.0E-02	AL45357.1	EST_HUMAN	Human cDNA clone, cytochrome P-450, complete cds
4833	17865	30735	0.89	8.0E-02	AF146566.1	EST_HUMAN	Human cDNA clone, cytochrome P-450, complete cds
4833	17865	30735	0.89	8.0E-02	AF146566.1	EST_HUMAN	Human cDNA clone, cytochrome P-450, complete cds
5832	18922	32105	2.87	8.0E-02	U72944.1	NT	Arabidopsis thaliana putative transcription factor (HUA2) mRNA, complete cds
5832	18922	32105	2.87	8.0E-02	U72944.1	NT	Arabidopsis thaliana putative transcription factor (HUA2) mRNA, complete cds
5903	19077	32274	3.28	8.0E-02	AF755448.1	EST_HUMAN	EST383236 MAGF, neurocancer, MAGA Homo sapiens cDNA
5903	19077	32274	3.28	8.0E-02	AF755448.1	EST_HUMAN	EST383236 MAGF, neurocancer, MAGA Homo sapiens cDNA
7386	19077	32274	1.44	8.0E-02	AF755448.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8405	21434	34851	3.74	8.0E-02	AL114893.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
9744	22685	36139	1.21	8.0E-02	X74206.1	NT	Bovine cholestanol 14 cDNA library under conditions of alloxan deprivation
9744	22685	36140	1.21	8.0E-02	X74206.1	NT	Bovine cholestanol 14 cDNA library under conditions of alloxan deprivation
10510	23441		0.6	8.0E-02	AL163209.2	NT	H. sapiens AGT gene, intron 4
11145	24105	37832	2.19	8.0E-02	AF17704.1	NT	H. sapiens AGT gene, intron 4
12493	25230	31789	6.54	8.0E-02	AJ053575.1	NT	Homo sapiens chromosome 21 segment HS21C009
13036	18342	31789	2.06	8.0E-02	490034.1	NT	Homo sapiens chromosome 21 segment HS21C009
2184	15169	26219	4.95	7.9E-02	BE200068.1	EST_HUMAN	protein 1 (AFRPP1) genes, complete cds
2692	16050	26871	8.43	7.9E-02	A652026.1	EST_HUMAN	Drasphila crata hunchback region
3954	19003	29809	5.68	7.9E-02	6981044.1	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREB2) mRNA
3954	19003	29809	5.68	7.9E-02	6981044.1	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREB2) mRNA
4722	17742	30633	1.08	7.9E-02	BF348454.1	EST_HUMAN	Mus musculus colony stimulating factor 1 receptor (CSF1) mRNA
4848	17868		1.49	7.9E-02	AB008019.1	NT	0620197001 NC_CGAP_Bim8 Homo sapiens cDNA clone IMAGE4165401 5'
6935	16908		1.06	7.9E-02	BF348454.1	EST_HUMAN	Arabidopsis thaliana EXON24L mRNA, partial cds
8568	21335	34747	3.26	7.9E-02	U72832.1	NT	RC3-GM004231080-004-0411 GM0042 Homo sapiens cDNA
10388	23310	36786	4.89	7.9E-02	A081644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of IMP2 Smtdp (SM14) gene, complete cds
							Out6806.61 NC_CGAP_Bp8 Homo sapiens cDNA clone IMAGE1602466 3' similar to WPC37A2.2 (CE08611)

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10368	23310	36789	4.89	7.8E-02	AI031844.1	EST_HUMAN	cd06063.t1 NCL_GGAP_B02 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2
1216	14253	27210	1.69	7.8E-02	AI793275.1	EST_HUMAN	cd06062.t6 NCL_GGAP_Lu05 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
1215	14253	27211	1.69	7.8E-02	AI793275.1	EST_HUMAN	cd06062.t6 NCL_GGAP_Lu05 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
5123	18804		3.26	7.8E-02	BE259468.1	EST_HUMAN	cd06063.t1 NCL_GGAP_Lu05 Homo sapiens cDNA clone IMAGE:286693 5'
7279	20013	33317	1.26	7.8E-02	U62654.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-X268TS protein (X268ORP), and blycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7279	20013	33318	1.29	7.8E-02	U62654.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-X268TS protein (X268ORP), and blycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8137	22103	36329	1.26	7.8E-02	BE67947.1	EST_HUMAN	cd06063.t1 NCL_GGAP_Lu05 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1
9232	22196	36329	0.6	7.8E-02	X78344.1	NT	S. cerevisiae CAT5 gene
9408	22373	39806	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP to mRNA, complete cds
9408	22373	39809	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP to mRNA, complete cds
9716	22744	39195	1.23	7.8E-02	AA469354.1	EST_HUMAN	ncfB08.t1 NCL_GGAP_P71 Homo sapiens cDNA clone IMAGE:777731
10181	23096	39593	0.95	7.8E-02	Z69124.1	NT	Bacillus subtilis complete genome (section 21 of 21), from 3069281 to 4214814
12114	24084	39595	1.64	7.8E-02	BF025981.1	EST_HUMAN	cd06063.t1 NCL_GGAP_Lu05 Homo sapiens cDNA clone IMAGE:3933063 5'
1399	15907	27402	0.93	7.7E-02	AF161897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3500	16945		2.05	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and 3' UTR repeat elements
9522	18718	31877	0.61	7.7E-02	AF002036.1	NT	Gallus gallus collagen type XI alpha-1(COL12A1) gene, promoter region and partial cds
9241	21210	34615	7.34	7.7E-02	AA029464.1	EST_HUMAN	cd06063.t1 NCL_GGAP_Lu05 Homo sapiens cDNA clone IMAGE:74117 5' similar to
10195	23120	39596	3.78	7.7E-02	P39596	SWISSPROT	TR.G173906 G173906 SPLICEOSOME ASSOCIATED PROTEIN ; PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR090C
10400	23412	39596	0.78	7.7E-02	AS16692.1	EST_HUMAN	cd06063.t1 NCL_GGAP_Lu05 Homo sapiens cDNA clone IMAGE:2906395 3' similar to gp-23676 60S
10400	23412	39596	0.78	7.7E-02	AS16692.1	EST_HUMAN	cd06063.t1 NCL_GGAP_Lu05 Homo sapiens cDNA clone IMAGE:2906395 3' similar to gp-23676 60S
11352	23632	31229	4.68	7.7E-02	11422767	NT	RIBOSOMAL PROTEIN L38 (HUMAN);
12671	25761		1.91	7.7E-02	11436659	NT	Homo sapiens RNU6B gene product (RNU6B) mRNA
							Homo sapiens nucleon regulatory factor 7 (RNF7) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3398	16447	25373	2.43	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:355403 5'
3419	16467	25387	1	7.6E-02	AA399447.1	EST_HUMAN	EST1112214 Cerebellum1 Homo sapiens cDNA 5' and similar to human 18S ribosomal RNA
6216	16260	32523	0.72	7.6E-02	AB013275.1	EST_HUMAN	EN54602.x1 Gaster Wilms tumor Homo sapiens cDNA clone IMAGE:168180 3'
6491	16569	32603	0.97	7.6E-02	BE376228.1	EST_HUMAN	601280402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:360440 5'
8775	22753	39200	1.35	7.6E-02	AL131016.1	NT	Homo sapiens SCL gene locus
10257	23182		1.42	7.6E-02	AL139078.2	NT	Campylobacter jejuni NC1511168 complete genome, fragment 5/6
10714	23435	39564	0.56	7.6E-02	BE108002.1	EST_HUMAN	RC11H105-02-02800-017-408.110345 Homo sapiens cDNA
10990	23502		0.56	7.6E-02	BE096038.2	EST_HUMAN	RC11H105-0475X1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:38338 10 3'
10952	23872	37384	0.67	7.6E-02	X62856.1	NT	Laccase human mRNA for tissue plasminogen activator
10952	23872	37385	0.67	7.6E-02	X62856.1	NT	Laccase human mRNA for tissue plasminogen activator
11895	24663	38456	1.9	7.6E-02	AW096945.1	EST_HUMAN	Q73-RN005F1-150400-15-404 EN0948 Homo sapiens cDNA
785	13845	25780	2.89	7.6E-02	5902063	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
785	13845	25791	2.89	7.6E-02	5902063	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1031	14659	27955	0.83	7.6E-02	AL153278.2	NT	Homo sapiens chromosome 21, segment H32,10q78
4356	17559	30447	0.63	7.6E-02	AB013481.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
5652	19037	32533	0.71	7.6E-02	AB01341.1	EST_HUMAN	w32602.x1 NCI_OGAP_K5111 Homo sapiens cDNA clone IMAGE:727257 3'
8681	21646	35071	1.01	7.6E-02	AB043987.1	EST_HUMAN	w32602.x1 NCI_OGAP_Bm235 Homo sapiens cDNA clone IMAGE:2428491 3' similar to ghbM14329 ALPHA ENCLASE HUMAN
8952	21919	35230	1.29	7.6E-02	AJ118913.1	EST_HUMAN	AUT118913 HEMBA100 Homo sapiens cDNA clone HEMBA100284 5'
10302	23314		0.45	7.6E-02	BF721730.1	EST_HUMAN	7081005.x1 NCI_OGAP_P1238 Homo sapiens cDNA clone IMAGE:3378004 3' similar to contains element
10338	23376	37379	0.9	7.6E-02	BF268909.1	EST_HUMAN	MEK27 repetitive element
10376	23937	37586	0.66	7.6E-02	X74900.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100446 5'
10739	13550	25478	1.24	7.6E-02	AW438547.1	EST_HUMAN	C-fim D5M1 20113 18S cDNA
1456	14459		1.08	7.6E-02	AF400027.1	NT	RC5L10054-280100-011-H09 L10054 Homo sapiens cDNA
2595	15548		0.89	7.6E-02	6755009	EST_HUMAN	Equine herpesvirus 4 strain NS60587, complete genome
3608	16653	28971	0.78	7.6E-02	AB07895.1	EST_HUMAN	Mus musculus period-like homeodomain transcription factor 1 (Pbx1), mRNA
47353	17733	30946	1.09	7.6E-02	L78810.1	NT	w43901.x1 Score: NFI1, TGR3 S1 Homo sapiens cDNA clone IMAGE:2353583 3'
4833	17850	30750	3.24	7.6E-02	6974442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl), mRNA
4870	17804	30883	2.32	7.6E-02	6974462	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Ubrp), mRNA
9543	19701		1.8	7.6E-02	RT1477.1	EST_HUMAN	y91468.f1 Score: infant brain TNIB Homo sapiens cDNA clone IMAGE:2389 5'
7707	20694	34031	0.78	7.6E-02	JA805132.1	EST_HUMAN	nc014602.x1 NCI_OGAP_AAT1 Homo sapiens cDNA clone IMAGE:1172589 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8203	21202	34808	1.2	7.4E-02	BE801112.1	EST_HUMAN	B01463866F NIH_HUGO_88 Homo sapiens cDNA clone IMAGE:3865584.5'
8848	21813	35233	1.01	7.4E-02	U60869.1	NT	Human keratin cytoplasmic protein 2 (KVP2) gene, exons 15 to 21, and complete cds
8521	22494	35960	1.02	7.4E-02	AW029605.1	EST_HUMAN	h67611.yt NCL_GCAP_GU1 Homo sapiens cDNA clone IMAGE:2867881.5' similar to SW_SCA2_HUMAN
8501	22484	35951	1.02	7.4E-02	AW029605.1	EST_HUMAN	h67611.yt NCL_GCAP_GU1 Homo sapiens cDNA clone IMAGE:2867881.5' similar to SW_SCA2_HUMAN
8754	21117	34510	0.48	7.4E-02	A672893.1	EST_HUMAN	O16127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.
8754	21117	34511	0.48	7.4E-02	A672893.1	EST_HUMAN	O16127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.
10178	20308	36578	0.93	7.4E-02	A672893.1	EST_HUMAN	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
10301	20328	36708	0.93	7.4E-02	BFS128.6.1	NT	Human LIN-Kinase1 and alternatively spliced LIN-Kinase1 (LINK1) gene, complete cds
12408	25181	38708	1.37	7.4E-02	BFS128.6.1	EST_HUMAN	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
12855	25903	33227	2.51	7.4E-02	AW37543.1	EST_HUMAN	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
486	13542	26465	1.3	7.3E-02	BE294691.2	EST_HUMAN	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
486	13542	26466	1.3	7.3E-02	BE294691.2	EST_HUMAN	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
685	13748	26674	5.46	7.3E-02	AE001786.1	NT	Human LINC00001 gene, complete cds
1477	13609	27468	3.94	7.3E-02	AW000281.1	EST_HUMAN	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
1802	13879		15.78	7.3E-02	AL183022.2	NT	Human LINC00001 gene, complete cds
3785	18928		0.72	7.3E-02	U60809.1	NT	Human LINC00001 gene, complete cds
9032	19046		1.00	7.3E-02	U12353.1	NT	Human LINC00001 gene, complete cds
8505	19855	33227	1.04	7.3E-02	AAT76977.1	EST_HUMAN	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
7708	20863	34020	2.47	7.3E-02	P0143	SWISSPROT	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
7708	20863	34030	2.47	7.3E-02	P0143	SWISSPROT	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
8508	21478		1.2	7.3E-02	7862107	NT	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
9585	22827		1.39	7.3E-02	AB011090.1	NT	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
11552	19855	33227	1.89	7.3E-02	AAT76977.1	EST_HUMAN	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
12825	25310		1.33	7.3E-02	Z73597.1	NT	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'
120	13229	26166	0.7	7.3E-02	AE000882.1	NT	h674602.x1 Soares_Diagnostic_cdon, NHGD Homo sapiens cDNA clone IMAGE:224818.3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Med Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
120	13229	25157	0.7	7.2E-02	AF000482.1	NT	Methanobacterium thermoautotrophicum from biogas 1025155 to 1039594 (section 68 of 148) of the complete genome
1472	14905	27478	2.77	7.2E-02	AL153301.2	NT	Homo sapiens chromosome 21 segment 11821C101
1472	14905	27479	2.77	7.2E-02	AL153301.2	NT	Homo sapiens chromosome 21 segment 11821C101
2555	15558		2.98	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 29 reverse transcriptase (pol) gene, internal fragment, partial cds
3900	16940	29851	0.74	7.2E-02	AF25822.1	EST HUMAN	U14794.2-94-95-96-97-98-99-100 CGAP Subst Homo sapiens cDNA clone IMAGE:2732040 3'
4373	17400	30260	4.57	7.2E-02	BF72307.1	EST HUMAN	80207767F1 NH1.MGC.82 Homo sapiens cDNA clone IMAGE:4251950 5'
5300	18425	31336	2.61	7.2E-02	U31351.1	NT	Methanococcus jannaschii section 78 of 180 of the complete genome
5391	18495	31337	5.14	7.2E-02	U31351.1	SWISSPROT	CALMODULIN
67289	19312	32132	0.73	7.2E-02	BF21068.1	EST HUMAN	801183056F1 NH1.MGC.57 Homo sapiens cDNA clone IMAGE:0595224 5'
7374	20344	33595	1.75	7.2E-02	BF21068.1	EST HUMAN	801183056F1 NH1.MGC.57 Homo sapiens cDNA clone IMAGE:0595224 5'
7391	20380	33712	0.6	7.2E-02	AF221126.1	NT	Zinc metalloprotease (tmpr8) genes, complete cds
7391	20380		1.74	7.2E-02	8834897	NT	Strongyloides purpuratus mitochondrion, complete genome
8320	21497	34612	0.89	7.2E-02	P06143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8529	21497	34613	0.89	7.2E-02	P06143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8410	22384		0.62	7.2E-02	V17217.1	NT	Lactococcus lactis cspE gene
8634	22681		0.63	7.2E-02	X16346.1	NT	Human gene for sex hormone-binding globulin (SHBG)
8970	22687	36590	1.95	7.2E-02	AV171452.1	EST HUMAN	AV171452 DCA Homo sapiens cDNA clone DCAUG01 5'
10117	23043	36593	3.63	7.2E-02	L14591.1	NT	AV171452 Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10274	23189	36593	1.17	7.2E-02	BF125399.1	EST HUMAN	901793623F1 NH1.MGC.20 Homo sapiens cDNA clone IMAGE:025458 5'
10352	23285	36762	2.29	7.2E-02	AF873187.1	EST HUMAN	hg3411.1x1 NO1 CGAP Adit Homo sapiens cDNA clone IMAGE:313333 3' similar to TRQ23240 Q82340
10552	23474	36659	0.54	7.2E-02	AA198304.1	EST HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN 1
10717	23639	37132	2.17	7.2E-02	U82965.2	NT	ca85507.1x1 NO1 CGAP G031 Homo sapiens cDNA clone IMAGE:131584 3'
10940	23760	37200	6.41	7.2E-02	BE56003.1	EST HUMAN	Homo sapiens zinc finger protein 92 (ZFP92), expressed Xc26F3 protein (Xc26F3), and blycane (BGN) genes
11044	23760	37200	6.41	7.2E-02	BE56003.1	EST HUMAN	90130395F1 NH1.MGC.53 Homo sapiens cDNA clone IMAGE:5685651 5'
11236	24270	37333	3.24	7.2E-02	BE30214.1	EST HUMAN	90130395F1 NH1.MGC.53 Homo sapiens cDNA clone IMAGE:5685651 5'
12111	25119	31942	1.38	7.2E-02	AF449874.1	NT	Partial cDNA of human transcription factor 1 (Tf1) (Tf1) gene, complete cds
12311	25119	31942	1.38	7.2E-02	AF449874.1	EST HUMAN	Partial cDNA of human transcription factor 1 (Tf1) (Tf1) gene, complete cds
12350	25145		5.13	7.2E-02	AJ237965.1	EST HUMAN	cdi146.L1 Soya, N1HMP0.51 Homo sapiens cDNA clone IMAGE:1048358 5'
							AJ237968 Homo sapiens beta (Sensid P) Homo sapiens cDNA clone P51305 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12459	25218		3.99	7.2E-02	U63028.1	NT	Homo sapiens, albumin binding protein (A1M) gene, complete cds
12464	25754		8.41	7.2E-02	AW006053.1	EST_HUMAN	CMA-111035-203530-110-111 NT1009 Homo sapiens cDNA
12860	25933		1.45	7.2E-02	AF020435.1	NT	Homo sapiens ATP-kinase like gene, exon 3
12864	25933		1.65	7.2E-02	AA01719.1	EST_HUMAN	257512.11 Sorensen, NHT Homo sapiens cDNA clone IMAGE:726454.5
1920	14944	27540	1.63	7.1E-02	U02260.1	NT	Human immunodeficiency virus type 1 (D) proviral structural capsid protein (gag) gene, partial cds
2200	15812	28332	8.39	7.1E-02	BF208802.1	EST_HUMAN	501122281F1 NH1_MGC_55 Homo sapiens cDNA clone IMAGE:4062681.5
8239	21209	34412	0.87	7.1E-02	A1125394.1	EST_HUMAN	9252415.21 Sorensen, NHT Homo sapiens cDNA clone IMAGE:4062681.5
12195	25038		8.33	7.1E-02	BE034784.1	EST_HUMAN	501143574F1 NH1_MGC_55 Homo sapiens cDNA clone IMAGE:4062681.5
529	13900	26516	1.42	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1469	14532		1.82	7.0E-02	Q56977.1	NT	Marfan's Marfan-1 gene
1778	14606	27751	1.19	7.0E-02	A035043.1	EST_HUMAN	256904.51 Strassman cation (453724) Homo sapiens cDNA clone IMAGE:406559.9
3042	16100	20715	1.75	7.0E-02	AW138152.1	EST_HUMAN	U1-HB1-495-470-0-0-J1 S1: C3AP S103 Homo sapiens cDNA clone IMAGE:2716020.3
3915	16953	26984	0.96	7.0E-02	A815438.1	EST_HUMAN	ab041241 Sorensen, NHT Homo sapiens cDNA clone IMAGE:2716020.3
4074	17110	30004	1.05	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN)
4184	17195		1.24	7.0E-02	AW162862.1	EST_HUMAN	Q14-570407-280100-089-410.5 (1407) Homo sapiens cDNA
4242	17271	30156	1.26	7.0E-02	AF077821.1	NT	Cenit, familial inducible nucleic oxide synthase mRNA, complete cds
4595	17871	30571	8.41	7.0E-02	BF381987.1	EST_HUMAN	50116251F1 NH1_MGC_55 Homo sapiens cDNA clone IMAGE:4060071.5
5457	18553		1.03	7.0E-02	T09143.2	NT	Lumbricus tubular mRNA for cyclophilin B
7830	20590	33953	0.9	7.0E-02	U680285.1	EST_HUMAN	AV680285 GRK Homo sapiens cDNA clone G160406.5
7894	20598	34186	0.9	7.0E-02	T19197.1	NT	Gallus gallus mRNA for partial actinin, XL spliced variant (ezr gene)
9454	22518	35856	1.2	7.0E-02	Q02801.1	NT	African swine fever virus, complete genome
9555	22983	35348	1.21	7.0E-02	Q02801.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
10312	23236	39718	0.76	7.0E-02	U27266.1	NT	Human myosin binding protein H (MYBP-H) gene, complete cds
11700	24895	38542	2.25	7.0E-02	A474295.1	EST_HUMAN	ab040511 Sorensen, NHT, T_GBC_51 Homo sapiens cDNA clone IMAGE:1327184.3 similar to gb1.14837
12039	25018	31170	1.98	7.0E-02	11421038	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN)
1365	25804		11.2	6.9E-02	A1163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
515	13360	25525	11.2	6.9E-02	A1163210.2	NT	Homo sapiens chromosome 21 segment H821C010
515	13360		11.2	6.9E-02	A1163210.2	NT	Homo sapiens chromosome 21 segment H821C010
1336	14370		1.88	6.9E-02		NT	Homo sapiens regulator of Gs-selective protein signalling (ZGAP1) mRNA, and translated products
3907	18947	29754	1.37	6.9E-02	Q03584	SWISSPROT	28S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN P107)
3207	18947	29755	1.37	6.9E-02	Q03584	SWISSPROT	28S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN P107)

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Single Exon Probes Expressed in Bone Marrow

Probe	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6183	21193	34561	1.01	6.7E-02	X62663.1	NT	H sapiens DNA for cGMP 3'-phosphodiesterase (gene 422)
8781	21746	35170	0.45	6.7E-02	AF038388.1	EST_HUMAN	35611.1 X1 Sra305, NR1, T, GBC, S1 Homo sapiens cDNA clone IMAGE:5860786.3
8958	22895	36347	0.73	6.7E-02	AF133386.1	EST_HUMAN	(U44)H4c-910-010-0111101 CGAP, S1/3 Homo sapiens cDNA clone IMAGE:2715433.3
9371	14435	27315	0.73	6.7E-02	AF133386.1	EST_HUMAN	(U44)H4c-910-010-0111101 CGAP, S1/3 Homo sapiens cDNA clone IMAGE:2715433.3
1371	14435	27315	0.9	6.8E-02	AF240116.1	NT	Proteinase 3, human
2192	18297	26236	2.66	6.8E-02	AF26841.1	NT	Mus musculus Ccr12 gene for carbon 12, pcoos 1-21, three alternative transcripts
3477	18357	25447	11.07	6.8E-02	RF63561.1	EST_HUMAN	17610.13 Sra305, p150cas, Nucleo Homo sapiens cDNA clone IMAGE:135679.3
3481	18357	25447	2.11	6.8E-02	RF63561.1	EST_HUMAN	17610.13 Sra305, p150cas, Nucleo Homo sapiens cDNA clone IMAGE:135679.3
4187	17141	29335	2.1	6.8E-02	7108357	NT	Homo sapiens macrolipin (MUSN), transcript variant 1, mRNA
4187	17141	29335	2.1	6.8E-02	7108357	NT	Homo sapiens macrolipin (MUSN), transcript variant 1, mRNA
5015	19029	30913	1.45	6.8E-02	AF26232.1	NT	Homo sapiens, TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5015	19029	30913	0.20	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-1-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI1 HEAVY CHAIN H2)
5015	19029	30914	0.20	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-1-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI1 HEAVY CHAIN H2)
6738	19782	33073	3.07	6.8E-02	X06411.1	NT	P-adaptor mRNA for choline synthase
6987	19828	33103	0.55	6.8E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN S1AUFEN
6987	19828	33106	0.55	6.8E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN S1AUFEN
8152	21091	33106	1.67	6.8E-02	D14667.1	NT	Pancellum uterine mitochondrial rRNA large rRNA gene and its flanking region
8279	21243	34660	1.06	6.8E-02	AF026372.1	NT	Homo sapiens choline oxidase receptor CXCR4 gene, promoter region and complete cds
8817	21784	35209	0.67	6.8E-02	AF006065.1	NT	Dysbetalipoproteinemia (beta2-microglobulin) gene, complete cds
9273	22239	35665	0.67	6.8E-02	9602188	NT	Human respiratory syncytial virus, complete genome
9273	22239	35667	0.67	6.8E-02	9602188	NT	Human respiratory syncytial virus, complete genome
10311	23235	36717	0.32	6.8E-02	AF458162.1	EST_HUMAN	167906.11 NC1 CGAP, L104 Homo sapiens cDNA clone IMAGE:2161496.3
10447	23309	36960	1.95	6.8E-02	Y07846.1	NT	Homo sapiens EWS, gnr22, nr22 and bmr22 genes
10447	23309	36960	1.95	6.8E-02	Y07846.1	NT	Homo sapiens EWS, gnr22, nr22 and bmr22 genes
11310	24290	37786	0.6	6.8E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
11310	24290	37786	4.9	6.8E-02	BF374248.1	EST_HUMAN	MRT-SN0084-010063-006-412 SN0084 Homo sapiens cDNA
12083	24596	38579	1.73	6.8E-02	C05789.1	EST_HUMAN	C05789 Homo sapiens cDNA clone h05156
12719	28373	39373	2.33	6.8E-02	8607891	NT	Mus musculus DFB gene (Dfb), mRNA
13024	29572	40572	1.31	6.8E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
584	13652	26566	2.67	6.8E-02	BF027636.1	EST_HUMAN	85167046F1 NH1_MGC_20 Homo sapiens cDNA clone IMAGE:384178.5
989	14041	26966	1.95	6.8E-02	7709068	NT	Homo sapiens EGF like protein (LOC612120), mRNA
1392	14426	27395	3.5	6.8E-02	AF47624.1	NT	Xenopus laevis alpha(E)-calinin mRNA, complete cds
1749	14778	27769	2.08	6.8E-02	AE000764.1	NT	Aquifex eolicus section 96 of 109 of the complete genome
5698	16734	31886	1.71	6.8E-02	AA438991.1	EST_HUMAN	2446h12.1 Soares away tumor N5H071 Homo sapiens cDNA clone IMAGE:746743.3 similar to g1aM06038
6693	16730	33027	0.83	6.8E-02	BF66840.1	EST_HUMAN	HLA CLASS I H1S100COMPATIBILITY ANTIGEN DR-8 BETA CHAIN (HUMAN); 62211887F1 NH1_MGC_38 Homo sapiens cDNA clone IMAGE:274629.5

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID/NO:	Expression Signal	Most Similar (BLAST E- Value)	Top Hit Database Source	Top Hit Descriptor
7165	16366	31241	1.17	6.E-02 U22651.1	NT	Arabinoside (AraC) LYC 9046 negative regulator (MucB) gene, partial cds
10302	23227	36709	0.55	6.E-02 BEK63200.2	EST_HUMAN	9018883771 NH_136367.1 Homo sapiens cDNA clone IMAGE:368537.3'
10302	23227	36710	0.55	6.E-02 BEK63200.2	EST_HUMAN	9018883771 NH_136367.1 Homo sapiens cDNA clone IMAGE:368537.3'
10832	23753	37352	0.53	6.E-02 BF108000.1	EST_HUMAN	9018883771 NH_136367.1 Homo sapiens cDNA clone IMAGE:368537.3'
11002	23068	37462	4.51	6.E-02 AA195948.1	EST_HUMAN	224263141 Soar1_NH0401.1 Homo sapiens cDNA clone IMAGE:985144.3'
12184	25017		4.18	6.E-02 M21485.1	NT	Neurofilament heavy chain related protein 2 (KRP2) gene, complete cds
12556	25255		7.31	6.E-02 J1125953.1	NT	Neurofilament heavy chain related protein 2 (KRP2) gene, complete cds
577	13546	26556	1.74	6.E-02 J264543.1	NT	A carboxyl terminal region of actinin-4/5 protein (ACT4/5) gene, complete cds
1746	14778	27750	0.93	6.E-02 J2601771.1	NT	Thermolysin maturation region 88 of 138 of the complete genome
1746	14778	27751	0.93	6.E-02 J2601771.1	NT	Thermolysin maturation region 88 of 138 of the complete genome
4633	16085	28007	1.16	6.E-02 0698023	NT	Mus musculus histone H2A.1 (H2A.1) mRNA
5282	18270		2.56	6.E-02 AA147572.1	EST_HUMAN	461604.1 Soar1_NH0401.1 Homo sapiens cDNA clone IMAGE:595470.5' similar to contains A19 repetitive element;
5235	18524	31559	1.19	6.E-02 A191958.1	EST_HUMAN	461604.1 Soar1_NH0401.1 Homo sapiens cDNA clone IMAGE:595470.5' similar to contains LTR b3
5235	18524	31560	1.19	6.E-02 A191958.1	EST_HUMAN	461604.1 Soar1_NH0401.1 Homo sapiens cDNA clone IMAGE:595470.5' similar to contains LTR b3
6324	19007	32565	4.18	6.E-02 AF032733.1	NT	Mus musculus IFN-response element binding factor 1 (IREB-1), mRNA
6324	19007	32566	4.18	6.E-02 AF032733.1	NT	Helicoverpa glycines beta-1, 4-endoglucanase-1 precursor (H-G-ang-1) gene, complete cds
6324	19007	32567	4.18	6.E-02 AF032733.1	NT	Helicoverpa glycines beta-1, 4-endoglucanase-1 precursor (H-G-ang-1) gene, complete cds
6324	19004	32568	0.72	6.E-02 AF072695.1	EST_HUMAN	wf75g12.1 Soar1_NH0401.1 Homo sapiens cDNA clone IMAGE:2348790.3'
6900	20213	33542	4.64	6.E-02 BE074448.1	EST_HUMAN	9018883771 NH_136367.1 Homo sapiens cDNA clone IMAGE:368537.3'
7593	20851	34015	0.52	6.E-02 AL192757.2	NT	Neshera meningitis serogroup A strain Z2481 complete genome, segment 87
8678	21647	34015	2.70	6.E-02 0755323	NT	Mus musculus chaperonin subunit beta (CpnB) mRNA
9012	21978	35397	4	6.E-02 AA003005.1	EST_HUMAN	K1419 seq. F Human fetal heart, Lambda ZAP Express Human cDNA clone CBDA1A10
9483	22447	35887	0.52	6.E-02 AF150165.1	EST_HUMAN	RC1-OT0083-150000-014-008 OT0083 Human sapiens cDNA
9444	22871		0.61	6.E-02 BEG34883.1	EST_HUMAN	Homo sapiens mRNA for KIA0054 protein, partial cds
10075	23002	35472	1.75	6.E-02 AB011128.1	NT	Homo sapiens DNA topoisomerase I beta (TOP2B) gene, exons 18, 17, and 16
10524	23549	37046	0.59	6.E-02 AF087150.1	NT	Homo sapiens DNA topoisomerase I beta (TOP2B) gene, exons 16, 17, and 18
10524	23549	37047	0.59	6.E-02 AF087150.1	NT	Homo sapiens DNA topoisomerase I beta (TOP2B) gene, exons 16, 17, and 18
12018	24895	38462	2.16	6.E-02 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-H) gene, Notc gene, and sodium phosphate transporter (NPT2) gene, complete cds
12018	24895	38463	2.16	6.E-02 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-H) gene, Notc gene, and sodium phosphate transporter (NPT2) gene, complete cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12424	26981		5.36	6.4E-02	AF107690.1	NT	Homo sapiens muscle 86 (MUS86) gene, partial cds
12476	25224	31793	5.66	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)15.4 protein
1789	14798	27164	2.76	6.3E-02	AF193905.1	NT	Mus musculus major histocompatibility locus class II regions Hsc70i, partial cds; smRNP, G7A, NG23, MuB hemopoic, CLOP, NG28, NG26, and NG28 genes, complete cds, and unknown genes
3818	16002		2.77	6.3E-02	F57932	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
4239	19332	32563	1.06	6.3E-02	BF10736.1	EST_HUMAN	61767331F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4057499 5'
4343	20416		1.36	6.3E-02	AF7848.1	NT	Homo sapiens gene encoding L1 subunit
4344	22297	38039	2.38	6.3E-02	AF587915.1	NT	Protein kinase domain, domain genes 1-3
10374	19229	39775	2.81	6.3E-02	AF57036.1	NT	Homo sapiens cDNA for p299 (NSA) region, partial cds, strain: CHIR-152
10374	22656		5.81	6.3E-02	AF57036.1	EST_HUMAN	AV188670 CNGC homologue, cDNA clone IMAGE:4057499 5'
10374	22656		5.81	6.3E-02	AF57036.1	EST_HUMAN	AV188670 CNGC homologue, cDNA clone IMAGE:4057499 5'
11070	19332	32463	2.76	6.3E-02	BF10736.1	EST_HUMAN	61167331F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4057499 5'
4278	17307	30166	2.46	6.3E-02	AL161372.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 68
4995	17392		1.12	6.2E-02	AF71235.1	NT	Rattus norvegicus differentiation-associated Nucleo-epithelial Inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4612	17633		6.96	6.2E-02	D65181	SWISSPROT	S2 KD RD PROTEIN (S2OGEN SYNDRONE TYPE A ANTIGEN (SSA)) (RQSS-A) (RQSS)
8683	20168	33513	0.87	6.2E-02	D46330.1	NT	Spaulding plasmid DNA for esterase, complete cds
7889	20833	34212	0.78	6.2E-02	U41483.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
6156	21096		0.58	6.2E-02	AL161443.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 48
9299	22052		0.53	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9699	22052	35106	0.53	6.2E-02	AA718450.1	EST_HUMAN	af20a05.1 Soares, total, fetus, N22H8 3w Homo sapiens cDNA clone IMAGE:1032178 3'
9435	22771	38228	1.25	6.2E-02	AE007750.1	NT	Mus musculus stomach cell derived factor receptor 2 (Sdrf2), mRNA
12269	25079		16.68	6.2E-02	AE007750.1	NT	Aquifex acidus section 62 of 109 of the complete genome
12595	25299		1.38	6.2E-02	BE793955.1	EST_HUMAN	60185731F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5'
12879	28346	31764	3.54	6.2E-02	BF112036.1	EST_HUMAN	737706x1 Soares, NSF, F6, 9w, OT, PA, P, 37 Homo sapiens cDNA clone IMAGE:3523813 3' similar to
285	13393	29278	3.09	6.1E-02	D11947.1	NT	Human mRNA, Xc terminal portion
4017	17596		15.65	6.1E-02	U75325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKIC1) gene, complete cds
8043	19126	32330	0.82	6.1E-02	7892463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
8043	19126	32331	0.82	6.1E-02	7892463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
8235	19338		1.64	6.1E-02	4507070	NT	Homo sapiens SVI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8605	21574	34866	3.52	6.1E-02	X69226.1	NT	H sapiens mRNA for BHLH DNA binding protein
8008	21974	35393	1.93	6.1E-02	BE971663.1	EST_HUMAN	601857068F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3934404 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9008	21674	30364	1.03	6.1E-02	E807163.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA clone IMAGE:393490.3'
11082	24044	37596	3.44	6.1E-02	E179543.1	EST_HUMAN	5L-H10516-115520-135-039 HT6318 Homo sapiens cDNA
12216	25897		2.42	6.1E-02	E170360.1	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
12779	25774		1.35	6.1E-02	E138551.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
12912	25491		7.44	6.1E-02	AL163307.2	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
12877	14302	27263	1.25	6.0E-02	E1001771.1	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
2684	15980	26596	1.17	6.0E-02	AW59546.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
2783	15776		1.86	6.0E-02	AB031290.1	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
2846	15213	36137	1.47	6.0E-02	AB118703.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
2846	15213	36138	1.47	6.0E-02	AB118703.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
3243	15208	35223	1.52	6.0E-02	AA372978.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
3243	15208	35223	1.52	6.0E-02	AA372978.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
5472	18575		0.76	6.0E-02	AW59211.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
6341	19410	32651	0.88	6.0E-02	AB67597.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
7180	18411	31212	2.76	6.0E-02	E174966	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
7180	18411	31213	2.76	6.0E-02	E174966	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
7384	20692	33714	2.08	6.0E-02	BF332249.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
7508	20473	33533	0.57	6.0E-02	BF210488.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
7644	20868	34277	1.71	6.0E-02	A204275.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
8795	21732		0.52	6.0E-02	A1480465	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
8927	22571	35020	1.17	6.0E-02	AB23167.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
8927	22571	35021	1.17	6.0E-02	AB23167.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
9761	22702	35750	2.03	6.0E-02	A245895.1	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
9761	22702	35760	2.03	6.0E-02	A245895.1	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
10265	23190	36575	0.86	6.0E-02	AA309797.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
10265	23190	36576	0.86	6.0E-02	AA309797.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
12475	28223	31752	3.08	6.0E-02	E1137702	NT	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
12845	25485		3.16	6.0E-02	AB69273.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA
232	13332	26255	5.34	5.9E-02	AW594718.1	EST_HUMAN	5S165-02(NH1) NH1, MGC, 51 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Exon Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10330	23590	37365	0.49	5.7E-02	2.69693.1	NT	Lin28a cpl1 gene
11521	24462	39013	3.22	5.7E-02	AJ752685.1	EST_HUMAN	en18030.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_en18030 random
11521	24462	39014	3.22	5.7E-02	AJ752685.1	EST_HUMAN	en18030.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_en18030 random
11676	26422	33677	1.89	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G193
12573	26762	34476	6.27	5.7E-02	D36320.1	NT	Pro DNA for SPAL2, complete cds
12794	26855	37372	3.72	5.7E-02	AJ2517490.1	NT	Homo sapiens fragin 160 cido reductase [FOR] gene, exons 8, 9, and partial cds
12830	26958	37373	5.53	5.7E-02	AJ2517490.1	NT	Pro trypsin-like epiproteinase-E gene, complete cds
1329	14662	27533	1.85	5.6E-02	AF094455.1	NT	Hydroxylase riboflavin ribosomal protein L18 (p18) gene, intron; chloroplast gene for chloroplast product
4671	17892	30578	1.92	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-AC38 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4725	17745	30528	1.21	5.6E-02	AJ426099.1	EST_HUMAN	245507.s1 NCI_GCAP_G081 Homo sapiens cDNA clone IMAGE:700416 3'
6817	19871	33160	5.93	5.6E-02	AW172708.1	EST_HUMAN	KIAA0905 PROTEIN ;
7075	20037	33407	0.77	5.6E-02	AA865182.1	EST_HUMAN	064712.s1 NCI_GCAP_G081 Homo sapiens cDNA clone IMAGE:137119 3' similar to contains Alu repetitive element/containing element L1 repetitive element ;
7358	20328	33677	2.94	5.6E-02	BC038001.1	EST_HUMAN	QY0-BN017-280-100-214-p07 BN0147 Homo sapiens cDNA
8141	21078	34476	0.61	5.6E-02	AH183983.1	EST_HUMAN	qf8491.1 x1 Scarec_NHT Homo sapiens cDNA clone IMAGE:1754003 3'
8154	22120	35548	2.47	5.6E-02	BE542693.1	EST_HUMAN	601087169F1 NH_VGC_10 Homo sapiens cDNA clone IMAGE:3453279 3'
8154	22120	35549	2.47	5.6E-02	BE542693.1	EST_HUMAN	601087169F1 NH_VGC_10 Homo sapiens cDNA clone IMAGE:3453279 3'
10171	23096	36576	1.08	5.6E-02	AA482864.1	EST_HUMAN	rf4807.s1 NCI_GCAP_AVT Homo sapiens cDNA clone IMAGE:523242 similar to TR:G768559 G768559
11801	24172	39279	1.87	5.6E-02	AF280223.1	NT	HOMO ASSOCIATED POLYPEPTIDE 1C ;
2653	15960	28678	8.23	5.6E-02	X79868.1	NT	Human alpha TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3228	16283	29207	3.44	5.6E-02	X79868.1	NT	Human alpha TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4244	17273	33017	1.13	5.6E-02	U14961.1	NT	Mus musculus SH3 domain protein 18 (SH3D18), mRNA
6742	18838	33017	3.09	5.6E-02	U14961.1	NT	Gal4 heteroprotein mRNA fragment
8141	19838	33017	3.81	5.6E-02	U01174	SWISSPROT	TROPONIN ALPHA CHAIN, TROPONIN MUSCLE
7603	20564	33925	1.85	5.6E-02	6759902	NT	TROPONIN ALPHA CHAIN, TROPONIN MUSCLE
8457	21426	34643	0.69	5.6E-02	AF170011.1	NT	Mus musculus titin (TITN), mRNA
8457	21426	34643	0.69	5.6E-02	AF170011.1	NT	Homo sapiens sodium-dependent Na/K-ATPase (SVC11) mRNA, complete cds
10013	22540	39405	0.63	5.6E-02	10847634	NT	Homo sapiens sodium-dependent Na/K-ATPase (SVC11) mRNA, complete cds
10013	22540	39405	0.63	5.6E-02	10847634	NT	Homo sapiens sodium-dependent Na/K-ATPase (SVC11) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Bone Marrow

[illegible]

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10618	23540		0.6	5.3E-02	U07007.1	NT	D-erio mRNA for ap-23 POU gene, splice variant (neura, 6-16 bp and polyomergs, 20-28 bp)
10619	23617	37111	0.69	5.3E-02	U08432.1	NT	B-erio poUc1 mRNA for transcription factor
12022	24993	38558	2.06	5.3E-02	U09435.1	NT	H-sapiens mRNA for HMG-CoA-synthase
2293	13005		86.73	5.2E-02		NT	Homo sapiens napin A, alpha (PABA peptide hydrolase) (MEPA) mRNA
3131	16188	20097	1.98	5.2E-02	U27768.1	NT	Homo sapiens napin A, alpha (PABA peptide hydrolase) (MEPA) mRNA
3131	16188	20098	1.98	5.2E-02	U27768.1	NT	Homo sapiens napin A, alpha (PABA peptide hydrolase) (MEPA) mRNA
3960	17000	29015	0.73	5.2E-02	AF258101.1	NT	Homo sapiens partial LMOT1 gene for LIM domain only 1 protein, exon 1
3962	17002		0.97	5.2E-02		NT	Aradopsid thalassa putative discoprotea diron protein (CDI) mRNA, complete cds
4307	17336	30714	3.38	5.2E-02	U07132.1	NT	Mus musculus cytochrome inducible S-acyl-CoA oxidizing protein 3 (Ctst3), mRNA
6025	19108	32510	0.66	5.2E-02	U14751.1	NT	Human zardox homologue zardox NAD(P)H dehydrogenase, complete cds
6228	19302		1.22	5.2E-02	AB30395.1	EST_HUMAN	SH3 domain containing GOSL1, Lym1? Homo sapiens cDNA clone IMAGE:2408193.3 similar to contains MER15.b1
7480	20454	33913				EST_HUMAN	MER15, similar to
8327	21505		3.16	5.2E-02	AF16322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) / DNA-BINDING GENE 18 (PROTEIN)
8327	21505		3.16	5.2E-02	AF16322.2	NT	Homo sapiens chromosome 21 segment HS21C004
10027	20014	36487	1.77	5.2E-02	D10827.1	NT	Tumto madozo virus genomic RNA for Capsid protein, complete cds
10027	20014	36488	1.77	5.2E-02	D10827.1	NT	Tumto madozo virus genomic RNA for Capsid protein, complete cds
11888	24769	38357	8.42	5.2E-02	F32065.1	EST_HUMAN	HSPD25907 HMB3 Homo sapiens cDNA clone s33000339A.02
11888	24769	38358	8.42	5.2E-02	F32065.1	EST_HUMAN	HSPD25907 HMB3 Homo sapiens cDNA clone s33000339A.02
12693	25338		1.55	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2072	13330		0.97	5.1E-02	AL134071.1	EST_HUMAN	DKFZ6547D078.1 347 (synonym: mbr1) Homo sapiens cDNA clone DKFZ6547D078.5
5041	18054		0.94	5.1E-02	AB031740.1	NT	Homo sapiens PBL gene for salivary proline-rich protein P-8, complete cds
6830	18884	33775	0.69	5.1E-02	AF280396.1	NT	Homo sapiens PBL gene for salivary proline-rich protein P-8, complete cds
7030	18371	31269	1.76	5.1E-02	BF378625.1	EST_HUMAN	HYUJ10051.23600-350-308 UMO351 Homo sapiens cDNA
8506	21594	34076	0.77	5.1E-02	M20434.1	NT	Human tyrosinase phosphatidylserine transferase (HPT) gene, complete cds
8506	21594	34076	0.77	5.1E-02	M20434.1	NT	Human tyrosinase phosphatidylserine transferase (HPT) gene, complete cds
9207	21858	35081	1.26	5.1E-02	A11955.1	NT	Spodopora littoralis mRNA for 3-dehydroxyketo-3-keto-reductase
9327	22203	35834	0.61	5.1E-02	P02633	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (CK 14)
9327	22203	35834	0.61	5.1E-02	P02633	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (CK 14)
10188	23083	35971	7.1	5.1E-02	AF012698.1	NT	Candida albicans protein phosphatase Sudt homology (SDST) gene, complete cds
10542	23464	38959	1.68	5.1E-02	P49393.0	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APC (PROTEIN CEX)
11176	24135	37865	2.19	5.1E-02	AF039393.1	NT	Homo sapiens ES18 mRNA, partial cds
11176	24135	37866	2.19	5.1E-02	AF039393.1	NT	Homo sapiens ES18 mRNA, partial cds

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12639	29339		1.75	5.1E-02	AF02467.1	NT	Cucurbita melo polygalacturonate acylase (PG3) mRNA, complete cds
12641	29331		1.6	5.1E-02	AA334104.1	EST_HUMAN	U75902.51 NC: CGAP Pro Homo sapiens cDNA clone IMAGE:598139
483	13556	25481	2.16	5.0E-02	AF098004.1	EST_HUMAN	Mus musculus 5'UTR acidic hydrolase gene, exon 10
635	13988	29038	4.85	5.0E-02	Z33896.1	NT	O. virginiana HEL377 microsatellite DNA
1208	14247	27203	4.03	5.0E-02	Z69104.1	NT	Bacillus subtilis complete genome (section 1 of 31) from 1 to 213080
2007	15028	28035	4.84	5.0E-02	P02810	SWISSPROT	4) (PIE-PFF-3) PROTEIN A (PROTEIN C) CONTAINS PEPTIDE P-C
2829	14040	26966	1.92	6.0E-02	U77242.1	NT	Oryzopsis glaberrima UDP-glucuronosyltransferase (UG*2B13) mRNA, complete cds
3348	19399		1.34	5.0E-02	Z703610	NT	Mus musculus Uuc-51 18a kinase 2 (C. elegans) (Uk2) mRNA
3605	19554		1.01	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 87 of 183 of the complete genome
3806	19738	25652	13.52	6.0E-02	U17769.2	NT	Anthrax toxin protective antigen protein homolog mRNA, complete cds
6253	19328	32357	0.71	5.0E-02	AF060584.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6441	19606		1.25	5.0E-02	AJ242323.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7181	18412	31214	0.6	5.0E-02	P38619	SWISSPROT	NEUROFILAMENT TRIPLET T-PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE (NFL))
7795	20738	34110	12.03	5.0E-02	P38619	SWISSPROT	NEUROFILAMENT TRIPLET T-PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE (NFL))
8008	20946		0.02	5.0E-02	AF002404.1	EST_HUMAN	Mus musculus Fc-gamma-interacting serine/threonine kinase 3 (Fgik3) mRNA, complete cds
10560	22482	36877	1.26	5.0E-02	AF065268.1	NT	Mus musculus Fc-gamma-interacting serine/threonine kinase 3 (Fgik3) mRNA, complete cds
11820	24703	36255	2.47	5.0E-02	U67000.1	NT	Neurospora crassa protein 142 of 150 of the complete genome
12238	28818		6.4	5.0E-02	G00047	SWISSPROT	NOON-TRANSPARENT A PROTEIN
228	13326		27.61	4.8E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
389	13498	26364	2.86	4.9E-02	AF75648.1	NT	Homo sapiens ABCA7 (ABCA7) gene, complete cds
389	13498	26365	2.86	4.9E-02	AF75648.1	NT	Homo sapiens ABCA7 (ABCA7) gene, complete cds
3302	16355	26741	1.54	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3884	16929		0.7	4.9E-02	AJ188940.1	EST_HUMAN	Zq4841.2.1 Striatum INT neuron (857233) Homo sapiens cDNA clone IMAGE:532226.3 similar to contains ALU repetitive element/contains element MSRI repetitive element ;
3805	16550	26599	0.86	4.9E-02	AA00014.1	EST_HUMAN	278603.51 Scores: Init1s_NHT Homo sapiens cDNA clone IMAGE:784228.3
3805	16550	26597	0.96	4.9E-02	AA00014.1	EST_HUMAN	278603.51 Scores: Init1s_NHT Homo sapiens cDNA clone IMAGE:784228.3
487	17884	30783	2.11	4.9E-02	AW167821.1	EST_HUMAN	XG5591.0.1 NC: CGAP UR Homo sapiens cDNA clone IMAGE:283289.3
487	17884	30784	2.11	4.9E-02	AW167821.1	EST_HUMAN	XG5591.0.1 NC: CGAP UR Homo sapiens cDNA clone IMAGE:283289.3
5441	18348	31659	1.71	4.9E-02	U00122.1	NT	Rat diaphanin II gene, exon 6
5441	18348	31659	1.71	4.9E-02	U00122.1	NT	Rat diaphanin II gene, exon 6
7146	20318	33656	2.83	4.9E-02	AE003880.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8963	21029		0.81	4.9E-02	AE002059.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
9107	22073	35600	0.8	4.9E-02	AL161569.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	TRANSCRIPTION FACTOR ES
10956	23576	37075	0.53	4.8E-02	P16832	SWISSPROT	Homo sapiens prouro placental (GF-beta gene, complete cds
11730	24616	38183	3.44	4.8E-02	P1080303.1	NT	
12879	26473		6.65	4.8E-02	M18954.1	NT	Human gamma-B-crystallin (gamma-1,3) and gamma-C-crystallin (gamma-2-1) genes, complete cds
330	13420	26344	1.08	4.8E-02	D16471.1	NT	Human alpha-2A-crystallin (alpha-2A) gene, complete cds
331	13420	26344	2.41	4.8E-02	D16471.1	NT	Human alpha-2A-crystallin (alpha-2A) gene, complete cds
489	13502	29468	12.99	4.8E-02	P503100.1	NT	Human alpha-2A-crystallin (alpha-2A) gene, complete cds
2281	15294	29518	2.24	4.8E-02	M51933.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
3222	16277	26523	1.93	4.8E-02	M51933.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
4098	17719	31690	0.24	4.8E-02	D16194.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
5174	18183	31690	0.24	4.8E-02	M51933.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
8477	21448	36593	1.95	4.8E-02	M51933.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
8483	21448	36593	0.76	4.8E-02	M51933.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
8483	22449	35550	0.76	4.8E-02	M51933.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
13505	25243		1.35	4.8E-02	9653395	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
7004	20130	33445	3.77	4.7E-02	V01183.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
7099	20091	33539	0.66	4.7E-02	BF986023.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
7099	20091	33540	0.66	4.7E-02	BF986023.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
7103	20037	33540	1.66	4.7E-02	M62752.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
8504	21962	34076	8.56	4.7E-02	X1543.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
8505	22270	35701	1.65	4.7E-02	X59211.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
9237	22262	35701	2.51	4.7E-02	AB026076.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
9502	22544	35695	7.94	4.7E-02	X1543.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
10005	23902	35695	0.95	4.7E-02	BF95237.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
10005	23918		0.96	4.7E-02	AB073042.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
12763	25970		1.97	4.7E-02	P52951	SWISSPROT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
13022	25570		1.56	4.7E-02	AJ278802.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
270	13366	26362	1.08	4.8E-02	BE13363.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
741	13802	26741	3.47	4.8E-02	AE000448.1	NT	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to
1391	14385	27966	3.62	4.8E-02	AV272056.1	EST_HUMAN	hsp2702.1 Homo sapiens, secreted, fibroblast, NHSEF Homo sapiens cDNA clone IMAGE:3256113 similar to

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2486	15496	28225	4.32	4.9E-02	AW28629.1	EST_HUMAN	3x2400.x1 NC_004611 Homo sapiens cDNA clone IMAGE:286485 3' similar to SW GRF1_HUMAN
2819	13388	28262	1.03	4.9E-02	BE13393.1	EST_HUMAN	PMCH10339-251189-003-305 HT0339 Homo sapiens cDNA
3020	10078	28990	0.87	4.9E-02	BE13393.1	EST_HUMAN	PMCH10339-251189-003-305 HT0339 Homo sapiens cDNA
3342	16078	28990	0.87	4.9E-02	BE13393.1	EST_HUMAN	PMCH10339-251189-003-305 HT0339 Homo sapiens cDNA
3357	16078	28990	0.91	4.9E-02	BE13393.1	EST_HUMAN	PMCH10339-251189-003-305 HT0339 Homo sapiens cDNA
4146	17180		1.24	4.9E-02	AF220953.1	NT	Plus muscular nuclear RNA helicase II(G) (d6221) gene, complete cds
5252	18280	31126	0.94	4.9E-02	AA079167.1	EST_HUMAN	2x1020.11 Stragene ovarian cancer (887219) Homo sapiens cDNA clone IMAGE:545394 3' similar to gp-2532.2 KERA-TIN, TYPE II, CYTOSKELETAL 7 (HUMAN).
5920	18913	32006	1.42	4.9E-02	AF076962.1	NT	Radicalism beta1in, gonadotropin-releasing hormone and GnRH-associated peptide precursor (Grim2)
6337	19426	32660	4.48	4.9E-02	VS1634.1	NT	Cathinidin 182 (463) mRNA
6337	19426	32660	4.48	4.9E-02	VS1634.1	NT	Cathinidin 182 (463) mRNA
6908	20191	33518	1.51	4.9E-02	AI14674.1	EST_HUMAN	cat500a.x1 Sarcos, alveolar, Bohnwies, 2x181P493W Homo sapiens cDNA clone IMAGE:178971 3' similar to cat500a.x1 Sarcos, alveolar, Bohnwies, 2x181P493W
8134	21071	34470	0.89	4.9E-02	BE15406.1	EST_HUMAN	Rattus norvegicus Cathinidin H (Grim) mRNA
9003	21969	35391	2.89	4.9E-02	BE15406.1	EST_HUMAN	PMCH10339-250400-009-012 HT0339 Homo sapiens cDNA
11731	24617	35164	5.31	4.9E-02	AA91328.1	EST_HUMAN	cd27052.x1 Sarcos, NFL, T, CBC, S1 Homo sapiens cDNA clone IMAGE:184737 3'
12761	23907		1.99	4.9E-02	L11892.1	NT	Oxytocin, ciliary, macrophage scavenger receptor type II mRNA, complete cds
12952	23552		8.41	4.9E-02	VS7806.1	NT	Human gamma immunoglobulin, lambda light chain gene
447	13520	28453	1.9	4.9E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1222	14260	27217	0.78	4.9E-02	AF005730.1	NT	Marburg virus strain, MIS Africa/Johannesburg/1975/Ozlin VP35 gene, complete cds
1222	14260	27218	0.78	4.9E-02	AF005730.1	NT	Marburg virus strain, MIS Africa/Johannesburg/1975/Ozlin VP35 gene, complete cds
1821	14948	27841	4.23	4.9E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2119	15135	28156	3.34	4.9E-02	AE033964.1	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
3738	18178	29691	4.42	4.9E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6338	19427	32670	1.63	4.9E-02	AI400877.1	NT	Homo sapiens chromosome 21 segment HS21C080
6556	19713	32960	0.84	4.9E-02	AL163280.1	NT	Methanococcus frisia carbon monoxide dehydrogenase large subunit (cdhA) gene, carbon monoxide dehydrogenase small subunit (cdhB) gene, complete cds
7052	20084	33592	0.96	4.9E-02	26487.1	NT	Methanococcus frisia carbon monoxide dehydrogenase large subunit (cdhA) gene, carbon monoxide dehydrogenase small subunit (cdhB) gene, complete cds
7052	20084	33593	0.96	4.9E-02	26487.1	NT	Methanococcus frisia carbon monoxide dehydrogenase large subunit (cdhA) gene, carbon monoxide dehydrogenase small subunit (cdhB) gene, complete cds
8736	21704	35128	2.34	4.9E-02	AF06684.1	NT	Arabidopsis thaliana COAT-box binding factor HAP3 homolog gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession Database No.	Top Hit Source	Top Hit Descriptor
10309	23233	38715	4.58	4.5E-02 AA325216.1	EST_HUMAN	EST128187	Cereadum II Homo sapiens cDNA 5' and similar to neuro-D4 protein
10460	23382	38875	0.43	4.5E-02 X95508.1	NT		A. europaeum mRNA for arginase-like protein
10577	23468	38981	0.81	4.5E-02 AB004470.1	NT		Cellular gallin mRNA for alpha1 integrin, complete cds
12440	25203	31828	2.95	4.5E-02	EST_HUMAN		Homo sapiens tel finger protein-like cDNA 5' mRNA
12823	26963	31140	7.33	4.5E-02 AA110971.1	EST_HUMAN	22431117	Stratagene 5' Homo sapiens cDNA clone IMAGE:633493 5'
222	13022		4.84	4.4E-02 BE072733.1	EST_HUMAN	8016021	Stratagene 5' Homo sapiens cDNA clone IMAGE:353384 5'
2107	15124		6.38	4.4E-02 AF31398	SWISSPROT		Human 5' Homo sapiens cDNA clone IMAGE:353384 5'
2498	15501	28527	2.11	4.4E-02 AF087547.1	EST_HUMAN	Q12-27001	Q12-27001 Homo sapiens cDNA
3954	16997	29812	2.01	4.4E-02 AF159160.1	NT		Homo sapiens alpha2 macroglobulin-like protein 1 (alpha2) gene, complete cds
4657	17978	30583	1.25	4.4E-02 AF103007.1	NT		Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4657	17978	30584	1.25	4.4E-02 AF103007.1	NT		Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7171	17931	33839	0.94	4.4E-02 AF022880.1	NT		Ovis aries CCAAT-enhancer binding protein epsilon gene
7232	20268	33840	0.59	4.4E-02 AF04894.1	NT		Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8103	22071	35407	2.17	4.4E-02 AF126059.1	EST_HUMAN		Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
11400	24353	37586	3.75	4.4E-02 AF090569.1	NT		Hepatitis E virus strain HEV/J22 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11533	24474	38025	2.56	4.4E-02 AA069738.1	EST_HUMAN	ea3304.1	Genes for Wilms tumor Homo sapiens cDNA clone IMAGE:607031 5'
12180	25014		2.22	4.4E-02 AB040026.1	NT		Homo sapiens mRNA for KIAA1463 protein, partial cds
12346	25800		1.83	4.4E-02 BF241245.1	EST_HUMAN	501878749F1	NH.MGC 55 Homo sapiens cDNA clone IMAGE:4107418 5'
761	13841	26786	5.03	4.3E-02 AF003246.1	NT		Monoclonal scabellin myosin heavy chain FKMA (FKMA) mRNA, complete cds
2575	15576	28595	1.4	4.3E-02 AF70487.1	EST_HUMAN	AF704878	AD8 Homo sapiens cDNA clone ADBA04088 5'
3343	16400	29409	8.93	4.3E-02 AL153210.2	NT		Homo sapiens chromosome 21 segment H521C010
3971	19714		1.25	4.3E-02 AF090568.1	NT		Homo sapiens prionylcysteinemia zinc finger protein (PLZF) gene, complete cds
6844	19702	32077	4.62	4.3E-02 F04427	SWISSPROT	PLECTIN	
6844	19702	32078	4.62	4.3E-02 F04427	SWISSPROT	PLECTIN	
8896	19048	33245	0.73	4.3E-02 AA652566.1	EST_HUMAN	h68612at1	NO2 CGAP P22 Homo sapiens cDNA clone IMAGE:1189588
8896	19048	33245	0.9	4.3E-02 AF003246.1	NT		Homo sapiens alpha2 macroglobulin-like protein 1 (alpha2) gene, complete cds; alternatively spliced
9163	21119	35546	0.95	4.3E-02 AF003246.1	NT		H. sapiens (H. sapiens) for neural cell adhesion
9163	21119	35547	0.95	4.3E-02 AF003246.1	NT		H. sapiens (H. sapiens) for neural cell adhesion
9163	21119	35547	0.95	4.3E-02 AF003246.1	NT		H. sapiens (H. sapiens) for neural cell adhesion
923	13981	29632	1.85	4.3E-02 AF123371.1	EST_HUMAN	AF123372	Homo sapiens cDNA clone NT281020020 5'
867	13923		2.98	4.3E-02 AF123371.1	EST_HUMAN	AF123372	Homo sapiens cDNA clone NT281020020 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
897	13932	29910	0.63	4.3E-02	AW03845.1	EST_HUMAN	w34g4.1 x1 NCL CGAP_P141 Homo sapiens cDNA clone IMAGE:254584.3 similar to TR.Q35261 Q83291
1733	14793		1.54	4.3E-02	AF44306.1	NT	L1 RE TROP-OSON, ORF2 mRNA, contains L1, is L1 repetitive element.
1733	14832	27808	1.02	4.3E-02	AF44306.1	NT	Thrombospondin domain complete genome, segment 4/6
3077	16720	26834	2.16	4.3E-02	Q23030	SWISSPROT	TRANSFORMING PROTEIN TAF
4774	17794	30886	0.73	4.3E-02	BF42864.1	EST_HUMAN	6023710F17.NCL CGAP_P141 Homo sapiens cDNA clone IMAGE:4125972.5
5959	18794	31957	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P-450 polypeptide 43 (CYP3A4) gene, partial cds; cytochrome P-450 polypeptide 44 (CYP3A4) and cytochrome P-450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P-450 polypeptide 5 (CYP3A5) gene, partial cds
5959	18794	31968	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P-450 polypeptide 43 (CYP3A4) gene, partial cds; cytochrome P-450 polypeptide 44 (CYP3A4) and cytochrome P-450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P-450 polypeptide 5 (CYP3A5) gene, partial cds
7175	19408	31203	0.73	4.2E-02	BE288285.1	EST_HUMAN	60124569F1.NHL MGC_8 Homo sapiens cDNA clone IMAGE:2885318.5
7789	20722	34094	4.52	4.3E-02	AF276752.1	NT	Ligandless pneumophila catalase-oxidase (lad) gene, complete cds
7793	20745	34118	0.61	4.3E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAR4.5
9162	22128	35559	3.74	4.3E-02	Q00095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS-LINKING PROTEIN)
10528	23447	38648	1.19	4.3E-02	Q10850	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-36)
11379	24328	37655	1.58	4.3E-02	AA076118.1	EST_HUMAN	on33b11 at NCL CGAP_L43 Homo sapiens cDNA clone IMAGE:1554461.3 similar to gb:MS220
11637	24574	38138	2.65	4.3E-02	BE115622.1	EST_HUMAN	INTERLEUKIN-12 BETA, CHAIN PRECURSOR (HUMAN)
11637	24574	38139	2.65	4.3E-02	BE115622.1	EST_HUMAN	PM3-BN0174-25050-009-410 BN0174 Homo sapiens cDNA
12594	25608		5.62	4.3E-02	AB34194.1	EST_HUMAN	w46510-1.NCL CGAP_P141 Homo sapiens cDNA clone IMAGE:2510850.3
12600	25650		1.89	4.3E-02	D14711.1	NT	Staphylococcus aureus HSP10 and HSP90 genes
911	13382	25033	0.76	4.1E-02	AF200526.1	NT	Homo sapiens HPS1 gene, intron 5
2685	15851	26959	1.16	4.1E-02	AE02530.2	NT	Chlamydia muridarum, section 6 of 66 of the complete genome
5039	17424		7.84	4.1E-02	AW060484.1	EST_HUMAN	Q1Y-NN0013.1B040-164-08 NN0013 Homo sapiens cDNA
5039	17424	31168	0.62	4.1E-02	BE02103	EST_HUMAN	Homo sapiens BRY (box-determining region 7)-box 10 (BOX10), mRNA
5275	18320		1.08	4.1E-02	BE21184.1	EST_HUMAN	601107335F1.NHL MGC_10 Homo sapiens cDNA clone IMAGE:334985.5
5728	19320	32050	1.08	4.1E-02	BE21184.1	EST_HUMAN	601107335F1.NHL MGC_10 Homo sapiens cDNA clone IMAGE:334985.5
7036	20088		1.19	4.1E-02	F5381.1	NT	A. thaliana mRNA for plasma membrane intrinsic protein 1a
7308	20277	33915	1.19	4.1E-02	AE02103.1	NT	Oreoplasma unguisum section 33 of 38 of the complete genome
7850	20709	34678	2	4.1E-02	785247	NT	Adenovirus protein removal insertion in the cDNA-phosphodiesterase (d beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (5' end) and 3' UTR
7850	20804	34180	0.7	4.1E-02	U02110.1	NT	Adenovirus protein removal insertion in the cDNA-phosphodiesterase (d beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (5' end) and 3' UTR

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7281	25669		0.79	3.7E-02	AF000983.1	NT	Aeropyrum pernix genomic DNA, section 877
7596	20887	34290	0.84	3.7E-02	AL06895.1	NT	Xyella fastidiosa, section 121 of 228 of the complete genome
10376	23286		0.99	3.7E-02	AF142616.1	EST HUMAN	af5509 at NCBI, GenBank, Homo sapiens cDNA clone IMAGE:426812.3
12226	23091	36028	0.94	3.7E-02	BF124974.1	EST HUMAN	601762171.F1 NCH.VOC.20 Homo sapiens cDNA clone IMAGE:426812.3
13883	29762	31220	2.34	3.7E-02	11180392	NT	Homo sapiens isolate cancer family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3967	16710	26025	1.04	3.6E-02	X73221.1	NT	H. vulgare S51 gene for sucrose synthase
							Homo sapiens genomic region containing hypervariable minisatellites chromosome 10 (0628.3) of Homo sapiens
3874	16717	26031	0.75	3.6E-02	AL068906.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10 (0628.3) of Homo sapiens
9253	16261	31130	2.27	3.6E-02	AL06810.1	NT	Homo sapiens gpi2, p88, and t61 genes for glyceroldehyde-3-phosphate, phosphoglycerate kinase and phosphoglycerate kinase
5501	19801	31914	0.8	3.6E-02	X89403.1	NT	C. glutamicum gpi2, p88, and t61 genes for glyceroldehyde-3-phosphate, phosphoglycerate kinase and phosphoglycerate kinase
5501	19801	31930	0.8	3.6E-02	X89403.1	NT	C. glutamicum gpi2, p88, and t61 genes for glyceroldehyde-3-phosphate, phosphoglycerate kinase and phosphoglycerate kinase
5578	18374	33333	0.95	3.6E-02	AF14722.1	NT	Homo sapiens RUGAS (RUG2) mRNA, complete cds
5683	18374	33333	0.97	3.6E-02	AF14722.1	EST HUMAN	OM2-EN0013-110600-192510 EN0013 Homo sapiens cDNA
5683	18374	33333	0.97	3.6E-02	AF14722.1	EST HUMAN	OM2-EN0013-110600-192510 EN0013 Homo sapiens cDNA
7150	19882	31270	0.5	3.6E-02	AF16751.1	NT	Mathemacoccus jamaicensis section 117 of 160 of the complete genome
7291	20263	33697	1.7	3.6E-02	AF125652.1	NT	Chromatium vibrio sulfur globule protein C/2 precursor (gpg2) gene, complete cds
							hw2065 at NCBI, GenBank, GCB0 Homo sapiens cDNA clone IMAGE:1241024.3 similar to gb:U00314.m2
7527	20491	33853	2.75	3.6E-02	AA174521.1	EST HUMAN	TUBULIN BETA-1 CHAIN (HUMAN)
7665	20338	34218	1.08	3.6E-02	BE143078.1	EST HUMAN	MRC-H701B9-00200-003308 HT0188 Homo sapiens cDNA
							Dichyatalium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9746	22697	35142	1.85	3.6E-02	U29008.1	NT	Dichyatalium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9746	22697	35143	1.85	3.6E-02	U29008.1	NT	Dichyatalium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9971	22848	35361	0.98	3.6E-02	BF147566.1	EST HUMAN	80220435F1 NC1 CGAP Em97 Homo sapiens cDNA clone IMAGE:4156116.5
896	13951	26009	0.9	3.6E-02	U06956.1	NT	Drosophila melanogaster tigm mRNA, complete cds
1010	14059	27011	1.38	3.6E-02	AF23417.1	NT	Homo sapiens nucleoside-specific lysozyme (NLSY) gene, complete cds
1506	14999	27874	1.3	3.6E-02	BF679068.1	EST HUMAN	62285135F1 NCH.VOC.20 Homo sapiens cDNA clone IMAGE:4268377.5
1508	14999	27874	1.3	3.6E-02	BF679068.1	EST HUMAN	62285135F1 NCH.VOC.20 Homo sapiens cDNA clone IMAGE:4268377.5
4241	17270	30165	1.05	3.6E-02	AE001773.1	NT	Thermococcus maritima section 86 of 136 of the complete genome
							CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
4344	17371	30253	3.87	3.5E-02	PS6790	SWISSPROT	

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Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (To) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5398	1873	32857	1.04	3.4E-02	P47144	SWISSPROT	HYPOTHETICAL 507 KD PROTEIN IN SODIUM-DEPENDENT INTERGENIC REGION
6347	19478		1.74	3.5E-02	J07283	NT	Maze strain 1 gene (Maze1), complete cds
8310	21279		0.78	3.4E-02	A20951.1	EST_HUMAN	IP44403.11 Soares ratna 1628R.Homo sapiens cDNA clone IMAGE:160266 5' similar to contains Alu
8670	21036	35392	2.87	3.4E-02	BC286970.1	EST_HUMAN	IP44403.11 Soares ratna 1628R.Homo sapiens cDNA clone IMAGE:302973 3'
10378	23331	30777	1.59	3.5E-02	X79832.1	NT	Human M251383 protein and gene
10425	23347	35832	0.47	3.4E-02	BC591042.1	EST_HUMAN	Human M251383 protein and gene
11623	24705	36228	1.61	3.4E-02	A1681641.1	EST_HUMAN	PH4-CT0035-261269-02-033 CT00328 Homo sapiens cDNA
12123	24706	36229	1.61	3.4E-02	A1681641.1	EST_HUMAN	PH4-CT0035-261269-02-033 CT00328 Homo sapiens cDNA
12977	25608		5.77	3.4E-02	BE279043.1	EST_HUMAN	65178765F.NIH_MGC_30 Homo sapiens cDNA clone IMAGE:35-4303 5'
650	13649	26582	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
550	13649	26583	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
581	13649	26582	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
581	13649	26583	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1083	14009	27049	2.4	3.4E-02	A127420.1	EST_HUMAN	X62607.X1 Soares N.F., T. GBC. S1 Homo sapiens cDNA clone IMAGE:2941283 3' similar to
1211	14249		6.51	3.4E-02	11345459	NT	SW-CH1_HUMAN PABP01 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR
2401	15408	28432	2.81	3.4E-02	T57160.1	EST_HUMAN	Human cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3444	18491	28410	1.19	3.4E-02	AL160263.2	NT	Human sapiens chromosome 21 segment HS21C009
3942	16982	28907	3.71	3.4E-02	A17794682.1	EST_HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4828	17849	30537	3.05	3.4E-02	X69799.1	NT	Musculus S-antigen gene promoter region
5100	18110		2.48	3.4E-02	Q29467	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
6114	18124	30986	1.93	3.4E-02	A1012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6330	18400		0.83	3.4E-02	BF131928.1	EST_HUMAN	05182844F.NIH_MGC_38 Homo sapiens cDNA clone IMAGE:4682434 5'
7032	18394	31251	3.87	3.4E-02	U24388.1	NT	Human lysozidase-like protein gene, exon 3
8604	21572		3.14	3.4E-02	A1895926.1	EST_HUMAN	W89004.X1 NCI CGAP B1928 Homo sapiens cDNA clone IMAGE:2433031 3'
9100	22088	35492	1.95	3.4E-02	A456698.1	EST_HUMAN	Human cDNA clone IMAGE:1216071 similar to contains Alu repetitive element contains element MER29 MER29 repetitive element
							tr.G101742s G101742s
9298	22234		0.2	3.4E-02	AA16308.1	EST_HUMAN	IP8IG6P.KYTL.SROGVLKATMRPNTETANL.TN.KESVTDATYANSSGTTKAFINVLDRPG
10139	23062		0.84	3.4E-02	A1027191.1	EST_HUMAN	PPT.GPVVDSYTESYTLKWEPPKQSGVYNYLLKRYSTAVYVETVATMTMKVMKL...
							0259038.X1 Soares_jaraphyroid tumor NH9PA Homo sapiens cDNA clone IMAGE:1083918 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
372	13498		6.24	3.3E-02	AJ399795.1	EST_HUMAN	275639.s1 Soares, Iwata, NHT Homo sapiens cDNA clone IMAGE:739198.3'
1171	14713	27166	14.48	3.3E-02	AJ393597.1	NT	Oryzopsis glabra cDNA clone IMAGE:739198.3'
1645	14677	27650	1.73	3.3E-02	AJ110763.1	NT	Human placenta cDNA clone IMAGE:739198.3'
1753	14782		1.28	3.3E-02	AJ500700.1	NT	Human placenta cDNA clone IMAGE:739198.3'
2096	15113		1.76	3.3E-02	U06112.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
2488	16402	28485	1.31	3.3E-02	U06112.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
3372	16422	26247	6.85	3.3E-02	U06112.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
4206	14677	27650	2.35	3.3E-02	AJ110763.1	NT	Human placenta cDNA clone IMAGE:739198.3'
4494	17419	30007	0.81	3.3E-02	U06112.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
4648	17863	30796	0.36	3.3E-02	AJ775963.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
4670	18300	32883	20.36	3.3E-02	B2745968.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
5370	18300	32883	20.14	3.3E-02	B2745968.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
5406	18300	32883	20.14	3.3E-02	B2745968.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
5677	22630	36094	0.71	3.3E-02	B115821.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
5677	22630	36095	0.71	3.3E-02	B115821.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
9779	22720	36174	0.72	3.3E-02	AA48202.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
9779	22720	36175	0.72	3.3E-02	AA48202.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
10564	23884		0.46	3.3E-02	AJ8106.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
11455	24368	37445	2.47	3.3E-02	B0891107.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
12425	25169		3.71	3.3E-02	B0645.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
12547	25270		1.69	3.3E-02	AJ280663.1	NT	Human placenta cDNA clone IMAGE:739198.3'
12577	25286		3.04	3.3E-02	AJ1890.1	NT	Human placenta cDNA clone IMAGE:739198.3'
132	13227	28168	1.27	3.3E-02	AJ02005.1	NT	Human placenta cDNA clone IMAGE:739198.3'
132	13227	28168	1.27	3.3E-02	AJ02005.1	NT	Human placenta cDNA clone IMAGE:739198.3'
1128	14171	27122	10.01	3.3E-02	AF065073.1	NT	Human placenta cDNA clone IMAGE:739198.3'
1128	14171	27122	10.01	3.3E-02	AF065073.1	NT	Human placenta cDNA clone IMAGE:739198.3'
2127	15144		3.6	3.3E-02	B2745968.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
3151	16028	29122	6.01	3.3E-02	B2745968.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
4246	17275		16.99	3.3E-02	U06112.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
4601	17816	30712	3.75	3.3E-02	AJ11482.1	NT	Human placenta cDNA clone IMAGE:739198.3'
5303	18300		1.34	3.3E-02	B0645.1	EST_HUMAN	Human placenta cDNA clone IMAGE:739198.3'
5913	19709	31666	1.38	3.3E-02	AJ08708.1	NT	Human placenta cDNA clone IMAGE:739198.3'
5913	19709	31667	1.38	3.3E-02	AJ08708.1	NT	Human placenta cDNA clone IMAGE:739198.3'

Table 4

Single Exon Probe Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8873	10730	33008	2.23	3.3E-02	U02437.1	NT	Rap1-p34/murinus left junction in cell line W6B.14
8978	18733		39.53	3.3E-02	T89897.1	EST_HUMAN	YAC311.2.1 Soares fetal liver spliced 1NF15 Homo sapiens cDNA clone IMAGE:110087.2 similar to contains Alu repetitive elements/containing 1.1 repetitive element
8983	18817	33097	4.01	3.3E-02	AF135445.1	NT	Negative coxixia tissue kallikrein gene, complete cds
8989	20978	34372	0.62	3.3E-02	11424048	NT	Homo sapiens cytochrome P450, subfamily 1B (phenobarbital-inducible) (CYP2B6) mRNA
8993	21611	35033	2.84	3.3E-02	6880695	NT	Mus musculus testis member 3c (M3c), mRNA
9286	22259		0.7	3.3E-02	AF109718.1	NT	Homo sapiens chromosome 17 region, member 1 region
9500	22542	35052	1.02	3.3E-02	AF109718.1	EST_HUMAN	qmt1704.4 NC1 CGAP LUS Homo sapiens cDNA clone IMAGE:182603.3'
9500	22542	35053	1.02	3.3E-02	A278971.1	EST_HUMAN	qmt1704.4 NC1 CGAP LUS Homo sapiens cDNA clone IMAGE:182603.3'
10417	23339		4.18	3.3E-02	AA1719795.1	EST_HUMAN	gbl.08441 CYTOCHROME C OXIDASE POLYPEPTIDE II (CYTOC),
10723	23845	37136	0.88	3.3E-02	U08782.1	NT	Mus musculus thymocyte receptor CDS mRNA, complete cds
12812	25078		1.43	3.3E-02	U00574.1	NT	Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-ras-1) with four exons
1285	14300		2.28	3.1E-02	4903418	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1308	14334	27309	1.87	3.1E-02	F18945	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN ALPHA-3 CHAIN PRECURSOR (GE-ALPHA-3)
1606	14803	27926	1	3.1E-02	6871864	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (A3-3), mRNA
1867	16012		1.18	3.1E-02	U05067.1	NT	Drosophila melanogaster mRNA for headcase protein
5338	18441	31164	1.28	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5434	18536		2.28	3.1E-02	A278478.1	EST_HUMAN	zab1a58.1 NC1 CGAP, G531 Homo sapiens cDNA clone IMAGE:703858.5'
5731	18528	32005	0.81	3.1E-02	BF58742.1	EST_HUMAN	40208783.F1 NH LMGC, 57 Homo sapiens cDNA clone IMAGE:705789.5'
5803	25946	32078	0.52	3.1E-02	AAJ581284.1	NT	Neseritis meningioma DNA for region 2 (fnaB) and fnaC-homolog, unknown genes and flanking genes, strain FAM18
10397	23313	38763	2.55	3.1E-02	AF04776.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1627	14690		2.21	3.0E-02	AF16125.1	NT	Phytoleaves mirvus cytochrome oxidase 1 gene, partial cds; mitochondrial gene for mitochondrial product
2590	15591	25608	0.97	3.0E-02	AA402242.1	EST_HUMAN	zab603.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:77263.3'
3560	18324	25545	0.91	3.0E-02	U0476.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3769	19329	25524	2.77	3.0E-02	AF27844.1	NT	Pseudomonas fluorescent family II emulxin/antifreeze gene, complete cds
3962	17309		0.88	3.0E-02	AA620223.1	EST_HUMAN	QV225026-19200-040-40b ST0268 Homo sapiens cDNA
3962	17309		1.45	3.0E-02	AA394003.1	EST_HUMAN	EST743020 Thelal gland II Homo sapiens cDNA, 5' end
5092	19102	30877	1.45	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5092	19102	30878	7.41	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
8465	18597		2.89	3.0E-02	AB047633.1	NT	Homo sapiens mRNA for KIAA1673 protein, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe Seq ID NO.	Exon Seq ID NO.	ORF Seq ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7657	21067	33942	0.67	2.9E-02	D29214.1	EST_HUMAN	HUMN22 Human epidermal keratinocyte Homo sapiens cDNA clone 282
8169	21077	34006	0.53	2.9E-02	AE003932.1	NT	Xiella fastidiosa, section 78 of 232 of the complete genome
8331	21300	34716	0.83	2.9E-02	AF128279.1	NT	Buchnera aphidicola natural-host Schilchehendallia chironomus gluconate-5-phosphate dehydrogenase (gnd) gene, partial cds
8331	21300	34717	0.83	2.9E-02	AF128279.1	NT	Buchnera aphidicola natural-host Schilchehendallia chironomus gluconate-5-phosphate dehydrogenase (gnd) gene, partial cds
1018	22073	36408	2.88	2.9E-02	AF1675979.1	EST_HUMAN	CNBP-T00744071286-051-cdt P10014 Homo sapiens cDNA
1020	22073	36409	2.88	2.9E-02	AF1675979.1	EST_HUMAN	CNBP-T00744071286-051-cdt P10014 Homo sapiens cDNA
1023	23136	35410	2.28	2.9E-02	AF1675979.1	EST_HUMAN	CNBP-T00744071286-051-cdt P10014 Homo sapiens cDNA
1023	23136	35410	2.28	2.9E-02	AF1675979.1	EST_HUMAN	CNBP-T00744071286-051-cdt P10014 Homo sapiens cDNA
10710	23532	37127	0.97	2.9E-02	AF1675979.1	EST_HUMAN	Neurospora tenuis genomic DNA, section 777
11388	16678	25840	1.6	2.9E-02	AF1675979.1	NT	Scaphylococcus aureus, section 11388
12531	16678	25840	1.6	2.9E-02	AF1675979.1	NT	Scaphylococcus aureus, section 11388
12531	16678	25840	1.6	2.9E-02	AF1675979.1	NT	Scaphylococcus aureus, section 11388
567	13837	23857	1.49	2.9E-02	AF1675979.1	EST_HUMAN	Human gene for alpha high-subunit keratin protein
3300	16426	20635	1.37	2.9E-02	AF1675979.1	EST_HUMAN	EST1382231 MAGE:102892 5'
3300	16426	20635	1.37	2.9E-02	AF1675979.1	EST_HUMAN	EST1382231 MAGE:102892 5'
3300	16426	20635	1.37	2.9E-02	AF1675979.1	EST_HUMAN	EST1382231 MAGE:102892 5'
4341	17368	20656	1.27	2.9E-02	AF1675979.1	NT	Homo sapiens retinal factor (RSF202) gene, exon 2
4341	17368	20656	1.27	2.9E-02	AF1675979.1	NT	Homo sapiens retinal factor (RSF202) gene, exon 2
4341	17368	20656	1.27	2.9E-02	AF1675979.1	NT	Homo sapiens retinal factor (RSF202) gene, exon 2
5298	18215	31090	3.2	2.9E-02	N87073.1	EST_HUMAN	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5298	18215	31090	3.2	2.9E-02	N87073.1	EST_HUMAN	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5298	18215	31090	3.2	2.9E-02	N87073.1	EST_HUMAN	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5595	18962	31922	10.89	2.9E-02	BE741063.1	EST_HUMAN	GLIANTIN TRANSGLYCOSYLASE
5595	18962	31922	10.89	2.9E-02	BE741063.1	EST_HUMAN	GLIANTIN TRANSGLYCOSYLASE
5595	18962	31922	10.89	2.9E-02	BE741063.1	EST_HUMAN	GLIANTIN TRANSGLYCOSYLASE
6091	20204	33533	1.13	2.9E-02	U78960.1	EST_HUMAN	Dengue virus type 2 non-structural protein 1 (NS1) gene, partial cds
8071	21639	35063	2.24	2.9E-02	U78960.1	EST_HUMAN	X01508.17 NIG_MXG_8 Homo sapiens cDNA clone IMAGE:394607 5'
9371	22336	35769	0.82	2.9E-02	AA007620.1	NT	X01508.17 NIG_MXG_8 Homo sapiens cDNA clone IMAGE:394607 5'
9371	22336	35769	0.82	2.9E-02	AA007620.1	NT	X01508.17 NIG_MXG_8 Homo sapiens cDNA clone IMAGE:394607 5'
9371	22336	35769	0.82	2.9E-02	AA007620.1	NT	X01508.17 NIG_MXG_8 Homo sapiens cDNA clone IMAGE:394607 5'
9593	22625	35974	1.03	2.9E-02	AF1675979.1	NT	Cratogeomys planatigaster mRNA for homeodomain leucine zipper protein (hs-1)
9593	22625	35974	1.03	2.9E-02	AF1675979.1	NT	Cratogeomys planatigaster mRNA for homeodomain leucine zipper protein (hs-1)
9593	22625	35974	1.03	2.9E-02	AF1675979.1	NT	Cratogeomys planatigaster mRNA for homeodomain leucine zipper protein (hs-1)
9967	22622	35974	0.71	2.9E-02	AE010622.1	NT	Caenorhabditis elegans, section 9967
10990	23000	37413	0.42	2.9E-02	BF527244.1	EST_HUMAN	Caenorhabditis elegans, section 10990
12815	25438		1.6	2.9E-02	RO6968.1	EST_HUMAN	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12815	25438		1.6	2.9E-02	RO6968.1	EST_HUMAN	Archaeoglobus fulgidus section 15 of 172 of the complete genome
12815	25438		1.6	2.9E-02	RO6968.1	EST_HUMAN	Archaeoglobus fulgidus section 15 of 172 of the complete genome
1485	14918	27491	1.07	2.7E-02	U69059.1	NT	Human gamma 1 cell receptor beta chain Dopamine-beta-hydroxylase-like, TRV1, TRV2, TRV3
3448	15492	29411	1.88	2.7E-02	AL161494.2	NT	TCRBV751P, TCRBV752A1NT, TCRBV651A1NT, TCRBV652A1NT, TCRBV752A1NT, TCRBV752A1NT
4230	17259	30149	2.01	2.7E-02	N47258.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 9
4230	17259	30149	2.01	2.7E-02	N47258.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 9
4230	17259	30149	2.01	2.7E-02	N47258.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 9

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Exon Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	17256	30144	2.01	2.1E-02/AF105000.1	EST_HUMAN	EST_HUMAN	Y68912.11 Soares, nulliparous, calcitriol, 2NcHSP Homo sapiens cDNA clone IMAGE:280487.5'
5319	18425	31178	0.52	2.1E-02/BF29672.1	EST_HUMAN	EST_HUMAN	X01856.011 FH, WGC, 57 Homo sapiens cDNA, 35ra IMAGE:03570.5'
5516	18518	31549	1.09	2.7E-02/RT2245.1	EST_HUMAN	EST_HUMAN	U01135.011 Homo sapiens NF- κ B Homo sapiens cDNA clone IMAGE:28897.5' similar to SP-IC294, IC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6005	19088	32289	0.68	2.1E-02/AB1070.1	NT	NT	T, section of 371120 mRNA for viral type V protein
6837	19167	32579	0.51	2.1E-02/AB1070.1	NT	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
6754	19805	33031	1.03	2.1E-02/AF105000.1	EST_HUMAN	EST_HUMAN	A bicupous p53A gene
7289	20034	33504	1.83	2.1E-02/AF105000.1	EST_HUMAN	EST_HUMAN	058503.41 Soares, total, fetus, N621F8, 3w Homo sapiens cDNA clone IMAGE:1624681.3'
8140	21077	34031	0.53	2.1E-02/A032456.1	NT	NT	Homo sapiens mRNA for FLJ00408 protein, partial cds
8160	21085	34097	0.59	2.1E-02	EST_HUMAN	EST_HUMAN	Mus musculus G21 protein (G21), mRNA
8807	21685		1.23	2.7E-02/AB17056.1	EST_HUMAN	EST_HUMAN	162820.81 Soares, total, fetus, N621F8, 3w Homo sapiens cDNA clone IMAGE:2065882.3' similar to centrin A1a repetitive element;
875	13840	26556	1.25	2.6E-02/AL185982.2	NT	NT	Homo sapiens chromosome 21, segment H32T082
2371	15352	28404	2.54	2.6E-02/AA60021.1	EST_HUMAN	EST_HUMAN	440250.2.11 Sindigene fetal retina, 537.202 Homo sapiens cDNA clone IMAGE:539561.3'
2376	15384	28406	3.05	2.6E-02	NT	NT	Mus musculus histidine rich calcium binding protein (Hr), mRNA
2376	15384	28407	3.05	2.6E-02	NT	NT	Mus musculus histidine rich calcium binding protein (Hr), mRNA
2376	15384	28407	3.05	2.6E-02	NT	NT	Mus musculus MHC class II region RD gene, partial cds; Bf, C2, G6A, TG22, G9, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
2926	15894		1.52	2.6E-02/AF105000.1	NT	NT	X81809.41 Soares, NF- κ B, S1 Homo sapiens cDNA clone IMAGE:2662409.3'
3068	17028	30048	3.25	2.6E-02/AW181945.1	EST_HUMAN	EST_HUMAN	Chenopodium rubrum R1 section 181 of 229 of the complete chromosome 1
4942	17058	30087	1.8	2.6E-02/AE002514.1	NT	NT	Chenopodium rubrum R1 section 181 of 229 of the complete chromosome 1
5104	18114			2.6E-02	EST_HUMAN	EST_HUMAN	X52504.1 NT, CGAP, S44 Homo sapiens cDNA clone IMAGE:2570383.3' similar to SW_7069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIA04069 ;
5128	18137	31014	3.05	2.6E-02/AW241164.1	EST_HUMAN	EST_HUMAN	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 83
5944	19030		0.6	2.6E-02/AL161983.2	NT	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 83
5942	19076		0.55	2.6E-02/AL161983.2	NT	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 83
6345	19414		6.38	2.6E-02/AZ0090.1	EST_HUMAN	EST_HUMAN	Q27191.1 NT, CGAP, K38 Homo sapiens cDNA clone IMAGE:176257.3'
6565	19925	32800	1.88	2.6E-02/BCG21748.1	EST_HUMAN	EST_HUMAN	Q01493.1371 NHT, MGC, 70 Homo sapiens cDNA clone IMAGE:388578.3'
7001	20127	33441	0.82	2.6E-02/265064.1	NT	NT	Vaccinia virus ORF1, strain Wyeth
7001	20127	33442	0.82	2.6E-02/265064.1	NT	NT	Vaccinia virus ORF1, strain Wyeth
7001	20127	33442	0.82	2.6E-02/265064.1	NT	NT	Vaccinia virus ORF1, strain Wyeth
7095	20028	33333	6.03	2.6E-02	SWISSPROT	SWISSPROT	Rattus norvegicus Nerve growth factor receptor, Iso (Ngr), mRNA
7516	20481	33942	0.95	2.6E-02/P1894	EST_HUMAN	EST_HUMAN	ALANYC-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALRS)
7850	21461	35237	0.71	2.6E-02/AA60946.1	EST_HUMAN	EST_HUMAN	062204.01 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1400719.3'
8850	21817	35237	0.71	2.6E-02/AA60946.1	EST_HUMAN	EST_HUMAN	062204.01 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1400719.3'
8715	22743	39164	1.27	2.6E-02	NT	NT	Homo sapiens KIA01070 protein (KIA01070), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10072	23999	36468	0.7	2.6E-02	AF114952.1	NT	Suchtharomyces deliensensis NRRL Y-12639(T) ATP synthase subunit 6 (ATP6) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10073	23999	36469	0.7	2.6E-02	AF114952.1	NT	Suchtharomyces deliensensis NRRL Y-12639(T) ATP synthase subunit 6 (ATP6) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10074	23999	37186	4.31	2.6E-02	AF114952.2	NT	Suchtharomyces deliensensis NRRL Y-12639(T) ATP synthase subunit 6 (ATP6) gene, mitochondrial gene encoding mitochondrial protein, complete cds
11717	24680	37186	2.02	2.6E-02	AF114952.2	NT	Suchtharomyces deliensensis NRRL Y-12639(T) ATP synthase subunit 6 (ATP6) gene, mitochondrial gene encoding mitochondrial protein, complete cds
11889	24770	38359	1.91	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
12467	25844	31313	1.98	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
533	13904	26522	1.85	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
533	13904	26523	1.85	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
670	13908	26817	8.18	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
810	13926	26884	6.9	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
2773	13795		2.28	2.6E-02	U12671.1	NT	Human sapiens chromosome 21 segment HS21C103
2598	16026	26949	3.43	2.6E-02	U12671.1	NT	Human sapiens chromosome 21 segment HS21C103
2598	16026	26950	3.43	2.6E-02	U12671.1	NT	Human sapiens chromosome 21 segment HS21C103
4075	18318	30095	1.02	2.6E-02	BE701185.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
4075	18318	30095	1.02	2.6E-02	BE701185.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
4233	17292	30148	8.32	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
7599	18991	32073	0.85	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
8317	18989		4.71	2.6E-02	BE701185.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
8334	19403	32763	4.42	2.6E-02	BE746886.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
8470	19535	32763	0.97	2.6E-02	U20026.1	NT	Human sapiens chromosome 21 segment HS21C103
7927	20970	34258	1.48	2.6E-02	BF526722.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
7927	20970	34259	1.48	2.6E-02	BF526722.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
8137	21074	34474	0.84	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
9177	22143	35970	0.82	2.6E-02	Q91713	SWISSPROT	Human sapiens chromosome 21 segment HS21C103
9315	22260	35710	0.48	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
10428	23348		0.65	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
10947	23667	37351	0.67	2.6E-02	AF114952.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C103
11881	24119	37646	2.15	2.6E-02	Q10335	SWISSPROT	Human sapiens chromosome 21 segment HS21C103
11881	24119	37647	2.15	2.6E-02	Q10335	SWISSPROT	Human sapiens chromosome 21 segment HS21C103

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
11227	24180		3.01	2.5E-02/AF50157.1	NT		Man muscular major histocompatibility locus class II region; major histocompatibility protein class II alpha chain (Majp) and major histocompatibility protein class II beta chain (Ebeta) genes, complete cds; biotinophyllin-like (NG9), biotinophyllin-like
12059	24032		1.47	2.0E-02/AB007546.1	NT		Human sapiens gene for ALE37, complete cds
12416	25896		3.35	2.9E-02	11420078	NT	Human sapiens similar to ALE37, complete cds
12508	26731		1.47	2.5E-02	11433220	NT	Human sapiens mitogen-activated protein kinase Mekk1 (meka), intron cDNA, complete cds
12696	26353		2.24	2.9E-02/U60186.1	NT		Dicycloanell discoidium pullulane protein kinase Mekk1 (meka), intron cDNA, complete cds
12709	23376	31770	3.17	2.4E-02/BE579327.1	EST_HUMAN		BT065288ER2.NT, MG2 C8 Homo sapiens cDNA, clone IMAGE335913.3
1275	32025	26203	0.98	2.4E-02/AJ378932.1	EST_HUMAN		U7207.111 Soares fetal liver spleen cDNA, clone IMAGE271149.5
1602	14634	27610	0.24	2.4E-02/HE6594.1	EST_HUMAN		H7811.11 Soares fetal liver spleen cDNA, clone IMAGE271149.5
2000	19894	28069	1.73	2.4E-02/01601	SWISSPROT		H2 CLAS3 HISTOCOMPATIBILITY ANTIGEN K3 ALPHA CHAIN PRECURSOR (H-2K3)
2000	16894	29059	1.73	2.4E-02/01601	SWISSPROT		H2 CLAS3 HISTOCOMPATIBILITY ANTIGEN K3 ALPHA CHAIN PRECURSOR (H-2K3)
4336	17424	30309	1.43	2.4E-02/J05110.1	SWISSPROT		H2 CLAS3 HISTOCOMPATIBILITY ANTIGEN, K3 ALPHA CHAIN PRECURSOR (H-2K3)
4549	17572	30461	1.43	2.4E-02/01601	SWISSPROT		H2 CLAS3 HISTOCOMPATIBILITY ANTIGEN, K3 ALPHA CHAIN PRECURSOR (H-2K3)
4549	17572	30462	1.43	2.4E-02/01601	SWISSPROT		H2 CLAS3 HISTOCOMPATIBILITY ANTIGEN, K3 ALPHA CHAIN PRECURSOR (H-2K3)
5227	18235		0.9	2.4E-02/AF1985.2	NT		Arabidopsis thaliana DNA chromosome 2, cent. fragment, NC 91
5343	19409	32650	0.97	2.4E-02/UG6860.1	EST_HUMAN		29P004.1.1 Soares fetal liver spleen cDNA, clone IMAGE271149.5
6495	19500	32811	0.95	2.4E-02/M31650.1	NT		Chicken myeloblastoid leukemia virus CR185 subgenus CR185, complete cds
6498	19600	32812	0.95	2.4E-02/M31650.1	NT		Chicken myeloblastoid leukemia virus CR185 subgenus CR185, complete cds
7431	20398	33750	1.38	2.4E-02/Z20573.1	EST_HUMAN		HSAA043X.1, Human adult B-lymphoblastoid cell line Homo sapiens cDNA
7448	20141	33797	1.05	2.4E-02/J12025.1	NT		Putative gene for uncoupling protein 1 (UCP)
7448	20141	33798	1.05	2.4E-02/J12025.1	NT		Putative gene for uncoupling protein 1 (UCP)
8159	21067	34495	0.52	2.4E-02/P48032	SWISSPROT		HEK293T.PRECURSOR (HUMORAL LECTIN)
8159	21067	34496	0.52	2.4E-02/P48032	SWISSPROT		HEK293T.PRECURSOR (HUMORAL LECTIN)
8222	21197		0.97	2.4E-02/AF163307.1	EST_HUMAN		NC3-370184-293309.4 (1905) 270.68 Homo sapiens cDNA
8275	21244		0.95	2.4E-02/AF163307.1	NT		Human melanotransferrin cDNA, 300 bp terminal repeat
8764	21761		0.53	2.4E-02/AF163307.1	EST_HUMAN		AF12205.1 Soares fetal liver spleen cDNA, clone IMAGE235578.3 similar to contains
8876	21843	35265	11.43	2.4E-02/NS98442.1	EST_HUMAN		2355911.11 Soares fetal liver spleen cDNA, clone IMAGE235578.3 similar to
9353	22303	35731	0.48	2.4E-02/A5001196.1	NT		gB(G2069P)ATSTRK Rat (RNA) contains A3R, A31 ASR, repetitive element
9363	22303	35731	0.48	2.4E-02/A5001196.1	NT		Borrelia burgdorferi (section 11 of 70) of the complete genome
9363	22303	35731	0.48	2.4E-02/A5001196.1	NT		2497 c008.11 Soares, Islets, NHT Homo sapiens cDNA, clone IMAGE744354.3 similar to gb:J04422 (SLT
9363	22303	35731	0.48	2.4E-02/A5001196.1	NT		ATM10 POLYPEPTIDE PRECURSOR (HUMAN); contains A10 repetitive element; contains XTR
9363	22303	35731	0.48	2.4E-02/A5001196.1	NT		ATM10 POLYPEPTIDE PRECURSOR (HUMAN); contains A10 repetitive element; contains XTR

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe Seq ID No.	Exon Seq ID No.	ORF SEQ ID No.	Expression Signal	Most Similar (Top) Ht BLAST E Value	Top Ht Accession No.	Top Ht Database Source	Top Ht Descriptor
10950	22977	39443	0.48	2.4E-02	AF124100.1	NT	Arabidopsis thaliana methylglutaryl synthase sulphydrylase (cys) gene, complete cds
10950	22977	39444	0.48	2.4E-02	AF124100.1	NT	Arabidopsis thaliana methylglutaryl synthase sulphydrylase (cys) gene, complete cds
10163	23090	36586	2.57	2.4E-02	AF582354.1	EST_HUMAN	AV928575 GK Homo sapiens cDNA clone GDC05C03.5'
10340	23284	39743	2.76	2.4E-02	AA403894.1	EST_HUMAN	FM767124.1 NC1 CGAP Thyl Homo sapiens cDNA clone IMAGE433583 similar to contains Alu repetitive element contains element TTTTb repetitive element
10376	23893		1.35	2.4E-02	BE237111.1	EST_HUMAN	U7274827.1 NH MGCC 20 Homo sapiens cDNA clone IMAGE3975002.5'
11900	24781	38308	1.81	2.4E-02	AF109005.1	NT	Mus musculus major histocompatibility locus class III regions H-2I genes, partial cds, smRNP, G7A, NG22, Mus homolog, QLOP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
11900	24781	38309	1.81	2.4E-02	AF109005.1	NT	Mus musculus major histocompatibility locus class III regions H-2I genes, partial cds, smRNP, G7A, NG22, Mus homolog, QLOP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
12260	25750		2.30	2.4E-02	0627609	NT	Mus musculus QLOP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
12283	25752	31655	1.7	2.4E-02	6733536	NT	Bacteriophage phiE7 complete genome
12418	25188	31623	3.48	2.4E-02	BE328699.1	EST_HUMAN	Mus musculus DnB1 homolog (E. coli) (DnB1) mRNA
12474	25222	31791	1.59	2.4E-02	U78197.1	NT	MRQ-T01715-310800-202-460 F01715 Homo sapiens cDNA
12474	25222	31853	1.59	2.4E-02	U78197.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor (GAMP-GEF1) mRNA, complete cds
12643	26327		7.68	2.4E-02	AB006999.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor (GAMP-GEF1) mRNA, complete cds
1889	14878		5.25	2.3E-02	W03350.1	EST_HUMAN	Carcinohedilia elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
1904	14878		8.44	2.3E-02	U6195.1	NT	285gD8.71 Sores
2359	15398	26338	3.16	2.3E-02	U74265.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
3894	17207	26950	0.5	2.3E-02	U74265.1	EST_HUMAN	3 chromosome chromosome IV reading frame ORF YOL245c
4178	17207	30093	0.5	2.3E-02	U74265.1	EST_HUMAN	HSAACGADH P: Human foetal Brain Whole tissue Homo sapiens cDNA
4178	17207	30094	0.8	2.3E-02	U74265.1	NT	Galus gallus contracta 45.8 (G45.8) gene, complete cds
4450	17478	30344	1.32	2.3E-02	AW091072.1	EST_HUMAN	Galus gallus contracta 45.8 (G45.8) gene, complete cds
4477	17503	30348	0.78	2.3E-02	BE639225.1	EST_HUMAN	Galus gallus contracta 45.8 (G45.8) gene, complete cds
4477	17503	30348	0.78	2.3E-02	BE639225.1	EST_HUMAN	Galus gallus contracta 45.8 (G45.8) gene, complete cds
4478	18317	30390	1.23	2.3E-02	AW091072.1	EST_HUMAN	Galus gallus contracta 45.8 (G45.8) gene, complete cds
4478	18317	30391	1.23	2.3E-02	AW091072.1	EST_HUMAN	Galus gallus contracta 45.8 (G45.8) gene, complete cds
4525	17646	30354	2.80	2.3E-02	BF026487.1	EST_HUMAN	Galus gallus contracta 45.8 (G45.8) gene, complete cds
4525	17646	30355	2.89	2.3E-02	BF026487.1	EST_HUMAN	Galus gallus contracta 45.8 (G45.8) gene, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probes	Exon Seq ID	ORF Seq ID NO:	Expression Signal	Most Similar (Ttp)Hit Value	Top Hit Assertion No.	Top Hit Descriptor
5203	18272	31069	1.19	2.3E-02 AF32710.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5203	18272	31087	1.19	2.3E-02 AF32710.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5449	19551	31463	3.35	2.3E-02 AF08303.1	EST_HUMAN	Guanosine crescentia topoisomerase IV PaeV subunit (PaeE) gene, complete cds, and prolinyl-CoA synthetase beta chain (psd3) homolog gene, partial cds
6393	19432	32675	0.35	2.3E-02 BF09646.1	EST_HUMAN	6012622 rat chn. (psd3) homolog gene, partial cds
7172	19403	33172	0.34	2.3E-02 AB141475.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment NC_17
7653	20558	34010	0.52	2.3E-02 AF18303.2	NT	MURC-H00960-01009-002-259 HT0090 Homo sapiens cDNA
8208	20558	34659	5.95	2.3E-02 AF08303.1	NT	Homo sapiens chromosome 21 segment HS21C103
8115	21152	35207	0.87	2.3E-02 AF028105.1	NT	Human placenta (HPL) gene, exons 5-32, and complete cds
8115	21152	35208	0.87	2.3E-02 AF028105.1	NT	Homo sapiens PDZK1 gene for bicyclic-containing component X, exons 1-11
9044	22010	35431	0.74	2.3E-02 AG85360.1	EST_HUMAN	wf7610.1 rat Source NH ₂ -TGCG 51 Homo sapiens cDNA clone IMAGE:235249.5
9044	22010	35432	0.74	2.3E-02 AG85360.1	EST_HUMAN	wf7610.1 rat Source NH ₂ -TGCG 51 Homo sapiens cDNA clone IMAGE:235249.5
9463	22143	35957	0.89	2.3E-02 AF1668	SWISSPROT	HYPOPHYSALIN 98.8 KD PROTEIN B2383 IN CHROMOSOME III PRECURSOR
10218	22143	36932	1.47	2.3E-02 F05632	SWISSPROT	CHROMOSOMAL ASSEMBLY PROTEIN ALX400 OF THE COMPLETE GENOME
10390	23312	36761	1.47	2.3E-02 AE00169.1	NT	Ectothioric acid L-17-MG165 section 18 of 400 of the complete genome
10390	23312	36762	1.47	2.3E-02 AE00169.1	NT	Ectothioric acid L-17-MG165 section 18 of 400 of the complete genome
11135	24095	37624	1.71	2.3E-02 F06840	SWISSPROT	GLUCANASE (NODKASAP)
12328	25392	37755	1.79	2.3E-02 BF07833.1	EST_HUMAN	601709369.HIT NIH_VGCC_71 Homo sapiens cDNA clone IMAGE:334939.5
12742	25392	37755	1.79	2.3E-02 BF07833.1	EST_HUMAN	60234362BF.NCI_GCAP_Bm67 Homo sapiens cDNA clone IMAGE:181454.5
12742	25392	37756	1.5	2.3E-02 BF07833.1	EST_HUMAN	60234362BF.NCI_GCAP_Bm67 Homo sapiens cDNA clone IMAGE:181454.5
12843	25453	37724	2.32	2.3E-02 U03394.1	NT	Supernatant ex alpha-1,3/4-Luciferase precursor gene, complete cds
12857	26993	37724	2.48	2.3E-02 U01071.1	NT	Dicyclohexyl succinylsuccinate-lygyl-regulated protein kinase (ERK1) mRNA, complete cds
13100	26933	37724	1.32	2.3E-02	NT	Homo sapiens discoid large ring (Discaliprin) like 1 (DLRL1), mRNA
730	18300	26738	1.62	2.2E-02 AF018207.1	NT	Columbia live nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1752	14751	26738	1.59	2.2E-02 AF018207.1	NT	Columbia live nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
2031	14751	26605	1.68	2.2E-02 Z62001.1	NT	S praemuricae psdA gene and open reading frame
3045	16703	26605	2.18	2.2E-02 AA077765.1	EST_HUMAN	m24604.s1 NCI_GCAP_Gast Homo sapiens cDNA clone IMAGE:1094782.3
3045	16703	26605	2.18	2.2E-02 AF08304.1	NT	Infectious brain disease virus segment B strain, LA VPI gene, complete cds
3397	18981	26814	1.26	2.2E-02 AW019137.1	EST_HUMAN	PMD-3170340-175100-004-803 BT0340 Homo sapiens cDNA
3397	18981	26814	1.26	2.2E-02 Z74293.1	NT	S cerevisiae chromosome IV reading frame ORF YOL246c

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Mean Similarity (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5105	16115	30988	1.17	2.2E-02	Z73897.1	NT	S cerevisiae chromosome XII reading frame ORF YPL241c
7498	20423	33780	3.37	2.2E-02	A766972.1	EST_HUMAN	A7669721 GRB Homo sapiens cDNA clone GIGAND03.3
8714	21882	33708	2.28	2.2E-02	AL161616.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8714	21882	33710	2.28	2.2E-02	AL161616.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9101	22127	33560	0.77	2.2E-02	Z79408.1	NT	P. vulgaris alpha tub 2 mRNA
10045	22072	36438	2.26	2.2E-02	A826888.1	NT	Homo sapiens DNA, DLEC1 to ORCLT4 gene region, section 1/2 (DLEC1, ORCLT3, ORCLT4 genes, complete cds)
10045	22072	36439	2.26	2.2E-02	A826888.1	NT	Homo sapiens DNA, DLEC1 to ORCLT4 gene region, section 1/2 (DLEC1, ORCLT3, ORCLT4 genes, complete cds)
10595	22487	36791	0.91	2.2E-02	U679140.1	NT	Human alpha 2(I) globulin gene, 5' flanking region and partial cds
11540	24481	36033	1.8	2.2E-02	BE276931.1	EST_HUMAN	601630308F12P10C17 Homo sapiens cDNA clone IMAGE:5068571.6
12802	23304		5.72	2.2E-02	A458353.1	EST_HUMAN	nc037497 at NC_037497.1 Homo sapiens cDNA clone IMAGE:500541.9 similar to contains Alu repetitive element
419	13462		5.37	2.1E-02	A7761192.1	EST_HUMAN	AV761802.M05 Homo sapiens cDNA clone M55A00691.6
449	13522		6.77	2.1E-02	U7020726.1	NT	Dipodomys deserti histidine kinase G (dHKG) mRNA, complete cds
1206	14305	27294	8.3	2.1E-02	U72073.1	NT	Bacillus subtilis cofilin cluster, Cofilin (cofilin), and apore coat protein Cofilin (cofilin) genes, complete cds
1387	14420	27298	0.99	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1387	14420	27299	0.99	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1707	14628	27611	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1707	14628	27612	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1707	14628	27613	1.26	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1960	15001	28004	1.07	2.1E-02	AF196989.1	NT	Tegula euredinella major ectodermal protein precursor (TMAP) mRNA, complete cds
2630	15068	28080	0.9	2.1E-02	BE072546.1	EST_HUMAN	PW2-810546-120100-001-411 B10546 Homo sapiens cDNA
2630	15068	28080	0.9	2.1E-02	BE072546.1	EST_HUMAN	PW2-810546-120100-001-411 B10546 Homo sapiens cDNA
2630	15068	28080	0.9	2.1E-02	BE072546.1	EST_HUMAN	PW2-810546-120100-001-411 B10546 Homo sapiens cDNA
2827	15068	28080	1.02	2.1E-02	AA225985.1	EST_HUMAN	nc037497 at NC_037497.1 Homo sapiens cDNA clone IMAGE:264841.6
3194	15068	28080	4.46	2.1E-02	BE072546.1	EST_HUMAN	PW2-810546-120100-001-411 B10546 Homo sapiens cDNA
3194	15068	28080	4.46	2.1E-02	BE072546.1	EST_HUMAN	PW2-810546-120100-001-411 B10546 Homo sapiens cDNA
3897	18842	28561	0.88	2.1E-02	BE072546.1	EST_HUMAN	PW2-810546-120100-001-411 B10546 Homo sapiens cDNA
4028	17068	28567	0.97	2.1E-02	BE072546.1	EST_HUMAN	PW2-810546-120100-001-411 B10546 Homo sapiens cDNA
4157	17186	30076	0.84	2.1E-02	Z12493.1	NT	S. cerevisiae histone H3C2, 17 Homo sapiens cDNA clone IMAGE:489407.6
4339	17986	30249	1.15	2.1E-02	BF340685.1	EST_HUMAN	602015030F12P10C17 Homo sapiens cDNA clone IMAGE:489407.6
4473	17469	30394	2.15	2.1E-02	U44914.1	NT	Bacillus burgdorferi pssm02 cys2-2, cys2-3, cys2-4 and cys2-5 genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4483	17558	36397	1.13	2.1E-02	AF06127.1	EST_HUMAN	hg61671.1f1 Scaevola_NSF_5B_SW_OT_PA_2_S1 Homo sapiens cDNA clone IMAGE:237169.3
4739	17750	36554	5.69	2.1E-02	Y05501.1	NT	A. thaliana mitochondrial genome, part A
4761	17781	36577	1.5	2.1E-02	AA66573.1	EST_HUMAN	445397.121 Gelsolin_Homo sapiens cDNA clone IMAGE:1176518.3
5265	18264	37133	1.07	2.1E-02	BF026405.1	EST_HUMAN	60167.111 UGC_7810_Homo sapiens cDNA clone IMAGE:39544.0.5
5723	18817	37698	0.76	2.1E-02	AY379529.1	EST_HUMAN	Chk1_H12.111119500.055 H19241 Homo sapiens cDNA
7289	20003	33303	0.65	2.1E-02	BF095196.1	EST_HUMAN	Q15-G00698-123000-339-413 GN0058 Homo sapiens cDNA
6864	21831	35294	0.56	2.1E-02	979229.1	NT	Wt3-300000 scd3f1 (Scd3) mRNA
9851	22797	36290	0.51	2.1E-02	AA084388.1	EST_HUMAN	smf8407.1 Stragena schizo brain S11 Homo sapiens cDNA clone IMAGE:1520732.3 similar to contains
9860	22810	36381	0.63	2.1E-02	AA084388.1	EST_HUMAN	Alu repetitive element contains element MER11 repetitive element;
9860	22810	36382	2.53	2.1E-02	AA084388.1	NT	Homo sapiens paraf 5-H1 receptor gene, exons 2 to 5
9860	22810	36382	2.53	2.1E-02	AA084388.1	NT	Homo sapiens paraf 5-H1 receptor gene, exons 2 to 5
10343	23367	36746	1.13	2.1E-02	26324.1	NT	Streptococcus pneumoniae HlgA, exocellinase, repressor protein, relaxase, UmuC MucB homolog, and
10421	23343	36829	0.68	2.1E-02	AA094288.1	EST_HUMAN	UmuC MucA homolog genes, complete cds; and unknown genes
12884	18345	37617	8.95	2.1E-02	Y19213.1	NT	smf8407.1 Stragena schizo brain S11 Homo sapiens cDNA clone IMAGE:1520732.3 similar to contains
12824	25736	31617	1.4	2.1E-02	L34170.1	NT	Alu repetitive element contains element MER11 repetitive element;
13003	25957	31693	3.5	2.1E-02	AF183913.1	NT	Homo sapiens putative parafinB, pseudogene for half keratin, exons 2 to 7
19	13139	26037	1.39	2.0E-02	BF008352.1	EST_HUMAN	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
20	13140	26038	10.76	2.0E-02	AF183913.1	EST_HUMAN	Asp1000.1 Brazilian major outer membrane protein OmpK precursor (ompA) gene, complete cds
269	13356	26280	3.29	2.0E-02	AF183913.1	EST_HUMAN	MER1 repetitive element;
265	13359	26317	2.85	2.0E-02	AF183913.1	EST_HUMAN	Q15-G00698-216400-37-105 NM0038 Homo sapiens cDNA
769	13568	28905	1.27	2.0E-02	979365.1	NT	Mer musculus Dms homolog (E. coli) (Dms), mRNA
1086	14133	27045	1.03	2.0E-02	AA096031.1	NT	Mer musculus Dms homolog (E. coli) (Dms), mRNA
1204	14243	27261	0.78	2.0E-02	802201.1	NT	Homo sapiens genomic region containing hypervariable minisatellite chromosome 11(p55.33) of Homo
1204	14243	27262	0.78	2.0E-02	802201.1	NT	Homo sapiens hypodermal protein FLJ10375 (FLJ10375), mRNA
1860	14019	27808	2.18	2.0E-02	802245.1	NT	Homo sapiens hypodermal protein FLJ10375 (FLJ10375), mRNA
1860	14019	27810	2.18	2.0E-02	802245.1	NT	Homo sapiens hypodermal protein FLJ10485 (FLJ10485), mRNA
2910	15955	29710	4.97	2.0E-02	AL14532.2	NT	Homo sapiens hypodermal protein FLJ10485 (FLJ10485), mRNA
3095	13139	26037	1.61	2.0E-02	BF008352.1	EST_HUMAN	Arabidopsis thaliana DNA Transomease 4, contig fragment No. 32
							765108.1 NCI CGAP P228 Homo sapiens cDNA clone IMAGE:309698.3 similar to contains MER1.13
							MER1 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top 3) Hit Vibrio	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3159	18218		1.83	2.0E-02	7095474	NT	Mus musculus alpha domain, Transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sem6B), mRNA
3241	18288		1.8	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein ZFP mRNA, complete cds
4022	17070	28971	1.4	2.0E-02	AF080581	NT	P. vulgaris hydroxyphenyl-rich glycoprotein (HRGP) mRNA, 3' end
4163	18183		1.71	2.0E-02	AF021965.1	EST_HUMAN	g950323.1 NCI_COAP_K103 Homo sapiens cDNA IMAGE1866078.3
5173	18183	31091	0.94	2.0E-02	AF116237.2	NT	Homo sapiens chromosome 21 segment HS21.0378
5718	18852	31092	0.94	2.0E-02	U34778.1	NT	Carotenoid desaturase alpha smn-2 mRNA, complete cds
6000	18905	32282	0.94	2.0E-02	AF020001.4	NT	Phycoerythrin aldehyde oxidase VII unconventional myosin (myo) gene, complete cds
7169	20751	34126	1.09	2.0E-02	AF020001.4	NT	Phycoerythrin aldehyde oxidase VII unconventional myosin (myo) gene, complete cds
7799	20751	34127	1.09	2.0E-02	AF020001.4	NT	Phycoerythrin aldehyde oxidase VII unconventional myosin (myo) gene, complete cds
10236	20161		1.59	2.0E-02	U04648.1	NT	Myosin heavy chain 13 gamma 2 gene, complete cds
10726	23048	37141	1.54	2.0E-02	AF040422.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
11005	23671	37495	1.54	2.0E-02	U04648.1	NT	Myosin heavy chain 13 gamma 2 gene, complete cds
11699	24694	38241	2.28	2.0E-02	D29818.1	NT	Myosin heavy chain 13 gamma 2 gene, complete cds
12148	18351	31296	1.93	2.0E-02	AF040556.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
12821	19002		1.99	2.0E-02	AF118152.2	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
13078	25008		3.4	2.0E-02	T60037.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
684	13798	26988	2.85	1.6E-02	AF57784.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
1163	14652	27618	1.93	1.9E-02	P14648	SWISSPROT	Myosin heavy chain 13 gamma 2 gene, complete cds
14074	15074	28033	3.04	1.9E-02	AF183033.2	NT	Myosin heavy chain 13 gamma 2 gene, complete cds
20355	15074	28033	3.04	1.9E-02	AF183033.2	NT	Myosin heavy chain 13 gamma 2 gene, complete cds
2514	15517	28540	3.04	1.9E-02	AF183033.2	NT	Myosin heavy chain 13 gamma 2 gene, complete cds
16974	18997		8.7	1.9E-02	AF183033.2	NT	Myosin heavy chain 13 gamma 2 gene, complete cds
2884	18022	28947	1.49	1.9E-02	U13955.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
3237	19327		0.72	1.9E-02	AF033851.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
3625	16668		1.36	1.9E-02	AF022201.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
3718	19761		9.23	1.9E-02	BE718068.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
3727	19769	29881	0.69	1.9E-02	AB01183.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
4077	17112	30008	1.59	1.9E-02	AF141940.1	EST_HUMAN	Myosin heavy chain 13 gamma 2 gene, complete cds
4222	17351	30137	1.62	1.9E-02	P00681	SWISSPROT	Myosin heavy chain 13 gamma 2 gene, complete cds
4222	17251	30138	1.62	1.9E-02	P00681	SWISSPROT	Myosin heavy chain 13 gamma 2 gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Description
8811	21778	35233	0.79	1.8E-02	AW905327.1	EST_HUMAN
8837	21824	35247	0.75	1.8E-02	6678949	NT
8849	22783	35235	0.5	1.8E-02	BF241924.1	EST_HUMAN
8846	22785	35239	0.5	1.8E-02	BF241924.1	EST_HUMAN
10000	23027		2.03	1.8E-02	AA697543.1	EST_HUMAN
10433	25345	36830	1.89	1.8E-02	BE76274.1	EST_HUMAN
10596	25698	37000	1.2	1.8E-02	AB5853.1	NT
11765	29030	37438	1.7	1.8E-02	AF02357.2	NT
11765	29030	37438	1.7	1.8E-02	AF02357.2	NT
11835	24818	38413	2.70	1.8E-02	AF020208.1	NT
11848	24827	38422	3.16	1.8E-02	UG2748.1	NT
13105	25926	31860	1.35	1.8E-02	R40235.1	EST_HUMAN
13105	25926	31861	1.35	1.8E-02	R40235.1	EST_HUMAN
907	13062	26918	0.8	1.7E-02	BC934903.1	EST_HUMAN
1806	14834	27823	2.15	1.7E-02	AW573183.1	EST_HUMAN
1808	14834	27824	2.15	1.7E-02	AW573183.1	EST_HUMAN
1887	14912		4.23	1.7E-02	AL193204.2	NT
2121	15138		11.19	1.7E-02	AB004916.1	NT
2301	18313	28333	1.03	1.7E-02	S74186.1	NT
2948	19545		1.18	1.7E-02	7897489	NT
3011	19089	28890	0.69	1.7E-02	AT17915.1	EST_HUMAN
3523	15869		5.82	1.7E-02	AW427368.1	EST_HUMAN
4198	17228		0.86	1.7E-02	AA698818.1	EST_HUMAN
4228	17287		2.04	1.7E-02	RO2503.1	EST_HUMAN
4462	17807	30398	0.7	1.7E-02	AB352579.1	EST_HUMAN

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4557	17800	30471	1.92	1.7E-02	AIW573183.1	EST_HUMAN	H54603.x1 Sources: N1L1_08C_S1 Homo sapiens cDNA clone IMAGE:2603740.3 similar to contains L1.1 L1 repetitive element.
4744	17784	30058	1.54	1.7E-02	AIW00441.1	NT	Messenger RNA for angiotensin (Lophius americanus) angiotensin II
4851	17868		7.05	1.7E-02	AIW01076.1	EST_HUMAN	0671622.x1 Sources: N1L1_08C_S1 Homo sapiens cDNA clone IMAGE:144955.3
5106	18116	30889	0.74	1.7E-02	6981288	NT	Retard navigation factor 1 (RNF1) mRNA
5229	18237		0.91	1.7E-02	AIJ29041.1	NT	Homo sapiens 5S1.05-15g between AML1 and CBF1 on chromosome 11q22; segment 1/3
6248	18321	32851	1.83	1.7E-02	AIJ78247.1	EST_HUMAN	W303060.x1 Sources: N1L1_08C_S1 Homo sapiens cDNA clone IMAGE:2387113.3 similar to T. alberta (ATG534821) 17kD gene for cyclo-oxygenase synthetase
6518	18678		0.94	1.7E-02	IJ28353.1	EST_HUMAN	0281533.x1 Sources: fetal liver spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:1872661.3
6731	18787	33095	1.37	1.7E-02	AIJ36263.1	EST_HUMAN	0281533.x1 Sources: fetal liver spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:1872661.3
7251	19688	33294	1.31	1.7E-02	AIJ9583.1	NT	Mouse fascicular protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7411	20378	33729	1.85	1.7E-02	6400716	NT	Homo sapiens nebulin (NEB) mRNA
7581	20543	33502	0.85	1.7E-02	AIJ7869.1	NT	Homo sapiens nebulin (NEB) mRNA
7581	20543	33502	0.85	1.7E-02	AIJ7869.1	NT	Homo sapiens nebulin (NEB) mRNA
7981	21543	34543	1.85	1.7E-02	AIJ0770.1	NT	Homo sapiens nebulin (NEB) mRNA
8016	21543	34543	1.85	1.7E-02	AIJ0770.1	NT	Homo sapiens nebulin (NEB) mRNA
8791	21741	34543	0.97	1.7E-02	IJ21854.1	NT	Homo sapiens nebulin (NEB) mRNA
10337	23834	36453	1.31	1.7E-02	AIJ04054.1	EST_HUMAN	DKFZ-341031.4, t1.434 (synonym: hms) Homo sapiens cDNA clone DKFZ-341031.4.3
12336	24656	38551	1.89	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE15) mRNA
12810	25810	31424	3.15	1.7E-02	AIW00482.1	EST_HUMAN	GM4-N11030-040400-130-06 N11030 Homo sapiens cDNA
13059	25695	31887		1.7E-02	AIJ46926.1	EST_HUMAN	0608604.x1 N1L1_08C_S1 Homo sapiens cDNA clone IMAGE:1855287 similar to contains element MSRT repetitive element
512	13583		2.22	1.6E-02	AIJ21929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 19/162
1665	14697	27673	0.91	1.6E-02	Y18886.1	NT	Treponema melophilum Me22, Me25 and Me26 genes for flagellin subunit proteins and CAP protein homologue
2572	15573	28593	0.95	1.6E-02	AIJ06345.1	NT	Homo sapiens K10CT1 gene
2851	15946	28671	1.45	1.6E-02	AIJ484972.1	EST_HUMAN	me81005.x1 N1L1_08C_S1 Homo sapiens cDNA clone IMAGE:910687
2704	15700		1.37	1.6E-02	AIJ014834.1	NT	Homo sapiens mRNA for K10A553 protein, partial cds
3537	15583	29506	4.46	1.6E-02	AIW50552.1	EST_HUMAN	IL3-17021P-162200-005-C07 C1021P Homo sapiens cDNA
4264	17235		2.14	1.6E-02	AF110230.1	NT	Mouse muscular major histocompatibility complex class II alpha chain (H2-DM) cDNA
4326	17357	30245	0.96	1.6E-02	AIW75407.1	EST_HUMAN	RFC1, Fan-binding protein, 80 kD isoform, full length, cDNA
5172	18181		0.76	1.6E-02	N607158.1	EST_HUMAN	02757032.1 40100-026107 T10121 Homo sapiens cDNA
5325	18431	31183	0.49	1.6E-02	AIJ21385.1	EST_HUMAN	245603.x1 Sources: fetal liver spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:267444.3
							04d3526.x1 N1L1_08C_S1 Homo sapiens cDNA clone IMAGE:186741.3

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6705	18800	31977	1.33	1.0E-02	6971716	NT	Mus musculus C25 antigen (C25), mRNA
6769	18803	33139	2.07	1.0E-02	AB015381.1	NT	Cardiac alpha 2B OCAO3 gene, complete cds
7117	20051	33354	0.93	1.0E-02	AB025711.1	NT	Swiss army protease CAL22 gene for cadmium resistance protein, complete cds
7177	20051	33355	0.93	1.0E-02	AB025711.1	NT	Swiss army protease CAL22 gene for cadmium resistance protein, complete cds
7078	20017	34308	1.08	1.0E-02	AL181508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8468	21427	34844	0.72	1.0E-02	AJ277662.1	NT	Human sapiens peritubular TUB gene for tubulin (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8519	21437		1.5	1.0E-02	X05151.1	NT	Human APC-1 gene for adenomatous polyposis coli
10400	23322		1.98	1.0E-02	AF076764.1	NT	Drosophila melanogaster enhancer of polycomb (E[Poly]) mRNA, complete cds
10785	23706	37206	1.2	1.0E-02	AA572818.1	EST_HUMAN	P29284 TELOKIN [H]
10785	23706	37207	1.2	1.0E-02	AA572818.1	EST_HUMAN	P19043 at NCL CGAP P-1 Homo sapiens cDNA clone IMAGE:594260 similar to SWI:TELO_RABIT
11235	25705	37750	1.83	1.0E-02	Z64828.1	NT	Gallus microsatellite DNA (LE0260) (= T18BEE11)
11547	24488	38042	1.7	1.0E-02	AL181508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11547	24488	38043	1.7	1.0E-02	AL181508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11839	24722	38307	1.96	1.0E-02	AB73558.1	EST_HUMAN	gdb10.011 Swiss army protease (E[Poly]) mRNA, complete cds
12347	18334	31172	1.39	1.0E-02	OQ4176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EC:3.1.1.1) (ESTERASE-22)
12347	18334	31173	1.39	1.0E-02	OQ4176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EC:3.1.1.1) (ESTERASE-22)
762	13813		20.73	1.0E-02	8922734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2152	13188	28184	4.44	1.0E-02	N36621.1	EST_HUMAN	y27007 at Swiss fetal liver spleen 1NF15 Homo sapiens cDNA clone IMAGE:243923 3'
2185	15200	28220	1.82	1.0E-02	AL18194.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
3074	10131	29043	2.54	1.0E-02	AJ065618.1	NT	Homo sapiens CACNA1F gene, exon 1 to 48
3074	10131	29044	2.54	1.0E-02	AJ065618.1	NT	Homo sapiens CACNA1F gene, exon 1 to 48
3737	16778	29522	1.06	1.0E-02	BF02642.1	EST_HUMAN	MRCT10115-080900-201-512 TN0116 Homo sapiens cDNA
9426	19400	32475	1.33	1.0E-02	C00771	SWISSPROT	HYPOPHOSPHATE CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
7541	20304		1.59	1.0E-02	11467262	NT	Cytophthora parvula cytochrome c, complete genome
8208	21176	33654	1.38	1.0E-02	AL181979.1	NT	Homo sapiens KIAA1005 protein (KIAA1005), mRNA
8213	21176	33655	1.5	1.0E-02	AL181979.1	NT	Homo sapiens KIAA1005 protein (KIAA1005), mRNA
9152	22146	35575	0.62	1.0E-02	BF345584.1	EST_HUMAN	gdb10.011 Swiss army protease (E[Poly]) mRNA, complete cds
9826	22072	35575	0.62	1.0E-02	BF345584.1	EST_HUMAN	gdb10.011 Swiss army protease (E[Poly]) mRNA, complete cds
9826	22072	35575	0.62	1.0E-02	BF345584.1	EST_HUMAN	gdb10.011 Swiss army protease (E[Poly]) mRNA, complete cds
9826	22072	35575	0.62	1.0E-02	BF345584.1	EST_HUMAN	gdb10.011 Swiss army protease (E[Poly]) mRNA, complete cds
9826	22072	35575	0.62	1.0E-02	BF345584.1	EST_HUMAN	gdb10.011 Swiss army protease (E[Poly]) mRNA, complete cds
10170	20095	36574	0.93	1.0E-02	B23667.1	EST_HUMAN	gdb10.011 Swiss army protease (E[Poly]) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit E-VALUE	Top Hit Accession No.	Top Hit Source	Top Hit Description
10170	23095	35575	0.95	1.5E-02	R32697.1	EST_HUMAN	h54510-7: 5' ends placenta h54510 Homo sapiens cDNA clone IMAGE:133531 5'
11903	24478	37997	2.75	1.5E-02	LA0956.1	NT	Plasmodium falciparum (disea. FC83) viridic-specific surface protein (var-2, var-3) genes, complete cds
11537	24478	38028	2.52	1.5E-02	AL11239.1	NT	Scytosin synthase 1 cDNA library under conditions of nitrogen deprivation
12994	25783		2.04	1.5E-02	AW750834.1	EST_HUMAN	RC4-CHN063-40100-01-1 c11 CN049 Homo sapiens cDNA
13078	26610		1.3	1.5E-02	AT76127.1	EST_HUMAN	w681603.1 NC1_CGAP_23.1 Homo sapiens cDNA clone IMAGE:2894693 3' similar to contains Alu
1120	14360	27115	5.44	1.4E-02	AE02253.2	NT	Human osteocalcin cDNA, complete cds
1281	14296		1.74	1.4E-02	U32800.1	NT	Human osteocalcin cDNA, complete cds
1301	14337		3.4	1.4E-02	U97179	NT	Human osteocalcin cDNA, complete cds
1320	14552		1.03	1.4E-02	AV725785.1	EST_HUMAN	Xenopus laevis neurokinin related 1b (XNGNR-1b) mRNA, complete cds
							AV725785 HTB Homo sapiens cDNA clone HTBAH111 5'
3226	16291	29204	2.04	1.4E-02	AF169899.2	NT	Bifidobacterium longum Na/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (agl-1) genes, complete cds; and Nucleoside/glucosamine/xylem repressor protein (nagOxR) gene, partial cds
3139	16489	29280	0.98	1.4E-02	AW074212.1	EST_HUMAN	3X09065.X1 NC1_CGAP_201 Homo sapiens cDNA clone IMAGE:2575763 3'
3109	16543	29437	6.29	1.4E-02	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3109	16543	29458	6.29	1.4E-02	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3109	16543	29458	6.29	1.4E-02	6999918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4510	17641	30427	6.1	1.4E-02	AW92288.1	EST_HUMAN	EST374761 IMAGE resequencer, MAGG Homo sapiens cDNA
4510	17641	30428	6.1	1.4E-02	AW92288.1	EST_HUMAN	EST374761 IMAGE resequencer, MAGG Homo sapiens cDNA
4911	17928	30818	8.08	1.4E-02	BE73142.1	EST_HUMAN	60159743F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4911	17928	30819	8.08	1.4E-02	BE73142.1	EST_HUMAN	60159743F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5130	18139	31017	1.01	1.4E-02	AW946453.1	EST_HUMAN	ON0-FR0041-120600-370-H09 FN0041 Homo sapiens cDNA
5988	23892		0.95	1.4E-02	XG1338.1	NT	Human osteocalcin cDNA, complete cds
							h111041-1 NC1_CGAP_312 Homo sapiens cDNA clone IMAGE:1028960 3' similar to contains Alu repetitive element
6555	19915	32380	4.9	1.4E-02	AA599030.1	EST_HUMAN	h111041-1 NC1_CGAP_312 Homo sapiens cDNA clone IMAGE:1028960 3' similar to contains Alu repetitive element
6555	19915	32381	4.9	1.4E-02	AA599030.1	EST_HUMAN	h111041-1 NC1_CGAP_312 Homo sapiens cDNA clone IMAGE:1028960 3' similar to contains Alu repetitive element
8478	21447		1.61	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 88/102
9249	22215	35648	0.77	1.4E-02	AB1702.1	NT	Candida bodini menadone oxidase (CDO1) gene, complete cds
9510	22473	35917	0.9	1.4E-02	AJ272968.1	NT	Homo sapiens PZ2 gene, transcript precursor, across 1-3
9735	22696	39153	2.15	1.4E-02	BE44491.1	EST_HUMAN	91018238F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:346241 5'
10243	23843		0.88	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21, segment 11S11C1018

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Probe SEQ ID NC	Exon SEQ ID NC	ORF SEQ IDNC	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12854	26980	38172	2.14	1.4E-02	AF24945.1	NT	Human FNAR1 gene for fibroblast alpha2beta1 receptor
12816	26312		1.47	1.4E-02	AF24985.1	NT	Arabidopsis thaliana F21U9.2 mRNA, complete cds
12853	26312		1.86	1.4E-02	U142698	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1972	14655	27604	2.05	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment H5210001
3227	19325	26205	2.31	1.3E-02	U07081.1	EST_HUMAN	90212875F11NH_MGC_36 Homo sapiens cDNA clone IMAGE:4285203 5'
3227	19325	26205	2.31	1.3E-02	U07081.1	EST_HUMAN	90212875F11NH_MGC_36 Homo sapiens cDNA clone IMAGE:4285203 5'
3953	17033		1.38	1.3E-02	AF16928.1	NT	Mus musculus beta-actin gene, complete cds
4664	17879	30859	1.06	1.3E-02	U6901.1	NT	Human germline T-cell receptor beta chain TCRBV7S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV26S1P, TCRBV15P1, TCRBV15S1, TCRBV10S1A1T, HVB reic, TCRBV28S1P, TCRBV34S1, TCRBV4S1, TCRBV5S1, TCRBV4S1A1T, TRV4, TRV5, TRV6, TRV7, TRV8, TCRBV1, TCRBV181, TCRBV162, >
5317	18423	31225	1.79	1.3E-02	AL049866.2	NT	Mus musculus p2 transmembrane X-connexin; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, transmembrane
5317	18423	31226	1.79	1.3E-02	AL049866.2	NT	Mus musculus p2 transmembrane X-connexin; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, transmembrane
6284	19360	32597	1.21	1.3E-02	U60017.1	NT	Homo sapiens basic transcription factor 2.64 (bTF2.4) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
6322	19393	32634	0.7	1.3E-02	U62902.1	NT	C. reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7154	18366	31228	1.25	1.3E-02	AL191546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7154	18366	31228	1.25	1.3E-02	AL191546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7829	20777	34155	4.86	1.3E-02	AA031563.1	EST_HUMAN	0W0505.x1 Soares_papillary_thyroid_tumor_NaHPA Homo sapiens cDNA clone IMAGE:1946072 3' similar to contains Alu repetitive element;
8520	21760	35216	1.48	1.3E-02	AF15989.1	NT	Homo sapiens human endogenous retrovirus W gag/33.37 G gag (gag) gene, complete cds
10367	23486	35981	2.18	1.3E-02	U63707.1	NT	Mouse kidney androgen-regulated protein (KARP) gene, complete cds
10541	23563	37059	0.63	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10663	23508	37421	0.44	1.3E-02	AA070741.1	EST_HUMAN	3724067.st Soares_pituitary_gland_NaHPG Homo sapiens cDNA clone IMAGE:412980 3'
11335	24286	37809	3.74	1.3E-02	AW266653.1	EST_HUMAN	X034403.x1 Soares_NFL_T_GBC_51 Homo sapiens cDNA clone IMAGE:2815938 3'
11335	24286	37810	3.74	1.3E-02	AW266653.1	EST_HUMAN	X034403.x1 Soares_NFL_T_GBC_51 Homo sapiens cDNA clone IMAGE:2815938 3'
12222	25253		1.4	1.3E-02	U289171.1	NT	Bacillus subtilis complete genome (section 14 of 21); from 2566451 to 2812870
12222	25253		2.51	1.3E-02	U633069	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
12665	25718		16.88	1.3E-02	AF152298.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
214	13314		0.87	1.2E-02	X87344.1	NT	Homo sapiens DNA, HLA-A21, IP22, LMP2, LMP7, TAP2, DOB, DOB2 and RING8, 6, 13 and 14 genes

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Single Exon Probes Expressed in Bone Marrow

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Table 4

Single Exon Probe Expressed in Bone Marrow

Probe Seq ID Seq ID NO.	Exon Seq ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (To) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6907	29234	36389	2.93	1.2E-02	AB31013.1	NT	Novel-like virus group 2 genes for capsid protein, complete cds
10300	22551	37423	1.26	1.2E-02	AL24003.1	NT	Homo sapiens Spast gene for spastin protein
13030	26116	31841	2.74	1.2E-02	AF16334	SWISSPROT	PERC10 CARDIAC PROTEIN 1 (CARDIAC PACEMAKER PROTEIN RIGU) (PERP)
13039	26493	32433	3.91	1.2E-02	C81818.1	EST_HUMAN	C78110 Human placenta cDNA (T7-14w) Homo sapiens cDNA clone GEN-397068 5'
13274	14399	27270	1.16	1.1E-02	AF070364.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
1719	14749	27743	1.8	1.1E-02	AF070364.1	NT	H-sapiens 1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
1719	14749	27743	1.8	1.1E-02	AF070364.1	NT	H-sapiens 1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
2054	15073	28052	4.98	1.1E-02	BF45363.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
2859	15648		3.91	1.1E-02	BN9623.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
3355	16581	29505	2.75	1.1E-02	AI65330.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
4051	17098		1.52	1.1E-02	BE144837.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
4133	17165		0.71	1.1E-02	AW813788.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
4897	17884	30772	2.22	1.1E-02	AL048832.2	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
6272	18345	32578	1.02	1.1E-02	U69486.1	NT	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
7635	20800	34176	2.47	1.1E-02	BE144837.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
8105	21042	34441	3.79	1.1E-02	8693294	NT	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
8887	21953	35377	0.7	1.1E-02	AW66160.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
9174	22140	35566	0.66	1.1E-02	CO4803.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
9283	22219	35650	7.21	1.1E-02	Q61842	SWISSPROT	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
10289	23214	36699	2.1	1.1E-02	AA832778.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
10454	23376	36869	3.79	1.1E-02	AA314955.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
11324	24374	37802	2.01	1.1E-02	11433503	NT	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
12184	26039		3.52	1.1E-02	AA688239.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
12960	17165		1.67	1.1E-02	AW813788.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
7	19127	26027	6.08	1.0E-02	AW64120.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
1528	14859	27530	1.07	1.0E-02	AW398128.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
2578	19579		1.28	1.0E-02	AA688239.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
3108	19163	28675	2.7	1.0E-02	BE833561.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'
3276	16330	29251	1.33	1.0E-02	BE988961.1	EST_HUMAN	hndes1.1 rat Stragene neuroepithelium (857283) Homo sapiens cDNA clone IMAGE:536624 3'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST H Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5061	18071	30981	1.01	9.0E-03	U70444.1	EST_HUMAN	pcr7508 at Stratiomys lung (8637210) Homo sapiens cDNA clone IMAGE:80919.3
5260	13258	31136	0.95	9.0E-03	575322.1	NT	hna muscular contractin-releasing hormone receptor 2 (CHR2), mRNA
5608	18034		1.2	9.0E-03	U89762.1	EST_HUMAN	hwt7043 at Source, NPL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2361831.3
6785	18640		0.81	9.0E-03	BE74958.1	EST_HUMAN	90197439 at NIH, YGC, 9 Homo sapiens cDNA clone IMAGE:3834792.5
7694	20590	34020	0.81	9.0E-03	AL425718	EST_HUMAN	g80512 at Source, NPL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:1863974.3
7712	20598	34035	0.81	9.0E-03	8622970.1	EST_HUMAN	hna muscle hypodermis protein FLJ10660 (FLJ10660), mRNA
8207	21177		0.99	9.0E-03	AL036291.1	EST_HUMAN	DKE72943 at U2, T, 431 (procyon, hna) Homo sapiens cDNA clone DKFZ34340412.5
8592	21500		0.55	9.0E-03	AF22309.1	NT	hna spleen calcium channel alpha 1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10221	23148	36035	1.42	9.0E-03	AP22309.1	NT	COLLAGEN ALPHA 1(V) OHAN PRECURSOR
11331	24281		1.6	9.0E-03	U9800.1	NT	Homo sapiens NF2 gene
12090	25695		2.12	9.0E-03	BE34638.1	EST_HUMAN	hwt7050 at NCI, GARP, L24 Homo sapiens cDNA clone IMAGE:3183181.3
12099	25549		15.47	9.0E-03	BF351141.1	EST_HUMAN	PM1410452.297265.091.409 HT0452 Homo sapiens cDNA
502	13574		3.01	8.0E-03	AA723007.1	EST_HUMAN	239403 at Source, gna, gna, HT0645 Homo sapiens cDNA
991	14043	29977	18.52	8.0E-03	AF106956.1	NT	Alu repetitive element
2105	15182	29202	1.96	8.0E-03	AF106956.1	NT	Homo sapiens adenovirus-like virus gene, complete cds
3321	18372	29203	1.12	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120203-011-349 HT0545 Homo sapiens cDNA
3370	16420	29445	0.93	8.0E-03	AF131016.1	NT	Homo sapiens SCL gene locus
3989	16732	29645	1.25	8.0E-03	P32844	SWISSPROT	HYPOPHOSPHATE 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3989	16732	29645	1.25	8.0E-03	P32844	SWISSPROT	HYPOPHOSPHATE 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4285	17514	30193	1.08	8.0E-03	BE640046.1	EST_HUMAN	GVO-FN0181-140700-304-10 FN0181 Homo sapiens cDNA
4410	17438	30226	5.3	8.0E-03	BF93327.1	EST_HUMAN	QMA-FN0119-300900-223-505 FN0119 Homo sapiens cDNA
4747	17767	30662	0.95	8.0E-03	PQ181	SWISSPROT	HYPOPHOSPHATE 127.0 KD PROTEIN
4747	17767	30663	0.95	8.0E-03	PQ181	SWISSPROT	HYPOPHOSPHATE 127.0 KD PROTEIN
5901	18967	31668	2.88	8.0E-03	AF10320.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28 (K1C1), Fes-binding protein, BING1, Ixasin, R4GDS-like, KE2, BING4, beta 1-3-galactosyl transferase, and RPS18 genes, complete cds, Sam21 gene, paralog
6323	20588	32535	1.39	8.0E-03	AP000002.1	NT	PROBABLY PEPTIDASE YVNA
6933	19665	33261	4.24	8.0E-03	P55577	SWISSPROT	Procyon carolinensis OT3 genomic DNA, 287001-344000 nt, position (27)
7104	20338		1.4	8.0E-03	P70109.1	NT	Human BK virus (HBMV) genome. (Closely related to SV40.)
7415	20352	33735	1.88	8.0E-03	MT1797.1	NT	A California (marine gastropod mollusk) neuropeptide gene (tag cel)
7760	20745		1.81	8.0E-03	AF036297.1	NT	Turpota truncatus mRNA for p10-phox, complete cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Source	Top Hit Descriptor
9235	22201	35631	0.95	9.0E-03	P08160	SWISSPROT	BASEMENT MEMBRANE SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9287	22227	35657	3.77	9.0E-03	AW806992.1	EST HUMAN	PRECURSOR (PSPC) (PSPC) (PSC) (PSC)
9270	22236	35665	0.52	9.0E-03	AL139073.2	NT	MR-571111-11 (MR-571111) Homo sapiens cDNA
9631	22265	35726	0.98	9.0E-03	9798966	NT	MR-571111-11 (MR-571111) Homo sapiens cDNA
10008	23232		5.16	9.0E-03	BE065599.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
11118	24078	37602	1.90	9.0E-03	BE178441.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
11330	24280		2.93	9.0E-03	Z44652.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
11940	24983	38196	2.50	9.0E-03	AF303327.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
11710	24973	38253	1.55	9.0E-03	AF438817.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
11710	24973	38253	1.55	9.0E-03	AF438817.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
12024	24903	38493	3.14	9.0E-03	AF045363.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
12203	25047		2.94	9.0E-03	M69035.1	NT	MR-571111-11 (MR-571111) Homo sapiens cDNA
12246	26077		2.6	9.0E-03	AB03191.1	NT	MR-571111-11 (MR-571111) Homo sapiens cDNA
9015	13757	29687	18.14	7.0E-03	AF097183.1	NT	MR-571111-11 (MR-571111) Homo sapiens cDNA
9015	13757	29688	18.14	7.0E-03	AF097183.1	NT	MR-571111-11 (MR-571111) Homo sapiens cDNA
978	14026	29683	4.68	7.0E-03	AF243376.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
1118	14162	27113	4.38	7.0E-03	AF731712.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
1396	14402		1.16	7.0E-03	Q81060	SWISSPROT	MR-571111-11 (MR-571111) Homo sapiens cDNA
1306	14430	27390	3.03	7.0E-03	AF688298.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
1502	14435	27390	3.04	7.0E-03	AF030596.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
1756	14765	27760	1.03	7.0E-03	AF650556.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
1756	14765	27770	1.03	7.0E-03	AF650556.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
2267	15889	28307	2.08	7.0E-03	P04629	SWISSPROT	MR-571111-11 (MR-571111) Homo sapiens cDNA
3571	16915	26337	0.57	7.0E-03	AF19273.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
3778	19820	26728	0.93	7.0E-03	AF444483.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
3825	19865	26769	1.45	7.0E-03	AF169344.1	NT	MR-571111-11 (MR-571111) Homo sapiens cDNA
4048	19820	26769	0.83	7.0E-03	AF444483.1	EST HUMAN	MR-571111-11 (MR-571111) Homo sapiens cDNA
4396	17393		0.69	7.0E-03	U06088.1	NT	MR-571111-11 (MR-571111) Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Probe Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4995	17938		1	7.0E-03	AW11771.1	EST HUMAN	3x3402.xt NCL_GCAP.U1 Homo sapiens cDNA clone IMAGE:260603 3' similar to TR-Q12867 Q12867
4629	17938		1.47	7.0E-03	AW18088.1	EST HUMAN	ACIDIC 82 KOA PROTEIN ;
5024	16038		1.81	7.0E-03	AL16378.2	NT	hNB603.yf NCL_GCAP_GUT1 Homo sapiens cDNA clone IMAGE:260603 5'
3228	16234	31108	1.4	7.0E-03	AV72419.1	EST HUMAN	Homo sapiens chromosome 21 segment HS210278
3228	16234	31108	1.4	7.0E-03	AV72419.1	EST HUMAN	AV72419 HTB Homo sapiens cDNA clone HTBCE08 5'
5918	19004		0.93	7.0E-03	HT108.1	EST HUMAN	AV72419 HTB Homo sapiens cDNA clone HTBCE08 5'
8233	28658		5.11	7.0E-03	AV181039.1	EST HUMAN	y8260.1.1 Soares fetal liver spleen NFI.S Homo sapiens cDNA clone IMAGE:211824 5' similar to
8447	10912	37163	1.38	7.0E-03	W6255.1	EST HUMAN	35x14728 CLUSTERIN PRECURSOR (HUMAN);
8537	10914	33016	3.18	7.0E-03	PA227126.1	EST HUMAN	RC1-C10286-050400-018-208 C10288 Homo sapiens cDNA
8717	18773	33052	0.91	7.0E-03	BE587985.1	EST HUMAN	233910.1 Soares fetal liver NFI.S Homo sapiens cDNA clone IMAGE:242475 5'
7284	20081	33567	1.92	7.0E-03	BE58133.1	EST HUMAN	RC1-C10286-050400-018-208 C10288 Homo sapiens cDNA
7783	20718	34068	5.31	7.0E-03	254938.1	EST HUMAN	RC1-C10286-050400-018-208 C10288 Homo sapiens cDNA
7783	20718	34068	5.31	7.0E-03	254938.1	NT	RC1-C10286-050400-018-208 C10288 Homo sapiens cDNA
8160	21150	34557	0.45	7.0E-03	AL22543.1	NT	RC1-C10286-050400-018-208 C10288 Homo sapiens cDNA
8160	21150	34558	0.45	7.0E-03	AL22543.1	NT	RC1-C10286-050400-018-208 C10288 Homo sapiens cDNA
8448	21417	34530	2.46	7.0E-03	BE17697.1	EST HUMAN	RC1-C10286-050400-018-208 C10288 Homo sapiens cDNA
8941	21927	35354	0.49	7.0E-03	AF281074.1	NT	Homo sapiens neocortical (NRP2) gene, complete cds, alternatively spliced
9752	22863		0.71	7.0E-03	AF11108.2	NT	Homo sapiens serine palmitoyl transferase, subunit I gene, complete cds, and LOC5049 genes
9953	22860	36344	0.85	7.0E-03	N62378.1	EST HUMAN	W48210.1 Soares fetal liver spleen NFI.S Homo sapiens cDNA clone IMAGE:240603 3' similar to occludin
10078	23005	36475	2.84	7.0E-03	P48962	SWISSPROT	Alu repetitive element
10078	23005	36475	2.84	7.0E-03	P48962	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10688	23860		1.08	7.0E-03	AV687376.1	EST HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10688	23873		0.95	7.0E-03	AV789734.1	EST HUMAN	AV687376 GKC Homo sapiens cDNA clone GKACF07 5'
11176	24132	37662	2.23	7.0E-03	AL006852.1	NT	wc37403.xt NCL_GCAP_P728 Homo sapiens cDNA clone IMAGE:220840 3'
11248	24201	37722	1.51	7.0E-03	AL006852.1	NT	Sox laurus mRNA for NUP52, complete cds
11248	24201	37722	1.51	7.0E-03	AL006852.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12734	28977		1.53	7.0E-03	H64065.1	EST HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12741	28391		1.91	7.0E-03	BE252053.1	EST HUMAN	W15001.1 Soares fetal liver spleen NFI.S Homo sapiens cDNA clone IMAGE:242833 3' similar to cortactin
12834	28451		1.99	7.0E-03	Y17455.1	NT	Alu repetitive element
							80114516492 NHR_10G.C, 19 Homo sapiens cDNA clone IMAGE:3160476 5'
							Homo sapiens USF2R gene, penultimate exon

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID No.	Exon SEQ ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10403	23325		2.06	6.0E-03	U42281.1	EST_HUMAN	U22622.X1 NC_024631 Homo sapiens cDNA clone IMAGE:2151202 3' similar to SW R15A_HUMAN
10523	23448	38543	0.87	8.0E-03	U011640.1	NT	R40429.03 RIBOSOMAL PROTEIN L18A; Bacterial sulfate ferro gene
10559	23551		1.03	8.0E-03	AF064555.1	NT	Homo sapiens oleic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10769	23930	37167	0.88	6.0E-03	U08596.1	NT	M. thermophilus complete plasmid pSV1 DNA
11096	24039	37560	1.61	8.0E-03	AW062164.1	EST_HUMAN	ES197237 IMAGE:38250000; MAGO Homo sapiens cDNA
11162	24120		1.55	8.0E-03	U154581.1	NT	Homo sapiens nucleoside diphosphate kinase 2-like protein FLJ14011 (FLJ14011). mRNA
11327	24277		3.89	8.0E-03	U14555.1	NT	Mus musculus glyceraldehyde 3-phosphate dehydrogenase 1 (GAPDH) mRNA, complete cds
11326	24276	37606	2.55	8.0E-03	BE27896.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3539747 5'
12319	25123		2.26	8.0E-03	AF010498.1	NT	Rhodospirillum rubrum 16S rRNA, complete cds
12422	25812		1.52	8.0E-03	BF027183.1	EST_HUMAN	502151024F1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:4292412 5'
12446	25744		6.26	8.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450295 (section 39 of 148) of the complete genome
12525	25807		2.71	6.0E-03	U07809.1	NT	Phaenocarpa carlini f. sp. ratii guanine nucleotide binding protein alpha subunit (gcg1) gene, complete cds
12576	25835		1.46	6.0E-03	Q62209.1	SWISSPROT	SYNAPTOMAL COMPLEX PROTEIN 1 (SCP-1) PROTEIN
12850	25459		2.18	8.0E-03	BE706019.1	EST_HUMAN	50140322F1 NIH_MGC_80 Homo sapiens cDNA clone IMAGE:3485398 5'
12869	25471		1.53	8.0E-03	U245480.1	NT	Breslaia nigra-sig gene for S-luciferase, complete cds
13043	25594		1.76	8.0E-03	BF110296.1	EST_HUMAN	7n58511.X1 NC_024631 Homo sapiens cDNA clone IMAGE:3536694 3'
670	13735	26061	2.34	5.0E-03	U25105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORF8, and gpeE-like protein, complete cds
670	13736	26062	2.34	5.0E-03	U25105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORF8, and gpeE-like protein, complete cds
671	13735	26061	3.43	5.0E-03	U25105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORF8, and gpeE-like protein, complete cds
671	13735	26062	3.43	5.0E-03	U25105.1	NT	Chlamydia trachomatis partial ORF8; aminocyclase synthase, complete cds; complete ORF8, and gpeE-like protein, complete cds
1114	14159	27706	1.03	8.0E-03	U04297.1	NT	Atalapha italiana mRNA for DEAD box RNA helicase R43
1574	14607		1.32	8.0E-03	U133677.1	EST_HUMAN	4274005.X1 Homo sapiens cDNA clone IMAGE:1735968 3'
2060	15889	29703	2.45	8.0E-03	U303305.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2847	16035	28840	3.89	8.0E-03	U252337.1	EST_HUMAN	10116479F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3153	16210	20125	3.89	8.0E-03	U252337.1	EST_HUMAN	10116479F1 Homo sapiens cDNA clone IMAGE:3538799 5'
3169	16224		3.65	8.0E-03	U1614491.2	NT	Atalapha italiana DNA chromosome 4, contig fragment No. 3

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Table 4
Antibodies Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID: NO.	Expression Signal	Most Similar SEQ ID BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9159	2125	33554	1.08	5.0E-03	D06723.1	NT	Escherichia coli genomic DNA (19.1 - 19.4 min)
6292	22298	33688	0.91	5.0E-03	M25000.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10196	23124	33811	0.97	5.0E-03	L2710.1	NT	Plasmodium berghei 58 kDa phosphogluconate kinase, partial cds
10330	23240	36732	0.88	5.0E-03	AB681888.1	EST_HUMAN	RQ3-271057-2710109-332-022 S10379 Homo sapiens cDNA
10518	23244	33808	0.84	5.0E-03	AA363148.1	EST_HUMAN	946H10.1 NC1 CGAP P18 Homo sapiens cDNA clone IMAGE:995587
10696	23618	37112	0.47	5.0E-03	7682357	EST_HUMAN	Human apolipoprotein A1 protein (APOA1), mRNA
10844	23712	37112	0.31	5.0E-03	AA653261.1	EST_HUMAN	ag90-10411 Gasteral Wilms tumor Homo sapiens cDNA clone IMAGE:1126260 3'
11075	24037	37112	4.17	5.0E-03	T19588.1	EST_HUMAN	BRF1 Heart Homo sapiens cDNA clone 694
11287	24287	37764	2.15	5.0E-03	AW170334.1	EST_HUMAN	wt9505.31 Soares, NH-CeC, cervical, tumor Homo sapiens cDNA clone IMAGE:2886043 3' similar to contains 1,12,12,1 repetitive element;
11287	24287	37765	2.15	5.0E-03	AW170334.1	EST_HUMAN	wt9505.31 Soares, NH-CeC, cervical, tumor Homo sapiens cDNA clone IMAGE:2886043 3' similar to contains 1,12,12,1 repetitive element;
11381	24328	37857	1.55	5.0E-03	T47619.1	EST_HUMAN	wt9505.31 Soares, NH-CeC, cervical, tumor Homo sapiens cDNA clone IMAGE:2886043 3' similar to contains 1,12,12,1 repetitive element;
11659	24565	37869	3.62	5.0E-03	BE049055.1	EST_HUMAN	1036047.1 Stratagene plasmids (8637225) Homo sapiens cDNA clone IMAGE:70898 5'
12463	25938	37844	5.42	5.0E-03	AF047874.1	EST_HUMAN	145604.7 NC1 CGAP Bm52 Homo sapiens cDNA clone IMAGE:2381622 5'
12925	25298	37855	3.19	5.0E-03	AF067253.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12888	25355	37855	3.7	5.0E-03	T10347.1	NT	Human Y chromosome marker
12743	25732	37855	1.89	5.0E-03	AA458997.1	EST_HUMAN	Human pro-alpha1(I) collagen (COL2A1) gene exons 1-34, complete cds
12822	24494	37702	5.67	5.0E-03	BF573392.1	EST_HUMAN	2075603.1 Soares pV190T Homo sapiens cDNA clone IMAGE:809548 3' similar to SW-DNA2.1, Moyses pV1488 PROBABLE DIPHEOL OXIDASE A2 COMPONENT
1235	13335	28239	3.21	5.0E-03	AY146908.1	EST_HUMAN	600777747.1T191, MGC, 82 Homo sapiens cDNA clone IMAGE:4233022 5'
1241	13413	28337	2.16	4.0E-03	AY501051.1	EST_HUMAN	UHF-8N-4648-480-001-11 NC1 CGAP S048 Homo sapiens cDNA clone IMAGE:2742416 3'
1241	13510	28337	2.16	4.0E-03	FA0482.1	EST_HUMAN	UHF-8N-4648-480-001-11 NC1 CGAP S048 Homo sapiens cDNA clone IMAGE:3079831 5'
695	3792	25658	1.15	4.0E-03	P54673	EST_HUMAN	94766.41 Soares infant tumor N1B Homo sapiens cDNA clone IMAGE:3568 3'
695	3792	25658	1.15	4.0E-03	P54673	EST_HUMAN	94766.41 Soares infant tumor N1B Homo sapiens cDNA clone IMAGE:3568 3'
973	13683	28865	4.85	4.0E-03	AA303381.1	EST_HUMAN	PH7324.1DTLNOSTO1, SKANASE 3 (P3-KANASE) (P1-DN3-KANASE) (P1-K3)
913	13983	28865	4.85	4.0E-03	FA0482.1	EST_HUMAN	94766.41 Soares infant tumor N1B Homo sapiens cDNA clone IMAGE:3568 3'
913	13983	28865	4.85	4.0E-03	FA0482.1	EST_HUMAN	94766.41 Soares infant tumor N1B Homo sapiens cDNA clone IMAGE:3568 3'
913	14039	28865	4.85	4.0E-03	AY146909.1	EST_HUMAN	600777747.1T191, MGC, 82 Homo sapiens cDNA clone IMAGE:4233022 5'
913	14039	28865	4.85	4.0E-03	AY146909.1	EST_HUMAN	600777747.1T191, MGC, 82 Homo sapiens cDNA clone IMAGE:4233022 5'
1305	14214	27169	1.32	4.0E-03	AA296747.1	EST_HUMAN	RQ3-106974-74000-022-021 UMR01 Homo sapiens cDNA clone IMAGE:510698 5'
1305	14214	27169	1.32	4.0E-03	AA296747.1	EST_HUMAN	RQ3-106974-74000-022-021 UMR01 Homo sapiens cDNA clone IMAGE:510698 5'
1337	14432	27306	1.64	4.0E-03	AA296747.1	EST_HUMAN	wt9505.31 NC1 CGAP G351 Homo sapiens cDNA clone IMAGE:701768 5'
1590	14622	27306	1.64	4.0E-03	AY703051.1	EST_HUMAN	AV70305.1 ADOc Homo sapiens cDNA clone ADOcB68 5'
1759	14793	27772	2.38	4.0E-03	U34721.1	NT	Rattus norvegicus tyrosine 1, alpha- and fatty-acyl-imbic associated protein AT1-46 mRNA, complete cds
2034	15035	28670	11.42	4.0E-03	AA309777.1	EST_HUMAN	221468.1T191 Synovial cistern (8607200) Homo sapiens cDNA clone IMAGE:510698 5'

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HTE BLAST E Value	Top Hit Accession No.	Top Hit Database Source
7273	20038	33038	1.22	4.0E-03	AL163278.2	NT
7273	20038	33038	1.22	4.0E-03	AL163278.2	NT
7404	20372	33723	4.12	4.0E-03	CG2817	SWISSPROT
7655	20624	33958	0.99	4.0E-03	A081483.1	EST_HUMAN
7657	20626	33960	0.72	4.0E-03	BE57076.1	EST_HUMAN
7797	20720		0.88	4.0E-03	352709.1	NT
8274	21343	34655	0.46	4.0E-03	CGT162	SWISSPROT
8333	21533	34765	0.82	4.0E-03	AF11894.1	NT
8445	21513	34630	1.92	4.0E-03		769287 NT
9094	22030	35493	7.41	4.0E-03	A059383.1	EST_HUMAN
9241	22027		4.72	4.0E-03	AL163209.2	NT
9250	22216	36646	3.66	4.0E-03	AL163278.2	NT
10287	23212	36659	0.97	4.0E-03	A35964.1	EST_HUMAN
10742	23664	37168	0.78	4.0E-03	AL161555.2	NT
11178	24133	37693	1.65	4.0E-03	A061935.1	EST_HUMAN
11464	24407	37854	4.53	4.0E-03	AL163209.2	NT
12431	25946		1.52	4.0E-03	BE51573.1	EST_HUMAN
12454	29213		3.2	4.0E-03	BE28820.1	EST_HUMAN
12533	29239		2.19	4.0E-03	AW504273.1	EST_HUMAN
12795	25400		7.22	4.0E-03	BF224123.1	EST_HUMAN
12801	25866		3.31	4.0E-03	A061456.1	EST_HUMAN
12814	25437		2.73	4.0E-03	AW818141.1	EST_HUMAN
13093	29519	31079	6.48	4.0E-03	11436965	NT
371	13487	26887	1.69	3.0E-03	AF011920.1	NT
880	13935	26884	3.09	3.0E-03	AF011920.1	NT
1669	14701	27078	5.52	3.0E-03	AA488110.1	EST_HUMAN
2288	15281		1.58	3.0E-03	AF05068.1	NT
2302	13314		8.06	3.0E-03	A32321.1	NT
2303	13315	28334	1.3	3.0E-03	U46958.1	NT
<p>Homo sapiens chromosome 21 segment HS21C078</p> <p>Homo sapiens chromosome 21 segment HS21C078</p> <p>MUCIN 2 PRECURSOR (NTES FINAL MUCIN 2)</p> <p>IGTGT12X1 NCI CGAP L104 Homo sapiens cDNA clone IMAGE:2271814.3</p> <p>7631602X1 NCI CGAP L104 Homo sapiens cDNA clone IMAGE:338403.3</p> <p>H. sapiens hexk gene</p> <p>ADAMTS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAMTS5) (AGRECANASE-2) (ADMP-2) (ADAMTS 11)</p> <p>Dipeptidylaminocyclase A24 development protein DGT122 (DGT122) gene, partial cds</p> <p>Homo sapiens LOC403434 gene product (NOA03343), mRNA</p> <p>94991 L1X1 Source_VFL_1_UBC_31 Homo sapiens cDNA clone IMAGE:286019.3 similar to contains Alu repeat</p> <p>Homo sapiens chromosome 21 segment HS21C039</p> <p>Homo sapiens chromosome 21 segment HS21C078</p> <p>JP45012.121 Sueren retina N2594R Homo sapiens cDNA clone IMAGE:190160.5</p> <p>Arabinoside thiolase RNA chromosome 4, coding fragment Nos. 55</p> <p>xx4704.x1 NCI CGAP L111 Homo sapiens cDNA clone IMAGE:2707169.3</p> <p>Homo sapiens chromosome 21 segment HS21C038</p> <p>PM4-BN0738-180602-002-508 BN0138 Homo sapiens cDNA</p> <p>601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029605.5</p> <p>UIHF-BN0481-P044-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:306322.5</p> <p>7674038.x1 NCI CGAP L104 Homo sapiens cDNA clone IMAGE:306322.5</p> <p>7674038.x1 NCI CGAP L104 Homo sapiens cDNA clone IMAGE:306322.5</p> <p>element contains element MER31 negative element:</p> <p>H02607.x1 NCI CGAP K1411 Homo sapiens cDNA clone IMAGE:2953932.3 similar to contains element LTR5 repetitive element:</p> <p>RC3-ST0281-240400-015-03 ST0281 Homo sapiens cDNA</p> <p>Homo sapiens GRG2-associated binder 2 (KIA00871), mRNA</p> <p>Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1</p> <p>Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1</p> <p>nc78058.x1 NCI CGAP P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element</p> <p>Homo sapiens MHC class 1 region</p> <p>S. cereale (cv. Halo) mRNA for triphosphate isomerase</p> <p>Mus musculus intestinal trefoil factor gene, partial cds</p>						

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2303	15315	20335	1.3	3.0E-03	U9858.1	NT	Mus musculus Interleukin 1 beta factor gene, partial cds
3006	16064		4.09	3.0E-03	Y09005.1	NT	Arabidopsis thaliana pto1 gene
3099	16156	20099	4.09	3.0E-03	BE370206.1	EST_HUMAN	8612719827 NIH_XLOC_44 Homo sapiens cDNA clone IMAGE:3509933 5'
3169	16221	20136	2.54	3.0E-03	AB602687.1	EST_HUMAN	U2340075-243030-358533 UNK078 Homo sapiens cDNA
3426	16478	25095	1.82	3.0E-03	U344008.1	NT	Mus musculus alpha-2(XII) collagen (COL18A1) gene, exon 1 and 2
3439	16486		6.72	3.0E-03	Y12250.1	NT	C elegans similar gene
4002	17041	29949	7.18	3.0E-03	AB762392.1	EST_HUMAN	AF103305 Homo sapiens cDNA clone M05B507 5'
4002	17041	29950	7.18	3.0E-03	AB762392.1	EST_HUMAN	AF103305 Homo sapiens cDNA clone M05B507 5'
4057	17203	29995	1.47	3.0E-03	AB762278.1	EST_HUMAN	AF103305 Homo sapiens cDNA clone M05B507 5'
4177	17208		1.08	3.0E-03	U23221.1	NT	S cerevisiae Gc40c1 Ylms1 tumor Homo sapiens cDNA clone IMAGE:115869 5'
4424	17461	30042	3.8	3.0E-03	AB11422.1	NT	S cerevisiae Gc40c1 Ylms1 tumor Homo sapiens cDNA clone IMAGE:115869 5'
4546	17569	30458	5.98	3.0E-03	AB153141.1	EST_HUMAN	RefSeq:103305 Homo sapiens cDNA 3'
4671	17888	30776	1.74	3.0E-03	AB12754.1	EST_HUMAN	af154645 Stragene lung (467210) Homo sapiens cDNA clone IMAGE:341142 3' similar to contains Alu repetitive element
4800	17967	30796	3.49	3.0E-03	BE737545.1	EST_HUMAN	af154645 Stragene lung (467210) Homo sapiens cDNA clone IMAGE:341142 3' similar to contains Alu repetitive element
5336	18443	31154	3.42	3.0E-03	86224081	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5635	18731	31653	1.22	3.0E-03	U249981.1	NT	Homo sapiens hypothetical protein ORF2 (ORF2), mRNA
6708	18803	31980	0.05	3.0E-03	U35233.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein, L2mp2, L2mp2 gene, complete cds
7739	19376	32540	10.04	3.0E-03	AA460701.1	EST_HUMAN	ant3101.1 Soares, NH-MP1, ST Homo sapiens cDNA clone IMAGE:813185 5'
7822	19446	32546	0.66	3.0E-03	U31977.1	NT	Figur rubripes mRNA for sodium channel alpha subunit, partial cds
7442	20379	33730	1.37	3.0E-03	AB114118.1	NT	Myxomycetes manducatus pop3 gene for putative cytochrome P450
7442	20379	33730	1.37	3.0E-03	AB114118.1	NT	Myxomycetes manducatus pop3 gene for putative cytochrome P450
7785	20718	34091	3.16	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
8145	21082	34481	0.49	3.0E-03	P29559	SWISSPROT	DNA REPAIR HELICASE RAD15 (RHPS)
8270	21239	34650	0.01	3.0E-03	BF333058.1	EST_HUMAN	RCO-B10812-250000-032-407 B10812 Homo sapiens cDNA
8270	21239	34650	0.01	3.0E-03	BF333058.1	EST_HUMAN	RCO-B10812-250000-032-407 B10812 Homo sapiens cDNA
8406	21464	34860	1.31	3.0E-03	AB22560.1	EST_HUMAN	12577004.1 Soares, Jarchow, tumor, NHP4 Homo sapiens cDNA clone IMAGE:304783 3'
8558	21626		0.77	3.0E-03	MA5498.1	NT	S cerevisiae UGA935 gene, complete cds
8604	21771		1.16	3.0E-03	P51069	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN P2 HOMOLOG 1 (HNRP2 A2A3)
8627	21794	35197	1.34	3.0E-03	AL143388.2	NT	Homo sapiens chromosome 21 segment RS210568
8633	21859	35217	1.25	3.0E-03	Q0Q0M1	SWISSPROT	NONSTRUCTURAL PROTEIN V
9343	22308		10.07	3.0E-03	AA613774.1	EST_HUMAN	rib60101 NC_004071 Homo sapiens cDNA clone IMAGE:2089133 3' similar to contains L1 L1 L1
9400	22345	35797	4.01	3.0E-03	AL181586.2	NT	Arabidopsis thaliana DNA chromosome 4, centric fragment No. 85

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9424	22388	38827	4.74	3.0E-03	U016573.1	EST_HUMAN	603812-1 NC1 CGAP K103 Homo sapiens cDNA clone IMAGE:193247 3' similar to gp-357138_rnet1
9424	22388	38866	0.83	3.0E-03	B533078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9764	22705	38866	0.85	3.0E-03	D29201.1	EST_HUMAN	622850-1 NC1 CGAP Bme6 Homo sapiens cDNA clone IMAGE:418388 5'
9802	21125	34520	0.81	3.0E-03	BE15470.1	EST_HUMAN	323230-1 NC1 CGAP K103 Homo sapiens cDNA clone IMAGE:193247 3' similar to gp-357138_rnet1
9804	22921	34520	0.82	3.0E-03	P00355	SWISSPROT	POLY(POLYPROTEIN) POLYPROTEIN REVERSE TRANSCRIPTASE: REVERSE TRANSCRIPTASE
10095	22922		5.33	3.0E-03	P08972	SWISSPROT	CIRCULISPOKITE PROTEIN PRECURSOR (CS)
10295	23180	38667	1.56	3.0E-03	P11360	SWISSPROT	RETROVIRUS-RELATED POLY(POLYPROTEIN) (CONTAINS REVERSE TRANSCRIPTASE);
10395	23279	38755	1.15	3.0E-03	P11360	SWISSPROT	RETROVIRUS-RELATED POLY(POLYPROTEIN) (CONTAINS REVERSE TRANSCRIPTASE);
10499	23421	38620	4.39	3.0E-03	AL183303.2	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2A1)
11194	24149		1.62	3.0E-03	6900328	NT	Homo sapiens chromosome 21 segment 1821G103
11708	24673	38250	1.47	3.0E-03	AF010222.1	NT	Homo sapiens ATP/GTP-binding protein (P2AB) mRNA
11778	24930	37451	1.86	3.0E-03	A536298.1	NT	Pneumococcal carboxy-terminal serine endonuclease mRNA, partial cds
11810	24995	38275	2.27	3.0E-03	AF044481.1	NT	Homo sapiens golgi-like protein (GLP) gene, complete cds
11810	24995	38275	2.27	3.0E-03	AF044481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-C5G8P (C5G8P) gene, complete cds
11811	24763	38348	1.47	3.0E-03	P11360	SWISSPROT	RETROVIRUS-RELATED POLY(POLYPROTEIN) (CONTAINS REVERSE TRANSCRIPTASE);
12199	25795		4.08	3.0E-03	A5325046.1	EST_HUMAN	promina-5.077: human Homo sapiens cDNA 5'
12232	25904	38162	1.83	3.0E-03	AA993154.1	EST_HUMAN	o17510.s1 Soares, Loid, Jaus, Nizhifg, Sw Homo sapiens cDNA clone IMAGE:182778 3' similar to
12292	25986		2.42	3.0E-03	A500988.1	NT	contains L18 MER29 repetitive element;
12478	26228	31784	2.01	3.0E-03	A256292.1	NT	Rattus norvegicus mRNA for CMP-N-acetylneuraminic acid hydrolase, partial cds
515	13597	26506	0.92	2.0E-03	Q04652	SWISSPROT	Rattus norvegicus mRNA for connexin38 (cx38 gene)
783	15951	26507	0.92	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
783	15951	27370	1.24	2.0E-03	T0874.1	EST_HUMAN	YF1803.1 Soares field liver spleen NF1.S Homo sapiens cDNA clone IMAGE:108341 5'
3363	14393	27370	1.19	2.0E-03	T08783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
3363	14402	27372	1.34	2.0E-03	A061695.1	EST_HUMAN	h08001.s1 NC1 CGAP A171 Homo sapiens cDNA clone IMAGE:1217563
1076	14410	27360	1.24	2.0E-03	A129446.1	NT	Homo sapiens tumor-related protein DRG2 (DRG2) gene, complete cds
1486	14519	27462	1.53	2.0E-03	P145209	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP-27) (MEMBRANE GLYCOPROTEIN SPA-1) (CD181 ANTIGEN)
1519	14551	27522	3.03	2.0E-03	45878361	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-oxoglutarase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1519	14651	27523	5.03	2.0E-03	4557936	NT	Homo sapiens phosphoglycerate 2-oxoglutarate 5-lyase (lysine hydroxylase, Elter-Ducloux syndrome type 1) cDNA
1595	14627		8.7	2.0E-03	P29400	SWISSPROT	CD44 (CELL SURFACE) CHAIN PRECURSOR
1786	14615	27800	1.28	2.0E-03	AA165138.1	EST - HUMAN	CD24 (10-FLUORESCIN) CELL SURF. M2H2R. 9w Homo sapiens cDNA clone IMAGE:789114 F
2011	15032	28042	1.52	2.0E-03	AF302591.1	NT	Homo sapiens protein expression factor-3-like protein gene, partial cds
2291	15275	28259	1.02	2.0E-03	AF163322.2	EST - HUMAN	Homo sapiens chromosome 21 segment H37C102
2384	15585		4.02	2.0E-03	JAV13752.1	EST - HUMAN	U-H-81 cell-9-10-JUL-11 NCI CGAP. SUG3 Homo sapiens cDNA clone IMAGE:2717010 3'
3427	16475	28544	4.82	2.0E-03	AA450138.1	EST - HUMAN	294310.11 Source: fetal fetus. M2H2R. 9w Homo sapiens cDNA clone IMAGE:789114 F
3474	16481	29400	0.8	2.0E-03	BF56855.1	EST - HUMAN	602153070.11 NH. MGC. 42 Homo sapiens cDNA clone IMAGE:430070 3'
3680	16723	29636	6.1	2.0E-03	N97344.1	NT	H sapiens DNA, DM6, HLA-Z1, IP2, LMP2, TAP1, TAP2, DOB, DOB2 and RING6, 9, 13 and 14 genes
3973	17013	30057	0.85	2.0E-03	AB049802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4140	17121	30059	2.7	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN CONTAINS: COAT PROTEIN GP52, COAT PROTEIN GP36
4243	17201	30121	1.29	2.0E-03	AA176893.1	EST - HUMAN	22713101.11 Stralagene fetal cells 967202 Homo sapiens cDNA clone IMAGE:503651 5'
4263	17201	30122	9.31	2.0E-03	AA176893.1	NT	Rattus norvegicus 5-hydroxytryptamine ₁ receptor gene, partial cds
4498	17484		1.01	2.0E-03	AW297368.1	EST - HUMAN	U-H-BW-01-2-03-0-UI-11 NCI CGAP. Sub8 Homo sapiens cDNA clone IMAGE:2703413 3'
4492	17485	30375	1.11	2.0E-03	AG04746.1	EST - HUMAN	HA0307 Human fetal liver cDNA library Homo sapiens cDNA
4677	17590	30483	1.99	2.0E-03	AA2512.1	NT	Drosophila melanogaster shortlegged class 2 (sls) mRNA, complete cds
4677	17590	30484	1.99	2.0E-03	AA2512.1	NT	Drosophila melanogaster shortlegged class 2 (sls) mRNA, complete cds
4735	17765	30549	1.05	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha 1E subunit (CACNA1E) gene, exons 7-46, and partial cds, alternatively spliced
4740	17760		1.84	2.0E-03	BB7775.1	EST - HUMAN	VC5462.1 1 Source: adult brain 102-HB55Y Homo sapiens cDNA clone IMAGE:180860 3'
5054	18006	30945	0.75	2.0E-03	AF034828.1	NT	Homo sapiens X-linked aniridia-related ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5163	18172	31051	1.02	2.0E-03	AF197974.1	NT	g Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
5261	18267	31149	2.28	2.0E-03	D89006.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
5554	18561	31607	1.33	2.0E-03	BF241410.1	EST - HUMAN	801878056.1 NH. MGC. 35 Homo sapiens cDNA clone IMAGE:410462 5'
5709	25943	31891	2.18	2.0E-03	AB014583.1	NT	Homo sapiens mRNA for KIA0365 protein, partial cds
5745	19887	32008	0.61	2.0E-03	AW766111.1	EST - HUMAN	NR2-UM0025-500505-102-002 UN0025 Homo sapiens cDNA
5795	19937	32066	0.61	2.0E-03	AW766111.1	EST - HUMAN	NR2-UM0025-500505-102-002 UN0025 Homo sapiens cDNA
5797	19969	32071	1.73	2.0E-03	AB7711.1	NT	Xenopus laevis nucleoside transporter
6231	18005	32530	3.79	2.0E-03	P25477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
8231	18005	32537	3.79	2.0E-03	P25477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
8480	19545	32785	15.16	2.0E-03	Q96203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-AP II) (CA-XI)

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8460	19646	32704	15.16	2.0E-03	G52633	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (GARP 1) (GAX)
8462	19647	32706	7.38	2.0E-03	BF30318.1	EST_HUMAN	5018743NF.NF1.MGC-17 Homo sapiens cDNA clone IMAGE4121408 5'
8521	19684	32842	2.26	2.0E-03	Q61KPA	SWISSPROT	ADAMTS 17 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN INTEGRIN-1) (ADAMTS-17) (ADAMTS17)
8522	19685	32843	0.77	2.0E-03	AV709075.1	EST_HUMAN	AV709075 Homo sapiens cDNA clone AC046708 5'
8564	19614	32879	1.36	2.0E-03	394483.1	NT	Leucosium mRNA for 3'-UTR RNA synthesis (L9485)
8795	19610		1.25	2.0E-03	A021090.1	EST_HUMAN	h42890.x4 Sarcos. Disintegrin, cDNA. NUCO Homo sapiens cDNA clone IMAGE252177 5' similar to SVRL20 HUMAN P2914.009 RBOSCHAL PROTEIN L29 sequence element (SRY) repetitive element ; 215at1.1at Sarcos. Adm. liver, spleen, TNE.S. S1 Homo sapiens cDNA clone IMAGE.430022 3'
7151	18303	31271	1.08	2.0E-03	AB038502.1	NT	Genomablastis elegans mRNA for galactid LEC-11, complete cds
7287	20094	33371	2.86	2.0E-03	BE057865.1	EST_HUMAN	CH4-870360-081289-254-201 BT0369 Homo sapiens cDNA
7351	20321	33666	0.84	2.0E-03	AI269883.1	EST_HUMAN	sm59211.x1 NCI, CGAP, Lufk Homo sapiens cDNA clone IMAGE1196885 3'
7511	20476	33837	0.77	2.0E-03	786599.1	EST_HUMAN	x777610.T Sarcos. fetal liver spleen TNE.S Homo sapiens cDNA clone IMAGE114308 5'
7877	20821	34198	1.55	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARILAGE LINK PROTEIN) (LP)
8386	21355	34763	1.95	2.0E-03	AW59204.1	EST_HUMAN	H37008.x1 Sarcos. VFL.T_GBC.S1 Homo sapiens cDNA clone IMAGE284035 5' similar to TR-Q60978 Q60978 JERRY.
8560	21528	34947	6.01	2.0E-03	N20287.1	EST_HUMAN	LY43508.a1 Sarcos melanocyte 216HM Homo sapiens cDNA clone IMAGE264442 3' similar to contains L1.12 L1 repetitive element ;
8590	21528	34948	6.01	2.0E-03	N20287.1	EST_HUMAN	LY43508.a1 Sarcos melanocyte 216HM Homo sapiens cDNA clone IMAGE264442 3' similar to contains L1.12 L1 repetitive element ;
8637	21575	34960	0.97	2.0E-03	G20350	SWISSPROT	LAMININ ALPHA3 328 KD PROTEIN C699.06 IN CHROMOSOME 1
8639	21597	35018	1.23	2.0E-03	P16137	SWISSPROT	LAMININ ALPHA3 328 KD PROTEIN C699.06 IN CHROMOSOME 1
8854	21652	35274	0.77	2.0E-03	6008659	NT	Homo sapiens Retin-derived POU-domain factor-1 (RPF-1), mRNA
8854	21652	35275	0.77	2.0E-03	6008659	NT	Homo sapiens Retin-derived POU-domain factor-1 (RPF-1), mRNA
9109	21727	35102	0.81	2.0E-03	AU136719.1	EST_HUMAN	AU136719 PLACE1 Homo sapiens cDNA clone PLACE104839 5'
8792	21728		0.67	2.0E-03	AJ003971.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
9450	19847	32668	0.66	2.0E-03	AV72611.1	EST_HUMAN	NP2-UM0025-300300-102-02 UM0025 Homo sapiens cDNA
9450	19847	32669	0.66	2.0E-03	AV72611.1	EST_HUMAN	NP2-UM0025-300300-102-02 UM0025 Homo sapiens cDNA
9595	22557	36007	0.66	2.0E-03	AF224960.1	NT	Homo sapiens mannitolase, beta A, (lysosomal) (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) cDNA, complete cds
9844	22837	36091	0.87	2.0E-03	U50832.1	EST_HUMAN	Y65609.x1 Sarcos. VFL.T_GBC.S1 Homo sapiens cDNA clone IMAGE162938 3'
9894	22837	36092	0.97	2.0E-03	U50832.1	EST_HUMAN	Y65609.x1 Sarcos. fetal liver spleen TNE.S Homo sapiens cDNA clone IMAGE162938 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

[illegible]

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Accession No.	Top Hit Descriptor
9405	23039		0.65	1.0E-03 U52111.2	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
9474	23438	35977	3.71	1.0E-03 M52471.1	NT	Human data II alpha2-macroglobulin (A2M) cDNA, complete cds
9474	23438	35978	3.71	1.0E-03 M52471.1	NT	Human data II alpha2-macroglobulin (A2M) cDNA, complete cds
9555	22842		0.45	1.0E-03 J1247482.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
9586	22833	36364	1.77	1.0E-03 AF511400.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
9586	22833	36365	1.77	1.0E-03 AF511400.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
10179	23104		0.8	1.0E-03 Q01129	SWISSPROT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
10524	23446	36844	1.55	1.0E-03 AF033529.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
10529	22451		0.79	1.0E-03 AF037485.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
10979	23601		1.12	1.0E-03 M024350.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
11025	23690	37519	1.65	1.0E-03 AW362363.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
11025	23690	37517	1.65	1.0E-03 AW362363.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
11102	24062	37685	2.81	1.0E-03 BET79859.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
11172	24129		2.21	1.0E-03 AB63847.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
11461	24434		2.59	1.0E-03 AV759946.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
11602	24598	38171	6.16	1.0E-03 AA12270.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
12176	25024	38621	6.74	1.0E-03 BE694468.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
12653	28915		1.53	1.0E-03 AB37385.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
12753	25338	31311	7.37	1.0E-03 BE767572.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
5765	18887		1.76	9.0E-04 P06727	SWISSPROT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
6388	18456		0.81	9.0E-04 J05343.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
6388	18456		0.81	9.0E-04 J05343.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
9533	18951		1.39	9.0E-04 P02391	SWISSPROT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
10001	22228		1.39	9.0E-04 AB07303.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
1484	14517		1.04	8.0E-04 AB5468.1	NT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
3350	19376		0.64	8.0E-04 R07303.1	EST_HUMAN	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds
4029	17238		4.49	8.0E-04 P08547	SWISSPROT	Human sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L1 (a RPL18a), Cdc42-Rac1-mediated dependent protein kinase 1 (CAMK1), creatine transporter (CRT19), CDM protein (CDM), sarcosine oxidase (SOD) and tubulin mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST Value	Top Hit Database Accession No.	Top Hit Database Source	Top Hit Description
3424	16472	20391	1.28	5.0E-04	AA448931.1	EST_HUMAN	hK27611 at NCI_QGAP_Ccd1 Homo sapiens cDNA clone IMAGE:101794 3' similar to contains ALU repetitive element
3728	16770	20882	0.95	5.0E-04	G9UKP4	SWISSPROT	ADAMTS7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-15)
5549	18646	31598	2.37	5.0E-04	AF548054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6784	19839	33124	5.54	5.0E-04	AA155269.1	EST_HUMAN	234305.77 Stridgens cdc (h63725) Homo sapiens cDNA clone IMAGE:58669 5'
7802	20583	33926	10.72	6.0E-04	M23604.1	NT	Corilla galls inducible gene medium alleles, complete cds
							gp150a.x1 Source: placenta_2608weeks_2100HP060W Homo sapiens cDNA clone IMAGE:172819 3'
							hK27611 at NCI_QGAP_Ccd1 Homo sapiens cDNA clone IMAGE:101794 3' similar to contains element (HUMAN) contains ALU1
8289	21288	34669	4.95	5.0E-04	AI118392.1	EST_HUMAN	hK27611 at NCI_QGAP_Ccd1 Homo sapiens cDNA clone IMAGE:101794 3' similar to contains element MER22 repetitive element
8549	21614	35036	0.82	5.0E-04	AA814619.1	EST_HUMAN	hK27611 at NCI_QGAP_Ccd1 Homo sapiens cDNA clone IMAGE:101794 3' similar to contains element
9532	22578	36026	1.97	5.0E-04	AA646546.1	EST_HUMAN	hK27611 at NCI_QGAP_Ccd1 Homo sapiens cDNA clone IMAGE:101794 3' similar to contains element
9726	22754	36207	0.82	5.0E-04	NG8786.1	EST_HUMAN	hK27611 at NCI_QGAP_Ccd1 Homo sapiens cDNA clone IMAGE:101794 3' similar to contains element
9878	22829	36283	0.94	5.0E-04	P29126	SWISSPROT	REPETITIVE ELEMENT
9938	22895	36358	4.35	5.0E-04	AW270983.1	EST_HUMAN	hK27611 at NCI_QGAP_Ccd1 Homo sapiens cDNA clone IMAGE:101794 3' similar to contains element
10940	23652		0.47	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
11320	24270		1.94	5.0E-04	AL046507.2	EST_HUMAN	DKFZ2658M2024_r1 586 (synonym: hule-1) Homo sapiens cDNA clone DKFZ2658M2024
12022	18948	31568	10.91	5.0E-04	AF246054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12296	26783		4.4	5.0E-04	AA569513.1	EST_HUMAN	hK27611 at NCI_QGAP_PRT Homo sapiens cDNA clone IMAGE:513878
674	13738	26955	1.46	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 83 of 183 of the complete genome
848	13904	26852	1.6	4.0E-04	A1720283.1	EST_HUMAN	hK27611 at NCI_QGAP_PRT Homo sapiens cDNA clone IMAGE:513878
848	13904	26853	1.8	4.0E-04	A1720283.1	EST_HUMAN	hK27611 at NCI_QGAP_PRT Homo sapiens cDNA clone IMAGE:513878
1481	14494	27468	2.78	4.0E-04	AW763366.1	EST_HUMAN	hK27611 at NCI_QGAP_PRT Homo sapiens cDNA clone IMAGE:513878
2095	15112	28133	1.57	4.0E-04	AL163278.2	NT	hK27611 at NCI_QGAP_PRT Homo sapiens cDNA clone IMAGE:513878
2143	15160		0.89	4.0E-04	AL046704.1	EST_HUMAN	hK27611 at NCI_QGAP_PRT Homo sapiens cDNA clone IMAGE:513878
2835	18634	28658	1.88	4.0E-04	U50871.1	SWISSPROT	hK27611 at NCI_QGAP_PRT Homo sapiens cDNA clone IMAGE:513878
3178	19233	29150	1.8	4.0E-04	AF281074.1	NT	hK27611 at NCI_QGAP_PRT Homo sapiens cDNA clone IMAGE:513878

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Table 4
Antibodies Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
4351	17376	30257	3.22	4.0E-04	AA457033.1	EST_HUMAN	nt010a01 NC1. COAP. Cofl Homo sapiens cDNA, clone IMAGE:591530 3' similar to gb:AA12121 T-CELL
4351	17376	30258	3.22	4.0E-04	AA457033.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN)
4351	17376	30259	3.22	4.0E-04	AA457033.1	EST_HUMAN	nt010a01 NC1. COAP. Cofl Homo sapiens cDNA, clone IMAGE:591530 3' similar to gb:AA12121 T-CELL
4358	17691	30494	1.31	4.0E-04	BE509690.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN)
4358	17691	30495	1.31	4.0E-04	BE509690.1	EST_HUMAN	nt010a01 NC1. COAP. Cofl Homo sapiens cDNA, clone IMAGE:59250 3'
5124	18153	31010	4.37	4.0E-04	AL163267.2	EST_HUMAN	60134569HF.1NT. JMC. 3 Homo sapiens cDNA, clone IMAGE:367890 5'
5268	18531		1.20	4.0E-04	AL163267.2	NT	Homo sapiens chromosome 21 segment H827C087
7483	20449	33906	1.28	4.0E-04	P46442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL
7790	20733		0.95	4.0E-04	AL115966.2	EST_HUMAN	CALCIUM-SENSING RECEPTOR
7897	20928	34321	0.68	4.0E-04	AF122076.1	EST_HUMAN	Autoblastip. Italiane DNA chromosome 4, contig fragment NO. 86
8861	21848	33289	1.97	4.0E-04	AF240712.1	EST_HUMAN	AUT122076 MAMMA1 Homo sapiens cDNA, clone IMAGE:1001820 5'
8869	21865	33276	1.96	4.0E-04	BF240712.1	EST_HUMAN	60176668HF.1NT. JMC. 35 Homo sapiens cDNA, clone IMAGE:4069760 5'
10048	22976	35442	1.11	4.0E-04	AF025666.1	EST_HUMAN	y636r1211 Scores melanocyte 200HM Homo sapiens cDNA, clone IMAGE:264142 5'
10249	23765		1.41	4.0E-04	AF025666.1	EST_HUMAN	y636r1211 Scores, Jwells, NHT Homo sapiens cDNA, clone IMAGE:1645441 3'
10249	23765		1.41	4.0E-04	AF025666.1	EST_HUMAN	Nucleus myoblast neoplasm-24a177 nDNA, alternatively spliced, complete cds
12684	25726		2.42	4.0E-04	AF258252.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds
187	13276	26187	3.45	3.0E-04	AF149429.1	EST_HUMAN	DK-281614221.1 Homo sapiens cDNA, clone IMAGE:592761 3'
197	13296	26226	1.65	3.0E-04	P42639	SWISSPROT	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
861	13368	26895	1.64	3.0E-04	AF03991.1	NT	264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
1856	14682	27878	1.65	3.0E-04	AF162100.1	EST_HUMAN	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
1871	14686		1.43	3.0E-04	AF039674.1	EST_HUMAN	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
3319	16171	26291	2.71	3.0E-04	P23147	SWISSPROT	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
4068	17120		3.21	3.0E-04	AF164445.1	NT	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
4120	17163		1.93	3.0E-04	BE140963.1	EST_HUMAN	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
4534	17371		5.39	3.0E-04	BE140963.1	EST_HUMAN	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
4534	17371		5.39	3.0E-04	BE140963.1	EST_HUMAN	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
5993	21919	33432	1.62	3.0E-04	AL163261.2	EST_HUMAN	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
7183	16414	31216	0.71	3.0E-04	AF063991.1	EST_HUMAN	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
7947	20764	34171	0.77	3.0E-04	P23446	SWISSPROT	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
8602	21730	34686	0.81	3.0E-04	P122607	SWISSPROT	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2
10280	23255	36689	1.44	3.0E-04	AA464935.1	EST_HUMAN	145 NO.264031 NC1. COAP. XG11 Homo sapiens cDNA, clone IMAGE:20261 1 and 2

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Table 4

Single Exon Probe Expressed in Bone Marrow

Probe SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description	
10538	23480	3.65	3.0E-04	AB02139.1	EST_HUMAN	h1461.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:281376 3'	
10825	23748	7.72	3.0E-04	AA76120.1	EST_HUMAN	h2409.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone 1391360 3' similar to gbl160072.60S RIBOSOMAL PROTEIN L7A (HUMAN)	
12245	25957	3.98	3.0E-04	AA22801.1	EST_HUMAN	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element	
12623	28602	3.33	3.0E-04	AB018592.1	NT	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element	
13014	25564	4.33	3.0E-04	AL134483.1	EST_HUMAN	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element	
177	13278	28204	2.0E-04	AF217708.1	NT	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element	
478	13551	28470	3.55	2.0E-04	AL146707.1	EST_HUMAN	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
908	13663	26919	4.01	2.0E-04	AB0524.1	NT	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
908	13663	26920	4.01	2.0E-04	AB0524.1	NT	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
1183	14224						
1190	14230						
1849	14875						
2184	15209						
2681	15562	28001	4.05	2.0E-04	U06081.1	NT	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
3040	16038	28771	1.13	2.0E-04	AI12429.1	EST_HUMAN	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
3445	16055	28413	2.44	2.0E-04	BE05217.1	EST_HUMAN	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
3903	16972	28655	1.21	2.0E-04	AW78441.1	EST_HUMAN	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
4137	17165						
4696	17717	30013	1.21	2.0E-04	U01025.1	NT	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
4696	17717	30013	1.21	2.0E-04	U01025.1	NT	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
4834	17851						
5070	18990	30981	1.21	2.0E-04	U04883.1	EST_HUMAN	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
5088	18108	31081	1.85	2.0E-04	U070707.1	NT	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
5823	18718	31878	1.29	2.0E-04	U064353.1	EST_HUMAN	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element
5965	18732	31894	1.78	2.0E-04	U060682.1	EST_HUMAN	h3494.11.1 Source: Jymna_NHFT.Homo sapiens cDNA clone IMAGE:1010450 similar to contains L12 L1 repetitive element

Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (%) Hit Score E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5843	18933	32117	1.15	2.0E-04	AJ260682.1	EST - HUMAN	EST11193 (Hs) Homo sapiens cDNA 5' end similar to EST containing 0 family repeat
6057	19138	32348	0.88	2.0E-04	4798179	NT	Homo sapiens cat cycle progression 3' region (DN3) mRNA
6066	19435	32678	0.8	2.0E-04	AF140708.1	NT	hls (Hs) Homo sapiens cDNA clone MAMM100708 5'
7440	20407		2.54	2.0E-04	AU17172.1	EST - HUMAN	AL021071 (Hs) Homo sapiens cDNA clone MAMM100708 5'
7546	20609		0.61	2.0E-04	AW950683.1	EST - HUMAN	Q1271 (Hs) REVERSE TRANSCRIPTASE HOMOLOG
7882	20829		15.1	2.0E-04	P08848	SWISSPROT	Q1271 (Hs) REVERSE TRANSCRIPTASE HOMOLOG
7892	20835	34215	1.21	2.0E-04	P46286	SWISSPROT	Q1271 (Hs) REVERSE TRANSCRIPTASE HOMOLOG
8170	21109	34908	0.93	2.0E-04	AL033722	EST - HUMAN	Q1271 (Hs) REVERSE TRANSCRIPTASE HOMOLOG
8170	21109	34909	0.93	2.0E-04	AL033722	EST - HUMAN	Q1271 (Hs) REVERSE TRANSCRIPTASE HOMOLOG
8288	21257	34687	2.13	2.0E-04	U32444.2	NT	Q1271 (Hs) REVERSE TRANSCRIPTASE HOMOLOG
8288	21257	34688	2.13	2.0E-04	U32444.2	NT	Q1271 (Hs) REVERSE TRANSCRIPTASE HOMOLOG
8927	21595	35015	1.21	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCT4 gene region, section 1/2 (DLEC1, ORCT3, ORCT4 genes, complete cds)
8927	21595	35016	1.21	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCT4 gene region, section 1/2 (DLEC1, ORCT3, ORCT4 genes, complete cds)
8911	21877	35203	1.9	2.0E-04	AF020503.1	NT	Homo sapiens FRAB3 common fragile region, diadenosine triphosphate hydrolase (FH17) gene, exon 5
8926	22051	35498	0.86	2.0E-04	AF57331.1	NT	Human immunoglobulin C(mu) and C(gamma) heavy chain genes (constant regions)
8989	22642	36700	0.61	2.0E-04	AF725700.1	EST - HUMAN	af22412.s1 Scores, letic, NHT Homo sapiens cDNA clone 1303518 3'
9774	22715	36710	0.65	2.0E-04	P18716	SWISSPROT	GASTRUL2 ZINC FINGER PROTEIN XLGFP26.1
10334	23288	36735	1.21	2.0E-04	BE149303.1	EST - HUMAN	RC3-H10284-151069-011-505 HT254 Homo sapiens cDNA
10377	23300	36776	2.74	2.0E-04	AA405777.1	EST - HUMAN	zu66511.1 Scores, letic, NHT Homo sapiens cDNA clone IMAGE742684 5'
11197	24152	37683	3.56	2.0E-04	AV730373.1	EST - HUMAN	AV730373 HTT Homo sapiens cDNA clone HTFAA01 5'
11810	24461		2.99	2.0E-04	AJ243213.1	NT	Homo sapiens partial EHT4 receptor gene, exons 2 to 6
11835	24572	38136	2.95	2.0E-04	AA40282.1	EST - HUMAN	10111.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE214028 3' similar to contains AU repetitive element
11755	24893	38622	2.49	2.0E-04	AF19740.1	EST - HUMAN	U28508.s1 Scores, melanocyte 2Nk-Ht Homo sapiens cDNA clone IMAGE 2717100 3'
798	19827	28771	0.81	1.0E-04	P68546.1	EST - HUMAN	U28508.s1 Scores, melanocyte 2Nk-Ht Homo sapiens cDNA clone IMAGE 262884 3' similar to contains L1/L1 repetitive element
951	14004	28955	2.03	1.0E-04	P48725	SWISSPROT	PERICENTRIN
1076	14121	27072	2.61	1.0E-04	P11589	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE ; (NONNUCLEASIS)]
11115	14160	27110	4.21	1.0E-04	AW018447.1	EST - HUMAN	U28508.s1 Scores, melanocyte 2Nk-Ht Homo sapiens cDNA clone IMAGE 2701825 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1118	14100	27111	4.21	1.0E-04	AW013947.1	EST_HUMAN	U4-HBD-sub-09-01-1 NC1_CGAP_Sb1t Homo sapiens cDNA clone IMAGE:270823 3'
1335	14389		3.08	1.0E-04	U02878.1	NT	Angiella anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1632	14695	27940	3.16	1.0E-04	AF148905.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, vFLIP, v-cyclin, latent nuclear antigen, ORF K14, vGPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
4335	14696	27941	3.16	1.0E-04	AF148905.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, vFLIP, v-cyclin, latent nuclear antigen, ORF K14, vGPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1375	15052	27953	2.87	1.0E-04	AF048424.1	NT	Human catallin DNA, chromosome 24q14, microsatellite TKY98
2039	15053	28100	1.08	1.0E-04	BE10833.1	EST_HUMAN	U4-HBD-sub-09-01-1 NC1_CGAP_Sb1t Homo sapiens cDNA clone IMAGE:376366 3'
2058	15694	28111	1.02	1.0E-04	BE10833.1	EST_HUMAN	U4-HBD-sub-09-01-1 NC1_CGAP_Sb1t Homo sapiens cDNA clone IMAGE:376366 3'
3297	16330	29235	1.14	1.0E-04	G02229	SWISSPROT	SPICEGLOVE, UNCLASSIFIED PROTEIN (GAP_62) (SPICEGLOVE FACTOR 3A SUBUNIT 2) (SF31068)
3748	16790	29702	0.93	1.0E-04	AI440282.1	EST_HUMAN	U4-HBD-sub-09-01-1 NC1_CGAP_Sb1t Homo sapiens cDNA clone IMAGE:270823 3' similar to contains AU repetitive element
4069	17123	30017	2.07	1.0E-04	M14942.1	NT	Mouse alpha 1 type-II collagen mRNA
4109	17143	30037	1.94	1.0E-04	AV047727.1	EST_HUMAN	AV047727 GLC Homo sapiens cDNA clone GLC8BD04.3
5132	18141	31019	1.87	1.0E-04	768201.S1NT	EST_HUMAN	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5137	18141	31020	1.87	1.0E-04	768201.S1NT	EST_HUMAN	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5137	18146	31028	0.92	1.0E-04	AI337156.1	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5690	19045	32244	1.19	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8033	19116	32319	0.92	1.0E-04	T19815.1	EST_HUMAN	735F Heart Homo sapiens cDNA clone 753
8033	19116	32320	0.92	1.0E-04	T19815.1	EST_HUMAN	735F Heart Homo sapiens cDNA clone 753
8576	19539	32905	0.9	1.0E-04	AA177111.1	EST_HUMAN	nc02412.1 NC1_CGAP_P1g Homo sapiens cDNA clone IMAGE:262
7012	20138	33455	0.86	1.0E-04	AA584551.1	EST_HUMAN	125804.1 NC1_CGAP_AA1 Homo sapiens cDNA clone IMAGE:953483 3' similar to pB197262
7952	20351	33719	12.66	1.0E-04	AI251980.1	EST_HUMAN	KALMANN SYNDROME PROTEIN PRECURSOR (HUMAN) contains AU repetitive element
7821	20351	33719	12.73	1.0E-04	AI251980.1	EST_HUMAN	q157510.x1 NC1_CGAP_O42 Homo sapiens cDNA clone IMAGE:1185583 3'
8328	21297	34712	0.89	1.0E-04	AA30453.1	EST_HUMAN	esb4068.at Stragene_NF1_7_GSC S1 Homo sapiens cDNA clone IMAGE:854564 3'
9662	22645	38102	2.18	1.0E-04	AI603220.1	EST_HUMAN	q157510.x1 NC1_CGAP_O42 Homo sapiens cDNA clone IMAGE:1185583 3'
9703	22656	38111	1.47	1.0E-04	O08969	SWISSPROT	q157510.x1 Stragene_NF1_7_GSC S1 Homo sapiens cDNA clone IMAGE:854564 3'
9780	22721		0.63	1.0E-04	T77153.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 6)
10074	23531	36394	1.69	1.0E-04	P08547	SWISSPROT	y47206.1 Source fetal liver spleen TNF-8 Homo sapiens cDNA clone IMAGE:113774 5'
10359	23461		6.91	1.0E-04	P08547	SWISSPROT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10578	23498	36960	0.91	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Source	Top Hit Descriptor
11897	24603		1.74	1.0E-04	M28387.1	NT	Mouse alpha interferon gene, complete cds
11898	24604	38433	1.15	1.0E-04	AB022988.1	NT	Human alpha interferon gene, complete cds
11899	24605	38432	1.48	1.0E-04	AV150461.1	EST	Human alpha interferon gene, complete cds
12032	24606	38502	1.81	1.0E-04	Q33664	SWISSPROT	Human alpha interferon gene, complete cds
12033	24608	38503	1.81	1.0E-04	Q33666	SWISSPROT	Human alpha interferon gene, complete cds
12413	25770		2.4	1.0E-04	BE876399.1	EST	Human alpha interferon gene, complete cds
13051	25977		1.38	1.0E-04	BE700353.1	EST	Human alpha interferon gene, complete cds
669	13761	20693	2.39	8.0E-05	AJ746933.1	EST	Human alpha interferon gene, complete cds
2020	15041	20652	1.09	8.0E-05	AJ746933.1	EST	Human alpha interferon gene, complete cds
6674	19155	32367	1.98	8.0E-05	AB06818.1	EST	Human alpha interferon gene, complete cds
7628	20776	34153	0.87	8.0E-05	AV150461.1	EST	Human alpha interferon gene, complete cds
7628	20776	34154	0.87	8.0E-05	AV150461.1	EST	Human alpha interferon gene, complete cds
9831	22960		2.89	8.0E-05	U00001.1	EST	Human alpha interferon gene, complete cds
9833	22962	38137	3.13	8.0E-05	AF150662.1	NT	Human alpha interferon gene, complete cds
11472	24415	37564	2.03	9.0E-05	AW023076.1	EST	Human alpha interferon gene, complete cds
11538	19155	32367	3.21	9.0E-05	Q68718	SWISSPROT	Human alpha interferon gene, complete cds
12485	25832		3.02	9.0E-05	AF120766.1	NT	Human alpha interferon gene, complete cds
822	13660	26931	1.76	8.0E-05	AJ251046.1	NT	Human alpha interferon gene, complete cds
866	13921		7.38	8.0E-05	AJ251046.1	NT	Human alpha interferon gene, complete cds
2581	18919		0.91	8.0E-05	M83575.1	NT	Human alpha interferon gene, complete cds
4657	17532	30415	0.87	8.0E-05	AW044605.1	EST	Human alpha interferon gene, complete cds
9101	22067	35463	3.463	8.0E-05	Y11696.1	NT	Human alpha interferon gene, complete cds
11485	24426	37979	3.06	8.0E-05	M69197.1	NT	Human alpha interferon gene, complete cds
13050	28815		2.74	8.0E-05	A4276933.1	EST	Human alpha interferon gene, complete cds
3417	13438	26358	6.11	7.0E-05	AW847448.1	EST	Human alpha interferon gene, complete cds
347	13438	26359	6.11	7.0E-05	AW847448.1	EST	Human alpha interferon gene, complete cds
569	13939	26953	1	7.0E-05	L49075.1	EST	Human alpha interferon gene, complete cds
569	13939	26954	1	7.0E-05	L49075.1	EST	Human alpha interferon gene, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mod Similar to EST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10079	23005	39477	0.71	0.0E-05	AW627665.1	EST_HUMAN	h57403.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:297444.3'
11100	24060	37584	2.27	6.0E-05	RT76939.1	EST_HUMAN	y06665.at Soares, placenta, N262P Homo sapiens cDNA clone IMAGE:143593.3' similar to contains Alu repetitive element/contains L1/T1 repeat
11847	24730	38316	2.71	6.0E-05	AA04015.1	EST_HUMAN	258302.21 Soares, placenta, N262P Homo sapiens cDNA clone IMAGE:487033.5'
12870	25013	31529	16.08	6.0E-05	AA080110.1	EST_HUMAN	W803103.5-51169-040-111 N262P Homo sapiens cDNA
1403	14438	27404	10.34	5.0E-05	AA032086.1	EST_HUMAN	Q1451024-41169-040-111 31023 Homo sapiens cDNA
1800	14905		1.15	5.0E-05	8623981	NT	Homo sapiens 29255 protein/contains monocyte protein/clone (LOC56955) mRNA
4004	17043	23951	3.54	5.0E-05	A1271894.1	NT	Homo sapiens partial BC122333 gene for extracellular monocyte transporter (EMT), exon 1
5903	18999	31070	11.74	5.0E-05	038955.1	NT	Homo sapiens partial gene for myoblastic myosin, elongin light chain, 3'UTR
6107	19189	32465	3.22	5.0E-05	A1053344.1	EST_HUMAN	AY85544.6L2 Homo sapiens cDNA clone GLC0403.3
6232	19394	32803	0.84	5.0E-05	A1053344.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7553	20516		1.18	5.0E-05	A007594.1	NT	Mus musculus gene for caldinin, exon 1
12462	25371	588	5.88	5.0E-05	F49153	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12717	25371		4.8	5.0E-05	A105334.1	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2518	13329		4.95	4.0E-05	A105334.1	NT	Human retin (REN) gene, 6' flanking region
4008	17933	30416	1.58	4.0E-05	A105334.1	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4008	17933	30417	1.58	4.0E-05	A105334.1	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4810	17427		0.89	3.0E-05	AF184988.1	NT	Cytoskeleton protein isolate Zebra 15.0a glycoprotein gp16 gene, partial cds
7127	20560	33586	0.71	4.0E-05	A105334.1	NT	Mosca musca hemoglobin (HP) gene, 5' region
9891	22834		8.43	4.0E-05	A105334.1	NT	Homo sapiens PF1200 mRNA, complete cds
10390	22823	36780	0.51	4.0E-05	A11369	SWISSPROT	RETROVIRUS-RELATED POLYMERASE
10771	23852	37188	0.66	4.0E-05	P21789	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
11120	24080	37904	3.91	4.0E-05	AA027046.1	EST_HUMAN	h39407.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2974360.3' similar to contains element MIR repetitive element
12423	25102		2.46	4.0E-05	AA117560.1	EST_HUMAN	xb5600.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:748252.3'
13001	25912		2.59	4.0E-05	AA117561.1	EST_HUMAN	z07611.at NC1 CGAP G0B1 Homo sapiens cDNA clone IMAGE:1694468.3' similar to contains Alu repetitive element/contains element KET repetitive element
681	13744	26871	0.78	3.0E-05	A1248061.1	EST_HUMAN	g14610.x1 Soares, total liver, spleen, N1FLS, S1 Homo sapiens cDNA clone IMAGE:2581409.3'
1091	14107	27057	1.89	3.0E-05	AA273951.1	EST_HUMAN	xc2498.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2581409.3'
1133	14176	27125	0.82	3.0E-05	BF037853.1	EST_HUMAN	601461463F1 NH, JMG, 60 Homo sapiens cDNA clone IMAGE:388142.5
1331	14178	27126	0.82	3.0E-05	BF037853.1	EST_HUMAN	601461463F1 NH, JMG, 60 Homo sapiens cDNA clone IMAGE:388142.5
4439	17437	30324	6.15	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0321-120200-001-410 HT0521 Homo sapiens cDNA
4409	17437	30325	6.15	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0321-120200-001-410 HT0521 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	QRF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8032	19102	32374	0.86	2.0E-05 Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA+/DICARBOXYLATE COTRANSPORTER)	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA+/DICARBOXYLATE COTRANSPORTER)
8291	18359	32559	0.68	2.0E-05 AL149272.1	EST_HUMAN	SwissProt	similar to contains 1,18 1L1 repetitive element;
8356	19426	32657	0.49	2.0E-05 F335055	SWISSPROT	SWISSPROT	similar to contains 1,18 1L1 repetitive element;
8778	19833	33116	2.32	2.0E-05 AF14380.1	EST_HUMAN	EST_HUMAN	similar to contains 1,18 1L1 repetitive element;
7086	20020	33322	1.52	2.0E-05 U09262.1	NT	NT	similar to contains 1,18 1L1 repetitive element;
7096	20033	33339	0.94	2.0E-05 A429890.1	EST_HUMAN	EST_HUMAN	similar to contains 1,18 1L1 repetitive element;
7108	20242		8.62	2.0E-05 M891025.1	EST_HUMAN	EST_HUMAN	similar to contains 1,18 1L1 repetitive element;
7360	20330	33978	2.22	2.0E-05 AF22482.1	NT	NT	similar to contains 1,18 1L1 repetitive element;
7390	20330	33980	2.22	2.0E-05 AF22482.1	NT	NT	similar to contains 1,18 1L1 repetitive element;
7592	20563		0.81	2.0E-05 AF179847.1	NT	NT	similar to contains 1,18 1L1 repetitive element;
8157	21095	34404	0.5	2.0E-05 U08651.1	NT	NT	similar to contains 1,18 1L1 repetitive element;
8217	21188	34596	1.25	2.0E-05 AB351040.1	EST_HUMAN	EST_HUMAN	similar to contains 1,18 1L1 repetitive element;
9477	22441	35381	0.52	2.0E-05 BE2344940.1	EST_HUMAN	EST_HUMAN	similar to contains 1,18 1L1 repetitive element;
9477	22441	35382	0.52	2.0E-05 BE2344940.1	EST_HUMAN	EST_HUMAN	similar to contains 1,18 1L1 repetitive element;
9500	23015	36015	0.57	2.0E-05 F44837	SWISSPROT	SWISSPROT	similar to contains 1,18 1L1 repetitive element;
9522	23566	36016	0.57	2.0E-05 F44837	SWISSPROT	SWISSPROT	similar to contains 1,18 1L1 repetitive element;
10363	23208	35953	0.87	2.0E-05 AL103207.2	NT	NT	similar to contains 1,18 1L1 repetitive element;
10494	23416	35914	0.87	2.0E-05 BF355595.1	EST_HUMAN	EST_HUMAN	similar to contains 1,18 1L1 repetitive element;
10554	23874	37317	2.1	2.0E-05 N41751.1	EST_HUMAN	EST_HUMAN	similar to contains 1,18 1L1 repetitive element;
10554	23874	37318	2.1	2.0E-05 N41751.1	EST_HUMAN	EST_HUMAN	similar to contains 1,18 1L1 repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10276	23201	36686	1.11	1.0E-05	AW291521.1	EST_HUMAN	UHFH2-agile-08-JUL-01 NC1_CGAP_5J24 Homo sapiens cDNA clone IMAGE:274588.3'
10544	23466		1.95	1.0E-05	AW460985.1	EST_HUMAN	h07610.x1 NC1_CGAP_4617 Homo sapiens cDNA clone IMAGE:2873010.3 similar to contains L12 L1 repetitive element;
11284	24216	37740	1.79	1.0E-05	U61328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-L) gene, h04rd gene, and sodium phosphate transporter (NPTS) gene, complete cds
11284	24216	37741	1.79	1.0E-05	U61328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-L) gene, h04rd gene, and sodium phosphate transporter (NPTS) gene, complete cds
12841	29500	31421	1.43	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2680	15676	28667	5.9	9.0E-06	AI88881.1	EST_HUMAN	h73608.x1 NC1_CGAP_7503 Homo sapiens cDNA clone IMAGE:2245368.3'
3112	18169	29079	4.25	9.0E-05	AI218955.1	EST_HUMAN	ag1103.x1 Scores, placenta, B2HSP8dW Homo sapiens cDNA clone IMAGE:1769191.3'
3524	18687		2.82	9.0E-05	M97195.1	NT	Human alpha2-macroglobulin embryonic form (A2M) gene, exon 1 and 2
5008	19091	32291	2.31	9.0E-05	U61328.1	NT	Homo sapiens differentiation antigen CD20 gene, exon 5, 6
7047	20360	33575	0.73	9.0E-05	BE503642.1	EST_HUMAN	RC1310313:10500-417-407 B10313 Homo sapiens cDNA
7874	20352	33988	0.84	9.0E-05	P08547	SWISSPROT	LINE1 REVERSE TRANSCRIPTASE HOMOLOG
8253	20906	34368	11.84	9.0E-06	AI034370.1	EST_HUMAN	cc2091.x1 Scores, fetal liver, spleen, INF1_S_51 Homo sapiens cDNA clone IMAGE:1666912.3' similar to contains Alu repetitive element
8587	21774	35200	1.18	9.0E-05	AL163269.2	NT	Homo sapiens chromosome 21 segment HS21C009
9334	22269	35728	2.51	9.0E-05	Q33769	SWISSPROT	SUSH1 REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9334	22269	35729	2.51	9.0E-05	Q33769	SWISSPROT	SUSH1 REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9377	22539	35900	4.44	9.0E-05	Q35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11285	24216	37763	3.85	9.0E-05	Q10384	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2353	15688	28659	2.23	9.0E-05	AW352639.1	EST_HUMAN	RC3-CT263-291119-01T-11T1 CT263 Homo sapiens cDNA
10899	23818	37326	0.64	9.0E-05	P24083	SWISSPROT	FASIGLII, II, PHOSPHATIDYLINOSITOL-LINKED ISOPREMI PRECURSOR (FAS II)
10996	23818	37327	0.64	9.0E-05	P24083	SWISSPROT	FASIGLII, II, PHOSPHATIDYLINOSITOL-LINKED ISOPREMI PRECURSOR (FAS II)
980	14031		2.14	7.0E-05	AI069726.1	EST_HUMAN	ab59010.1 Stragelung (h697210) Homo sapiens cDNA clone IMAGE:354291.3 similar to contains MER22.11 MER20 repetitive element;
1433	14467	27444	3.05	7.0E-05		79821771 NT	Homo sapiens KIA00585 gene product (KIA00585), mRNA
2884	15643		7.94	7.0E-05	AI066552.1	EST_HUMAN	h076105.x1 NC1_CGAP_106 Homo sapiens cDNA clone IMAGE:1991229.3 similar to contains Alu repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) Blast E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3576	10621		0.78	7.0E-06	AA398542.1	EST_HUMAN	EST162026 Thyroid Homo sapiens cDNA 5' and similar to EST containing 11 repeat
3780	10622		5.16	7.0E-06	AW88344.1	EST_HUMAN	OV2-CT00682-260400-173-01 OT0082 Homo sapiens cDNA
5902	10699	32179	0.81	7.0E-06	N98945.1	EST_HUMAN	Y95607.1 Score1_mutable_sclerosis_ZNHHMSP Homo sapiens cDNA IMAGE:278412 5'
8141	22107	35533	0.7	7.0E-06	11420706	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF6851E), mRNA
10200	23165		0.64	7.0E-06	Q81147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	26327	31307	2.85	7.0E-06	BF215972.1	EST_HUMAN	001815227 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4063972 5'
2323	13585	28607	1.27	6.0E-06	BE99785.1	EST_HUMAN	QV2-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
3703	17149	25644	1.08	6.0E-06	BE99785.1	EST_HUMAN	QV2-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4783	19370	28935	2.35	6.0E-06	Q01488	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4794	17311	30703	2.54	6.0E-06	AD40993.1	EST_HUMAN	Q65402.x1 Score1_fetal_liver_spleen_infr.5_31 Homo sapiens cDNA clone IMAGE:1695738 3' similar to contains MER21 MER21 repetitive element
8422	18528	31403	2.21	6.0E-06	AF167441.1	NT	Plus mucosin E-cadherin binding protein E7 mRNA, complete cds
6483	18533	31495	1.05	6.0E-06	AF167441.1	SWISSPROT	PROTEIN XE1
10218	23140		1.52	6.0E-06	AW59132.1	EST_HUMAN	TC-UM0075-10400-365-322 UM0075 Homo sapiens cDNA
13041	26582	31769	1.74	6.0E-06	11419197	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
6178	19254	32467	3.86	5.0E-06	AL182345.2	NT	Homo sapiens chromosome 21 segment H521C046
6171	19538	32784	3.95	5.0E-06	U07591.1	NT	Human ABL gene, exon 1b and intron 1b, and partial 16S04.1 Med protein (16S04.1 Med) gene, complete cds
7444	20410	33762	1.14	6.0E-06	AB007548.1	NT	Homo sapiens gene for ECT2, complete cds
8803	21770	35165	0.49	6.0E-06	AW85697.1	EST_HUMAN	RC1-CT0392-120200-013-02 CT0392 Homo sapiens cDNA
8803	21770	35166	0.48	5.0E-06	AW85697.1	EST_HUMAN	RC1-CT0392-120200-013-02 CT0392 Homo sapiens cDNA
10402	23384	39877	7.1	5.0E-06	AA113922.1	EST_HUMAN	EST185493 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and
12101	24972	38569	2	5.0E-06	Q28039	SWISSPROT	SODIUM AND CHLORIDE DEPENDENT GLYCINE TRANSPORTER 1 (SLYT-1)
12928	28912	31769	2.14	5.0E-06	AL065045.1	EST_HUMAN	HQ0377 Human fetal liver cDNA library Homo sapiens cDNA
848	13714	28635	6.89	4.0E-06	R19297.1	EST_HUMAN	Y945003.1 Score1_invent brain NIH Homo sapiens cDNA clone IMAGE:53254 5' similar to contains A1u repetitive element/contains 11 repetitive element
847	13803	28681	6.33	4.0E-06	AW103544.1	EST_HUMAN	xc6891.1 x1 NC1_OGAP_Exc2 Homo sapiens cDNA clone IMAGE:2685974 3' similar to contains A1u repetitive element/contains element MER21 repetitive element
1337	14371	27540	4.22	4.0E-06	AL334928.1	EST_HUMAN	1833406.x1 NC1_OGAP_Exc2 Homo sapiens cDNA clone IMAGE:2095168 3'
1470	14503	27477	2.88	4.0E-06	BF795612.1	EST_HUMAN	1833406.x1 NC1_OGAP_Exc2 Homo sapiens cDNA clone IMAGE:2095168 3'
2214	15267	28513	3.05	4.0E-06	AW015401.1	EST_HUMAN	OV2-NT0046-200800-250-07 NT0046 Homo sapiens cDNA
3078	19133	29046	0.84	4.0E-06	AF195448.1	NT	UIH-B01-0407-050-01.1 NC1_OGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
							Gallus gallus Dn22 protein (Dn22) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3309	16949	23890	1.1	4.0E-09	AW84295.1	EST_HUMAN	L33-C10214-1/5020-374-B03 C10214 Homo sapiens cDNA
4846	17893	30766	2.18	4.0E-09	A1899909.1	EST_HUMAN	W94C10.1X1 NCI CGAP_Bmd8 Homo sapiens cDNA clone IMAGE:2452962 3' similar to contains element
8944	21811	33200	0.96	4.0E-09	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9132	22118	33545	3.6	4.0E-09	A100690.1	SWISSPROT	Homo sapiens T cell receptor beta locus, TCRBV/TS3A2 to TRBV/TS2 region
10066	22683	39482	1.14	4.0E-09	AJ272265.1	NT	Homo sapiens SPZ2 gene for secreted phosphoprotein 24 precursor, exons 1-8
11778	23693	37454	2.81	4.0E-09	AB007865.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript RUC0486
2173	15189	28209	1.9	3.0E-09	AA700592.1	EST_HUMAN	254608.x1 Soares, field_jiver_gdenn_INRLS_31 Homo sapiens cDNA clone IMAGE:326903 3' similar to contains L1 L1 repetitive element.
2173	15189	28210	1.8	3.0E-09	AA700592.1	EST_HUMAN	254608.x1 Soares, field_jiver_gdenn_INRLS_31 Homo sapiens cDNA clone IMAGE:326903 3' similar to contains L1 L1 repetitive element.
2276	15288		1.89	3.0E-09	AF502895.1	NT	contains L1 L1 L1 repetitive element.
2833	15981	28911	0.95	3.0E-09	A4969218.1	EST_HUMAN	484911 at Soares, field_NHT1 Homo sapiens cDNA, clone IMAGE:1400262 3' similar to contains LTR1.8
3279	16333		2.32	3.0E-09	A857779.1	EST_HUMAN	LTR1 repeat, NSI, CGAP_1111 Homo sapiens cDNA clone IMAGE:2428193 3' similar to TR.060734 C000734
3797	16837	28743	1.12	3.0E-09	BE047084.1	EST_HUMAN	LINE-1/LIKE PROTEIN, contains L1, L2, L1, repetitive element.
3797	16837	29744	1.12	3.0E-09	BE047084.1	EST_HUMAN	NS44123x1 NCI CGAP_1N13 Homo sapiens cDNA clone IMAGE:3124151 3'
4851	17326	30411	0.67	3.0E-08	T60265.1	EST_HUMAN	NS44123x1 NCI CGAP_1N13 Homo sapiens cDNA clone IMAGE:3124151 3'
4534	17815	30593	4.02	3.0E-08	X54819.1	NT	4578510.1 Sindigene ovary (4637217) Homo sapiens cDNA clone IMAGE:72276 6' similar to contains L1 repetitive element
5254	18389	32629	0.74	3.0E-08	A1168412.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-blau, exons 1-5 (preceding alpha-1-microglobulin, N-terminus).
5254	18389	33525	0.66	3.0E-08	A1168412.1	EST_HUMAN	AUT189412 THYROT1 Homo sapiens cDNA clone THYROT101602 3'
5974	20197	33528	0.86	3.0E-08	Z76478.1	NT	H.sapiens low-sorted chromosome 8 Tel fragment, SC09A055
7459	20408		1.9	3.0E-08	BE042684.1	SWISSPROT	H.sapiens low-sorted chromosome 8 Tel fragment, SC09A055
7459	20408	34769	0.76	3.0E-08	BE042684.1	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9632	21898	35417	0.64	3.0E-08	AW382282.1	SWISSPROT	6013362131 FH1, MGC_44 Homo sapiens cDNA clone IMAGE:3698314 5'
12631	26317		6.4	3.0E-09	AW382282.1	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
1303	13304		3.24	2.0E-09	P45695	SWISSPROT	RC05-L10001-86119941-L403 L10001 Homo sapiens cDNA
1572	14605		5.6	2.0E-09	P21414	SWISSPROT	HOMEOBOX PROTEIN GOOSECOCK
2337	16395	29420	2.64	2.0E-09	AB72139.1	EST_HUMAN	POLY(ADP-RIBOSE) POLYMERASE 1 (PARP1)
2474	16478	28901	2.73	2.0E-09	P04929	SWISSPROT	POLY(ADP-RIBOSE) POLYMERASE 1 (PARP1)
							W94603.x1 NCI CGAP_1X111 Homo sapiens cDNA clone IMAGE:2207068 3' similar to contains MER30.b1
							MER30 repetitive element.
							HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2573	15574	25594	1.84	2.0E-06	P08719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3331	15577	29500	1.29	2.0E-06	AV67555.1	EST_HUMAN	AV67555 GJC Homo sapiens cDNA clone GJC0803.3
3774	16816	29728	1.56	2.0E-06	AA173518.1	EST_HUMAN	p202a5-r1 Stragelange ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:595232.5
3783	16824	29732	0.87	2.0E-06	AW49215.1	EST_HUMAN	UHR-BB-alky-95-GUJ s1 NCI CGAP SubB9 Homo sapiens cDNA clone IMAGE:2738178.3
3789	16830	29736	1.74	2.0E-06	AB030906.1	NT	Mus muscular gene for odorant receptor A16, complete cds
6208	16292			2.0E-06	AA974632.1	EST_HUMAN	nc34K01 s1 NCI CGAP LuB Homo sapiens cDNA clone IMAGE:159569.9 similar to contains Alu repetitive element
8241	18314	32544	0.93	2.0E-06	AI39448.1	EST_HUMAN	1857165.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:209241.3 similar to TRC13337
8381	18411	32508	3.37	2.0E-06	AI81942.1	EST_HUMAN	CI1337 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.:
8260	21219		0.81	2.0E-06	AW68629.1	EST_HUMAN	W95603.s1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:341008.3
8426	21393	34066	0.63	2.0E-06	U1228.1	EST_HUMAN	MR5-SN0387.20400-002.02 SNO067 Homo sapiens cDNA
9188	22154		0.61	2.0E-06	AA172497.1	EST_HUMAN	2447R Heart Homo sapiens cDNA clone X447
8200	22196	33598	1.83	2.0E-06	H6205.1	EST_HUMAN	252761 s1 Soares_Pituitary_Island_NSPC0 Homo sapiens cDNA clone IMAGE:413300.3 similar to
9571	22533	35963	0.97	2.0E-06	AF03526.1	NT	TRC49470487 REVERSE TRANSCRIPTASE 1
9571	22533	35964	0.87	2.0E-06	AF03526.1	NT	YAC109-10 Homo sapiens cDNA clone IMAGE:231974.5 similar to pX-174629
9581	22533		0.48	2.0E-06	AA173440.1	EST_HUMAN	KEB1.N1 TYPE II CYTOSKELETAL 8 (HUMAN)
10059	22298	39454	0.92	2.0E-06	N30578.1	EST_HUMAN	Homo sapiens p13capin 3 (GPC3) gene, partial cds and flanking repeat regions
10279	23204		0.81	2.0E-06	AV174896.1	EST_HUMAN	Homo sapiens p13capin 3 (GPC3) gene, partial cds and flanking repeat regions
12111	24681	36361	2.21	2.0E-06	O15533	SWISSPROT	W95943.s1 Soares_Pituitary_Islands_R205weeks_2NbhP89bW Homo sapiens cDNA clone IMAGE:257123
12111	24681	36362	2.21	2.0E-06	O15533	SWISSPROT	AF174896 NRC Homo sapiens cDNA clone NRCX3003.5
12540	25028	31309	2.97	2.0E-06	P23249	SWISSPROT	PYRIN (MARENGOSTRIN)
36	13159	29057	3.02	1.0E-06	O70982	SWISSPROT	PYRIN (MARENGOSTRIN)
658	13724	26849	1.96	1.0E-06	AF084954.1	NT	PROTEIN MOV-10
1445	14478	27454	1.61	1.0E-06	P09125	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH AFFINITY SODIUM-DEPENDENT CARNITINE CO-TRANSPORTER)
1527	14590	27531	1.97	1.0E-06	AL03278.2	NT	Mus muscular DMMB protein (DMMB) mRNA, complete cds
1578	14609	27582	1.22	1.0E-06	AA034141.1	EST_HUMAN	MEROZOITE SURFACE PROTEIN OAZ-8
1578	14609	27582	1.22	1.0E-06	AA034141.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1578	14609	27582	1.22	1.0E-06	AA034141.1	EST_HUMAN	Z00412.s1 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:426862.3 similar to contains Alu repetitive element
1578	14609	27582	1.22	1.0E-06	AA034141.1	EST_HUMAN	Z00412.s1 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:426862.3 similar to contains Alu repetitive element

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4804	17821	30716	3.87	8.0E-07	M285596.1	EST_HUMAN	q8207.x1 Sorex, NHIMP2, S1 Homo sapiens cDNA clone IMAGE187876.3'
4804	17821	30716	3.87	8.0E-07	M285596.1	EST_HUMAN	q8207.x1 Sorex, NHIMP2, S1 Homo sapiens cDNA clone IMAGE187876.3'
5988	18073	31651	6.55	8.0E-07	P21414	SWISSPROT	PO1 POLYPROTEIN [CONTAINS: PROTEASE, REVERSE TRANSCRIPTASE, ENDONUCLEASE]
8335	21304		11.24	8.0E-07	AF135418.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11943	24823	31651	6.78	8.0E-07	T07770.1	EST_HUMAN	ES105660 Fetal brain, Strategene (cat#836206) Homo sapiens cDNA clone HBEN69
12163	25031		9.17	8.0E-07	AF193280.2	NT	Homo sapiens chromosome 21 segment H521C050
5507	18886	31651	0.73	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5507	18886	31651	0.73	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1628	14952	27448	4.99	9.0E-07	AW605556.1	EST_HUMAN	OMG-C10277-221099-029-424-011 CT0277 Homo sapiens cDNA
2500	15503	26530	5.98	8.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing laccase X (laccase-X) gene, partial cds, cytchrome P450 21-
3986	17036		2.25	8.0E-07	P41479	SWISSPROT	HYPOPHOSPHATE 241 KD PROTEIN IN LEF4P33 INTERGENIC REGION
6407	22461	35002	2.17	6.0E-07	AF016887.1	EST_HUMAN	q8407.x1 NC1 CGAP, C016 Homo sapiens cDNA clone IMAGE3314149.3' similar to TRC075920 075920
12462	25889		3.45	6.0E-07	AF016887.1	EST_HUMAN	q8407.x1 NC1 CGAP, C016 Homo sapiens cDNA clone IMAGE3314149.3' similar to TRC075920 075920
320	13147		2.45	6.0E-07	AF016887.1	EST_HUMAN	q8407.x1 NC1 CGAP, C016 Homo sapiens cDNA clone IMAGE3314149.3' similar to TRC075920 075920
1085	14108		2.45	6.0E-07	AF016887.1	EST_HUMAN	q8407.x1 NC1 CGAP, C016 Homo sapiens cDNA clone IMAGE3314149.3' similar to TRC075920 075920
3044	16101		0.89	5.0E-07	AF016887.1	EST_HUMAN	q8407.x1 NC1 CGAP, C016 Homo sapiens cDNA clone IMAGE3314149.3' similar to TRC075920 075920
4676	17897	30984	1.19	5.0E-07	AF140741.1	NT	Homo sapiens OGG-2 homologous protein (OGG-2) gene, partial cds
6242	18315	32348	1.23	5.0E-07	U65057.1	NT	Homo sapiens OGG-2 homologous protein (OGG-2) gene, partial cds
7296	20001	33500	1.68	5.0E-07	A335081.1	EST_HUMAN	q8407.x1 NC1 CGAP, C016 Homo sapiens cDNA clone IMAGE3314149.3' similar to TRC075920 075920
7296	20001	33501	1.68	5.0E-07	A335081.1	EST_HUMAN	q8407.x1 NC1 CGAP, C016 Homo sapiens cDNA clone IMAGE3314149.3' similar to TRC075920 075920
7571	20534	33982	15.74	5.0E-07	AW070985.1	EST_HUMAN	q8407.x1 NC1 CGAP, C016 Homo sapiens cDNA clone IMAGE3314149.3' similar to TRC075920 075920
8618	21886	35002	0.87	5.0E-07	Q0WUQ1	SWISSPROT	ADAM-TS1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
8835	21602		1.86	5.0E-07	P09560	SWISSPROT	ADAM-TS1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
10732	23654	37147	5.39	5.0E-07	A008597.1	EST_HUMAN	ADAM-TS1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
11845	24728	39314	3.52	5.0E-07	P11087	SWISSPROT	ADAM-TS1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
11806	24787		2.12	5.0E-07	A1271735.1	NT	ADAM-TS1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
12842	26780		4.14	5.0E-07	AW605556.1	EST_HUMAN	ADAM-TS1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top 5) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4024	17652	28964	1.91	4.0E-07/AL039800.1	EST_HUMAN	EST_HUMAN	wash4b5.x1 NCI G0AP_C03 Homo sapiens cDNA clone IMAGE:264497 3'
7394	20334	33864	0.93	4.0E-07/AL027265.1	NT	EST_HUMAN	Human sapiens SPF2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7482	20448	33864	1.33	4.0E-07/02Q2V8	SWISSPROT	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHD1A)
7482	20448	33864	1.33	4.0E-07/02Q2V8	SWISSPROT	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHD1A)
6255	71224	33662	0.52	4.0E-07/AL183207.2	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
6255	71224	33662	0.52	4.0E-07/AL183207.2	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
12458	23504	36904	0.48	4.0E-07/BE014193.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
12458	23504	36904	0.48	4.0E-07/BE014193.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
10468	23810	36905	0.46	4.0E-07/AL183218.2	NT	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
10468	23810	36905	0.46	4.0E-07/AL183218.2	NT	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
10982	23810	37108	0.47	4.0E-07/AL183218.2	NT	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
11284	24234	37760	2.6	4.0E-07/AL176528.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
11284	24234	37761	2.6	4.0E-07/AL176528.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
11655	24495	37761	2.72	4.0E-07/BE001628.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
441	13515	28446	4.71	3.0E-07/AL17619.1	NT	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
585	13553	28597	3.11	3.0E-07/AL271735.1	NT	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
1375	14409	27370	2.82	3.0E-07/M69449.1	NT	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
1530	14903		2.48	3.0E-07/M64871.1	NT	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
2082	15080		1.91	3.0E-07/AL52785.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
2298	15308	28330	2.59	3.0E-07/M69148.1	NT	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
2477	15481	28505	6.03	3.0E-07/BE003071.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
2477	15481	28508	6.03	3.0E-07/BE003071.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
3047	16041	28018	0.8	3.0E-07/AL039799.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
3175	16228	28144	1.71	3.0E-07/P23749	SWISSPROT	SWISSPROT	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
4700	17727		1.68	3.0E-07/AL52785.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
4758	17718	36073	4.48	3.0E-07/AL52785.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
4758	17718	36760	0.81	3.0E-07/AL70728.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
5103	16113	30685	2.02	3.0E-07/TS7690.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
5103	18143	30686	2.02	3.0E-07/TS7690.1	EST_HUMAN	EST_HUMAN	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
5749	18843	32028	9.02	3.0E-07/068807	SWISSPROT	SWISSPROT	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'
6585	19165	32377	0.73	3.0E-07/AL02480	SWISSPROT	SWISSPROT	WASH4B5.X1 NCI G0AP_L034_1 Homo sapiens cDNA clone IMAGE:265654 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6801 18914	7762 20705	34074	5.12	3.0E-07	AA31675.1	EST_HUMAN	cc04c10.41 NCL CGAP CG81 Homo sapiens cDNA clone IMAGE:133690 3'
7925 20898			3.26	3.0E-07	AW787168.1	EST_HUMAN	QV1-UN0036-200300-15-022 UN0038 Homo sapiens cDNA
13083 28514				3.0E-07	AB91095.1	EST_HUMAN	W29111.x1 NCL CGAP CG81 Homo sapiens cDNA clone IMAGE:2291037 3' similar to contains Alu repetitive element/contains element MSR1 MSR1 repetitive element;
31 13161	20051		7.27	3.0E-07	AJ132452.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
155 13259	20165		4.19	2.0E-07	AF262883.1	NT	Homo sapiens TRP2-interacting leucine RAP1 protein (RAP1) mRNA, complete cds
155 13259	20165		6.54	2.0E-07	L77690.1	NT	Homo sapiens D(George syndrome critical region, telomeric end
183 13283	20209		6.54	2.0E-07	U38848.1	NT	Homo sapiens D(George syndrome critical region, telomeric end
749 13810	20751		152.91	2.0E-07	U38848.1	NT	Fig1 (ubiquitin-like-cytosolic)(vascular) actin gene, complete cds
749 13810	20751		1.29	2.0E-07	AF033300.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
749 13810	20751		1.29	2.0E-07	AF033300.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
760 13820			0.87	2.0E-07	P11969	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE : ENDONUCLEASE]
642 13695	26047		3.12	2.0E-07	AA23390.1	EST_HUMAN	Z08807.at Stratiotes NT2 neuronal precursor 93720 Homo sapiens cDNA clone IMAGE:88599 3' similar to gp131860 GLYCOPHORN A PRECURSOR [HUMAN] contains Alu repetitive element;
643 13695	26048		7.18	2.0E-07	T8042.1	EST_HUMAN	X15694.at Stratiotes lung (937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1167 14208	27102		1.16	2.0E-07	U28706	SWISSPROT	18 AUTANTOXIN
1604 14208	27102		2.35	2.0E-07	U28706	SWISSPROT	HYPOPHOSPHATIDYL CO PROTEIN C27.10 IN CHROMOSOME 1
3833 16793	27513		0.85	2.0E-07	BF13397.1	EST_HUMAN	X17618.at NCL CGAP CG81 Homo sapiens cDNA clone IMAGE:405481 5'
3700 16743	28455		11.94	2.0E-07	AF133848.1	EST_HUMAN	X17618.at NCL CGAP CG81 Homo sapiens cDNA clone IMAGE:405481 5'
4195 17228	30115		1.42	2.0E-07	AB163883.1	EST_HUMAN	RC3/NK0036-350002-02-311 NK0038 Homo sapiens cDNA
4177 25520	31391		0.71	2.0E-07	AF133848.1	EST_HUMAN	U1-H-815-465-01-01-01 NCL CGAP CG81 Homo sapiens cDNA clone IMAGE:273408 3'
6702 25558	33371		0.9	2.0E-07	AF133848.1	EST_HUMAN	955503.11 Sarcos. beta. NMT Homo sapiens cDNA clone IMAGE:183517 3'
6520 18974	34153		1.93	2.0E-07	AJ289715.1	EST_HUMAN	955503.11 Sarcos. beta. NMT Homo sapiens cDNA clone IMAGE:183517 3'
6832 19895	33178		0.81	2.0E-07	AA72963.1	EST_HUMAN	955503.11 Sarcos. beta. NMT Homo sapiens cDNA clone IMAGE:183517 3'
8813 21760	34780		4.23	2.0E-07	AF176690.1	EST_HUMAN	AV176360 HTO Homo sapiens cDNA clone HTCA002 5'
9443 22002	35400		0.96	2.0E-07	AA035198.1	EST_HUMAN	322750.11 Sarcos. pregnant. uerue. NHPU Homo sapiens cDNA clone IMAGE:471698 3'
10119 23045	10119		1.8	2.0E-07	AA035198.1	EST_HUMAN	Homo sapiens chromosome 21 segment H521C103
10380 23562	37062		6.11	2.0E-07	AW892507.1	EST_HUMAN	CMA-NK0003-280300-124-005 NK0003 Homo sapiens cDNA
10955 23175	37272		0.92	2.0E-07	P00761	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/G3 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GB9) (PBF2)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9653	22636		0.54	6.0E-08	AA427075.1	EST_HUMAN	ds56c0.5s1 NCL_GGAP_G031 Homo sapiens cDNA clone IMAGE:135398 3' similar to contains MER12 repetitive element.
11744	24629	38208	1.91	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ; ENONUCLEASE)
85	13201	25123	3.22	5.0E-08	AL183303.2	NT	Homo sapiens chromosome 21 segment 185210183
2245	16289	28285	1.95	5.0E-08	AA400851.1	EST_HUMAN	COMPLEMENT C2 PRECURSOR (C2/C3 CONVERTASE)
12185	25032		10.16	5.0E-08	P06691	SWISSPROT	CYCLOPHILIN A (CYCLOPHILIN A13 CYTO23) Homo sapiens cDNA
12342	25162	31814	1.93	5.0E-08	AW651878.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
1775	14804	27789	1.07	4.0E-08	P28723	SWISSPROT	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
10093	22890		0.82	4.0E-08	P06857	SWISSPROT	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
10893	22815		0.85	4.0E-08	AI016542.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
10732	23874	37171	3.67	4.0E-08	AI050027.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
11411	24335	37889	1.51	4.0E-08	AA430927.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
11411	24335	37890	1.51	4.0E-08	AA430927.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
11283	24370	37607	3.11	4.0E-08	BF652463.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
11283	24370	37608	3.11	4.0E-08	BF652463.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
12300	25007		4.96	4.0E-08	W76150.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
12300	25468		1.84	4.0E-08	AI043493.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
3438	16465	29404	0.94	3.0E-08	AI03242.1	NT	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR
5692	18787	31938	3.05	3.0E-08	BE016348.1	EST_HUMAN	DOUGAL CENTRAL PATTERNING TOLL-RECEPTOR PRECURSOR

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) E-Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7168	18390	31345	4.23	3.0E-08	AF792737.1	EST_HUMAN	4q27b11 y6NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:164046 5'
7787	20740	34113	1.41	3.0E-08	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C046
8025	20962		3.85	3.0E-08	AI438352.1	EST_HUMAN	9q30b0.x1 Scores_NSIF_Fq_giv_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:216273 3' similar to TR-Q13337 Q13337 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
10258	23185		0.57	3.0E-08	AF065098.1	NT	Homo sapiens MHC class I region
12157	25013		2.76	3.0E-08	RI18420.1	EST_HUMAN	XP0204.r1 Scores Trifid brain IN1B Homo sapiens cDNA clone IMAGE:30948 6' similar to contains AU repetitive element
2077	13308		10.54	2.0E-08	AW30296.1	EST_HUMAN	x37708.x1 NCL_CGAP_L028 Homo sapiens cDNA clone IMAGE:2767139 3'
230	13330		8.83	2.0E-08	AA42598.1	EST_HUMAN	2v4807.r1 Scores_tota_fewa_NB2HF8_5w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains AU repetitive element/contains element MER18 repetitive element ;
497	13659	28492	1.3	2.0E-08	AF119348.1	NT	Gallus gallus Dactyl protein (Dactyl) mRNA, complete cds
861	13727	23651	9.73	2.0E-08	AW38438.1	EST_HUMAN	NR0-OT0086-240200-007.g8 OT0080 Homo sapiens cDNA
902	13727	23652	9.73	2.0E-08	AW38438.1	EST_HUMAN	NR0-OT0086-240200-007.g8 OT0080 Homo sapiens cDNA
1346	14381		17	2.0E-08	BE230477.1	EST_HUMAN	80116527.F1 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3130859 5'
1795	14784	27350	1.83	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1872	14897		3.87	2.0E-08	AF176271.1	EST_HUMAN	3v4807.r1 NCL_CGAP_FNT1 Homo sapiens cDNA clone IMAGE:3364169 5'
2550	15652		1.7	2.0E-08	K02378.1	NT	3v4807.r1 NCL_CGAP_FNT1 Homo sapiens cDNA clone IMAGE:273749 5'
3221	16276	29200	8.15	2.0E-08	C42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3221	16276	29201	8.15	2.0E-08	C42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3873	16912		1.62	2.0E-08	AW113320.1	EST_HUMAN	RCS-3710192-15109-012-03 ST0197 Homo sapiens cDNA
4104	17138	39033	0.68	2.0E-08	AB2388.1	NT	Homo sapiens beta case, alternatively spliced products, complete cds
4434	17481		1.2	2.0E-08	AA459040.1	EST_HUMAN	af22507.r1 NCL_CGAP_CG31 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1/2 L1 repetitive element ;
4694	18009		2.97	2.0E-08	AW172881.1	EST_HUMAN	ht1708.x2 NCL_CGAP_CNA1 Homo sapiens cDNA clone IMAGE:2010327 3' similar to contains AU repetitive element
5719	18413	31922	1.26	2.0E-08	AA613264.1	EST_HUMAN	ab0811.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18.83
5932	19018	32213	0.99	2.0E-08	AW088924.1	EST_HUMAN	x32204.x1 NCL_CGAP_DV03 Homo sapiens cDNA clone IMAGE:1377189 3'
8337	21306	34721	1.89	2.0E-08	PI10272	SWISSPROT	MER18 MER18 repetitive element ;
9447	21416	34829	1.47	2.0E-08	AA400121.1	EST_HUMAN	POLYPROTEIN [CONTAINS: PROTEASE, REVERSE TRANSCRIPTASE, ENDONUCLEASE]
9440	22004		0.77	2.0E-08	AU139078.1	EST_HUMAN	af02205.x1 Shiga toxin fetal ref1a 837822 Homo sapiens cDNA clone IMAGE:839874 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (100) Hit DUSTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6828	16886		1.59	8.0E-09/AJ27015.1	EST_HUMAN	repetitive element;	cu86c11.x1 NC_023647 Homo sapiens cDNA clone IMAGE:197894 3' similar to contains L1.8 L1
7479	20445	33301	7.91	8.0E-09/AJ65000.1	EST_HUMAN	contains MBR1.L1 MBR1 repetitive element;	q42607.x1 Soares_fetal_hes1 NBH16W Homo sapiens cDNA clone IMAGE:1732164 3' similar to
8333	21302	34719	3.04	8.0E-09/AJ690180.1	EST_HUMAN		CMO-NY1004-100000-273-a08 NN1004 Homo sapiens cDNA
9340	22205		2.64	8.0E-09/AJ69892.1	EST_HUMAN		q74408.L1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:189276 3'
3821	16894		1.91	7.0E-09/B6842.1	NT		Homo sapiens DNA for 3-ketocoad thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4034	17072		1.22	7.0E-09/J50871.1	EST_HUMAN		Human Familial Alzheimer's disease (STM2) gene, complete cds
8234	21203		0.99	7.0E-09/BF108795.1	EST_HUMAN		contains MBR20.b2 MBR20 repetitive element;
8392	21351		0.91	7.0E-09/AJ25200.1	EST_HUMAN		z86003.r1 Soares_NHHPUL_S1 Homo sapiens cDNA clone IMAGE:691662 5' similar to contains L1.12 L1
9915	22559	39038	3.05	7.0E-09/J6793.1	NT		repetitive element;
10343	23455	39560	1.17	7.0E-09/BE24650.1	EST_HUMAN		g61m117351.NHL_NBC_18 Homo sapiens cDNA clone IMAGE:351834 5'
10711	23633		0.59	7.0E-09/AJ65628.1	EST_HUMAN		z56107.1 Soares_retina V24-IR Homo sapiens cDNA clone IMAGE:331186 3' similar to contains L1.12 L1
11033	23695		3.65	7.0E-09/J7350.1	EST_HUMAN		W53432.s1 Soares_fetal liver spleen_NFL_S1 Homo sapiens cDNA clone IMAGE:121818 3'
2102	15778		0.39	8.0E-09/LJ00493.1	EST_HUMAN		DXF24342.CS314.L1 834 (Synonym: Nica3) Homo sapiens cDNA clone IMAGE:104024 similar to contains L1.12 L1
4059	17095	20990	0.98	8.0E-09/AJ657940.1	EST_HUMAN		repetitive element;
5017	19031	30917	5.44	8.0E-09/BE199421.1	EST_HUMAN		PM1-HT0527-160200-201-H05 HT0327 Homo sapiens cDNA
5444	18569	31467	5.55	8.0E-09/AJ195784.1	EST_HUMAN		xs8506.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8922	21883	33515	0.88	8.0E-09/BE191863.1	EST_HUMAN		MR3-HT1446-260300-201-H12 HT0449 Homo sapiens cDNA
8531	22404	35942	2.12	8.0E-09/4503710	NT		Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10039	23591		4.42	8.0E-09/AF20023.2	NT		Homo sapiens thapsigargin-specific kinase substrate (TSKS) gene, complete cds
1413	14449	27181	4.43	8.0E-09/BE149294.1	EST_HUMAN		RC2-HT0262-120200-01-H10 HT0262 Homo sapiens cDNA
1870	14583	27894	1.02	8.0E-09/AL163284.2	NT		Homo sapiens chromosome 21 segment HS21084
6550	16911	32672	2.31	8.0E-09/AJ359454.1	EST_HUMAN		EST189148 Fetal lung Homo sapiens cDNA 5' end
							Human gamma T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRV1, TRV2, TRV3, TCRBV2/ISIP, TCRBV2/23A2N1, TCRBV9/5A1N1, TCRBV9/5A1N1, TCRBV6/5A1N1, TCRBV1/5S3, TCRBV/5P7, TCRBV/5SA2T, TCRBV/1932A1T, TCRBV/952A2P1, TCRBV/752A1N4T, TCRBV/1359/135P
7025	18357	31277	0.59	8.0E-09/U96056.1	NT		

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Table 4
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5168	18207	31081	0.68	2.0E-09	M2161.1	NT	Human transposon-like element mRNA
5008	18888	32081	0.69	2.0E-09	A004092.1	EST_HUMAN	d47006.atl Source: testis_NHT Homo sapiens cDNA clone IMAGE:101897.9
6273	19346	32081	0.65	2.0E-09	AL03249.2	NT	Homo sapiens chromosome 21 segment HS210049
6947	20171		0.8	2.0E-09	AA357407.1	EST_HUMAN	EST18142 Kidney IX-Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7684	20542	34006	7.6	2.0E-09	AA451430.1	EST_HUMAN	z63008.1 Source: testis_Nb2F8_5w Homo sapiens cDNA clone IMAGE:706187.6 similar to contains Alu repetitive element
7768	20719	34062	0.63	2.0E-09	W28834.1	EST_HUMAN	92311 Human retina cDNA randomly primed sublibrary/Homo sapiens cDNA
8128	21083	34461	0.62	2.0E-09	AW862126.1	EST_HUMAN	NR1-CT03932-24/0200-105-106 CT03932 Homo sapiens cDNA
9002	22028	35452	2.25	2.0E-09	AJ271735.1	NT	Homo sapiens Xa pseudosubclonal region, segment 1/2
12705	13871		22.38	2.0E-09	X18674.1	NT	H sapiens PA08P1.1 gene for NAD(+) ADP-ribosyltransferase
12772	28975		1.07	2.0E-09	AA28070.1	EST_HUMAN	nc110032.1 NC1_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element
12778	28929		1.47	2.0E-09	AW301837.1	EST_HUMAN	X58402.1 NC1_CGAP_K411 Homo sapiens cDNA clone IMAGE:2788234.3
12813	25462		1.98	2.0E-09	U62668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
11111	14195	27105	1.1	1.0E-09	531623	NT	Homo sapiens CGAAT-box-binding transcription factor (CBF2) mRNA
11111	14195	27105	1.1	1.0E-09	531623	NT	Homo sapiens CGAAT-box-binding transcription factor (CBF2) mRNA
1638	14670		0.31	1.0E-09	AJ22641.1	NT	Homo sapiens 89912 contig between NAL1 and CBR1 on chromosome 21/222 segment 1/3
2510	15513		1.16	1.0E-09	A350086.1	EST_HUMAN	90461.1 NC1_CGAP_P1/25 Homo sapiens cDNA clone IMAGE:2016812.3 similar to contains MER12.12 MER12 repetitive element
2000	19559	28378	1.83	1.0E-09	A300171.1	NT	Homo sapiens basic transcription factor 2 p44 (b2p44) gene, partial cds, nuclear apoptosis inhibitory
2037	15905	28515	4.07	1.0E-09	V28929.1	NT	Human 10p11 and 10p12 genes containing a 10p11-10p12 gene overlap
2037	15905	28515	4.07	1.0E-09	V28929.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3051	16108	26222	0.69	1.0E-09	BE031440.1	EST_HUMAN	601059022.1 NHX_MJC_10 Homo sapiens cDNA clone IMAGE:344317.5
4838	17853		5.63	1.0E-09	AA719297.1	EST_HUMAN	5319003.atl Source: spinal_dorsal_XBPPO Homo sapiens cDNA clone IMAGE:444028.3 similar to contains Alu repetitive element/containing element MER22 repetitive element
9102	18171	31050	0.84	1.0E-09	T00216.1	EST_HUMAN	XC22608.1 Sitagliptin kind (6637210) Homo sapiens cDNA clone IMAGE:81424.9 similar to contains Alu repetitive element/containing MER28 repetitive element
5551	18977	31640	0.82	1.0E-09	AL63283.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS210083
9530	19016	32211	1.35	1.0E-09	U07000.1	NT	Homo sapiens chromosome 21 segment HS210083
6267	19340	32572	3.11	1.0E-09	P29804	SWISSPROT	CIRCUINPROPOZOITE PROTEIN PRECURSOR (CS)
8113	21050	34449	0.63	1.0E-09	AV728545.1	EST_HUMAN	AV728545 HTG Homo sapiens cDNA clone HTG01007.9
8733	21701	35127	0.87	1.0E-09	A688474.1	EST_HUMAN	wd3805.atl Source: VHL_T_CGC_S1 Homo sapiens cDNA clone IMAGE:233487.1 similar to contains MER23.1 MER23 repetitive element

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Table 4
Cytokines Expressed in Bone Marrow

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Table 4
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12221	20098		1.64	9.0E-10	AW971620.1	EST_HUMAN	EST394012 IMAGE:resseques, IMAGE: Homo sapiens cDNA
781	19321		5.01	5.0E-10	AL046804.1	EST_HUMAN	DKFZ34342N9.1 134 (synonym: Hies3) Homo sapiens cDNA clone DKFZ34342N9.5
3459	16335	29460	1.63	5.0E-10	Q01039	SWISSPROT	HYPOPHOSPHATASE 1
5028	18040	30023	1.1	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7544	20507		1.74	5.0E-10	BF087591	EST_HUMAN	60122184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413.5
9834	22847	35203	1.98	5.0E-10	P34678	SWISSPROT	HYPOPHOSPHATASE 1
9834	22847	35204	1.98	5.0E-10	P34678	SWISSPROT	HYPOPHOSPHATASE 1
111	13222		1.27	4.0E-10	AZ21083.1	EST_HUMAN	q95669.x1 Sorensen, placenta, bioRxiv, 2N14P1625W Homo sapiens cDNA clone IMAGE:1759049.3
55	13551	28265	0.75	4.0E-10	A4976260.1	EST_HUMAN	similar to contains L188.021 L188 repetitive element
2012	15033	26043	1.4	4.0E-10	AW594709.1	EST_HUMAN	np58403.x1 NC_023647.3 Homo sapiens cDNA clone IMAGE:524648.3
2680	15581	28500	5.49	4.0E-10	AL103503.2	NT	np58403.x1 NC_023647.3 Homo sapiens cDNA clone IMAGE:204844.3 similar to contains ALU repetitive element
7382	20932	33703	17.71	4.0E-10	AF224690.1	NT	Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
10555	24737	36771	0.53	4.0E-10	AW202343.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
10812	23733	37283	0.87	4.0E-10	U207342.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
10933	23953	37569	0.45	4.0E-10	BE166208.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
10933	23953	37569	0.45	4.0E-10	BE166208.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
916	13970	28924	1.8	3.0E-10	N61113.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
1353	14389		4.9	3.0E-10	AV05150.1	NT	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
4595	17869	30480	1.04	3.0E-10	AL163203.2	NT	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
5530	18628	31554	1.06	3.0E-10	NS0106.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
9327	19397	32539	4.03	3.0E-10	BE020670.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
9469	18551	32501	3.08	3.0E-10	BE020670.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
8036	20973	34367	1.42	3.0E-10	AV743302.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
8036	20973	34368	1.42	3.0E-10	AV743302.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
9082	22048	35471	1.04	3.0E-10	H67208.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
9404	22369	35503	1.8	3.0E-10	AW560731.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)
9404	22369	35504	1.8	3.0E-10	AW560731.1	EST_HUMAN	U183233.1 Homo sapiens chromosome 21 segment 13521C103 (IMAGE203)

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Table 4
Cytokines Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Descriptor
5060	2246		0.73	3.0E-10	AF20903.1	NT
10028	23749		2.05	3.0E-10	AF20903.1	EST_HUMAN
10027	23749		1.78	3.0E-10	AF20903.1	EST_HUMAN
10027	10957		1.057	1.3E-09	AF20903.1	EST_HUMAN
12865	25458		1.958	2.0E-10	AF20903.1	EST_HUMAN
31	13157	26028	0.81	2.0E-10	AF20903.1	SWISSPROT
37	13157	26038	1.55	2.0E-10	AF20903.1	SWISSPROT
1913	13157		1.88	2.0E-10	U06071.1	NT
2550	16057		0.68	2.0E-10	BF75947.1	EST_HUMAN
5901	18938		3.12	2.0E-10	U29640	SWISSPROT
6379	1947	32583	1.55	2.0E-10	AF280107.1	NT
7005	20560	33920	6.24	2.0E-10	BE791082.1	EST_HUMAN
8347	21319	34730	0.54	2.0E-10	U29609	SWISSPROT
8347	21319	34731	0.54	2.0E-10	U29609	SWISSPROT
9957	22800		0.85	2.0E-10	BF34565.1	EST_HUMAN
1509	14542		2.84	1.0E-10	AF287707.1	EST_HUMAN
1811	14643		3.27	1.0E-10	AF287707.1	EST_HUMAN
2596	15587		1.92	1.0E-10	AF282001.1	EST_HUMAN
3511	16557	29481	0.81	1.0E-10	AF282001.1	EST_HUMAN
3250	16958		0.81	1.0E-10	AF282001.1	EST_HUMAN
3585	18958		0.34	1.0E-10	AF282001.1	EST_HUMAN
4043	17081		6.46	1.0E-10	AF219841.1	NT
4154	17185	30072	5.55	1.0E-10	U52112	NT
4154	17185	30073	5.55	1.0E-10	U52112	NT
4180	17181	30083	2.48	1.0E-10	AB031086.1	NT

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4199	17200		2.63	1.0E-10	M30623.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, test exon
5212	18221		0.62	1.0E-10	A077745.1	EST_HUMAN	w8204.x1 Source: fetal liver; spleen, NFIL3, S1 Homo sapiens cDNA clone IMAGE:2847616 3' similar to contains MER31.1 MER31 repetitive element;
6875	19028	33226	0.91	1.0E-10	A683123.1	EST_HUMAN	ng87a25.at NC1, CGAP, C69 Homo sapiens cDNA clone IMAGE:1183704 3'
6991	20214	33543	0.49	1.0E-10	A003523.1	NT	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7718	20873		0.99	1.0E-10	A093548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7947	20888	34279	0.63	1.0E-10	AU126584.1	EST_HUMAN	AU12684 NT2RP2 Homo sapiens cDNA clone NT2RP2003761 5'
8382	21550	34068	1.11	1.0E-10	AW-08900.1	EST_HUMAN	IB_044 Fetal brain library Homo sapiens cDNA
9002	21968		1.1	1.0E-10	A288340.1	EST_HUMAN	gm04e10.x1 NC1, CGAP, Lu6 Homo sapiens cDNA clone IMAGE:1800374 3' similar to contains L1, L1 L1 repetitive element;
10562	23484		3.95	1.0E-10	A081898.1	EST_HUMAN	zz23p06.l1 Strikagene neuroepithelium NT2RAM 937234 Homo sapiens cDNA clone IMAGE:548314 5'
11259	24271	37734	3.25	1.0E-10	A036280.1	EST_HUMAN	cy65053.x1 Source: fetal liver; spleen, NFIL3, S1 Homo sapiens cDNA clone IMAGE:1072661 3'
12166	18354		2.46	1.0E-10	A077244.1	NT	H. sapiens DNA, DMB, HLA-2T, JP22, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 6, 13 and 14
261	3357	26382	0.98	1.0E-10	A077244.1	EST_HUMAN	DKFZ10331201026.216-c8 H10283 Homo sapiens cDNA
2114	15131	28161	6.21	0.0E-11	AL134395.1	EST_HUMAN	DKFZ56470228.11 5'UT (Pharynx; hb11) Homo sapiens cDNA clone DKFZ56470228 5'
2114	15131	28162	6.21	0.0E-11	AL134395.1	EST_HUMAN	DKFZ56470228.11 5'UT (Pharynx; hb11) Homo sapiens cDNA clone DKFZ56470228 5'
3394	16443	26370	2.6	0.0E-11	AL134395.1	EST_HUMAN	DKFZ56470228.11 5'UT (Pharynx; hb11) Homo sapiens cDNA clone DKFZ56470228 5'
3394	16443	26371	2.6	0.0E-11	AL134395.1	EST_HUMAN	DKFZ56470228.11 5'UT (Pharynx; hb11) Homo sapiens cDNA clone DKFZ56470228 5'
4328	17552	30440	0.72	0.0E-11	A4715985.1	EST_HUMAN	acc3801.at Strikagene embryo brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5654	18760		3.89	0.0E-11	BE079780.1	EST_HUMAN	RC6-B10627-140200-011-E06 B10627 Homo sapiens cDNA
10514	23436	39534	1.22	0.0E-11	A4324690.1	EST_HUMAN	EST17872 Cervicalium II Homo sapiens cDNA 5' end
10514	23436	39535	1.22	0.0E-11	A4324690.1	EST_HUMAN	EST17872 Cervicalium II Homo sapiens cDNA 5' end
12546	20289	31809	4.59	0.0E-11	C16635.1	EST_HUMAN	C16635 Cervicalium human sort1 mRNA (46572) Homo sapiens cDNA clone GEN-508808 5'
3133	16190		8.85	0.0E-11	H19071.1	EST_HUMAN	yt33111.at Source: adult brain N264-B857 Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4071	17109	30033	4.35	0.0E-11	NH2312.1	EST_HUMAN	yt46506.at1 W. Kozmin, Olfactory Epithelium Homo sapiens cDNA clone IMAGE:265589 3'
5890	18678	32170	0.65	0.0E-11	AW674916.1	EST_HUMAN	yt45111.x1 NC1, CGAP, Bm50 Homo sapiens cDNA clone IMAGE:2600682 3'
6829	19883		0.65	0.0E-11	AW169158.1	EST_HUMAN	MER10 repetitive element;
1442	14475	27452	1.87	7.0E-11	A4330442.1	EST_HUMAN	EST134392 Embryo, 6 week1 Homo sapiens cDNA 5' end

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Table 4
Single Xlon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3885	18625	28834	1.11	7.0E-11	AJ27546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8843	21810	35229	2.79	7.0E-11	AF163884.1	NT	Homo sapiens SNCA, isoform (SNCA) gene, complete cds, alternatively spliced
10590	25512		1.19	7.0E-11	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ; ENONUCLEASE)
4121	13465	26421	6.97	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGF) gene, complete cds
412	13465	26422	6.97	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGF) gene, complete cds
6884	19638	33232	0.88	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from Hlamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
7657	20580	34281	3.22	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8707	21675	35100	7.37	6.0E-11	AJ727689.1	EST_HUMAN	AV727689 HTCC Homo sapiens cDNA clone HTCC0308.5
6666	22621	39072	0.42	6.0E-11	BC065509.1	EST_HUMAN	CAC4810281-407189-387-430 B10281 HS21C083 cDNA
12	13132	26030	0.75	5.0E-11	AL162983.2	NT	Homo sapiens chromosome 21 segment HS21C083
3377	13132	26030	1.31	5.0E-11	AL162983.2	NT	Homo sapiens chromosome 21 segment HS21C083
4250	17585	31617	1.51	5.0E-11	P48034	SWISSPROT	CD58 MOLECULE EXPRESSED
6650	19722	32697	1.81	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7774	20727	34069	1.91	5.0E-11	AL167090	NT	Homo sapiens proteobacterin beta 3 (PDBH3), mRNA
1461	14434		1.88	4.0E-11	AJ438042.1	EST_HUMAN	zfp012.11 Soares, testis, NHT Homo sapiens cDNA clone IMAGE730559.5
2802	15764	28812	7.63	4.0E-11	BE888552.1	EST_HUMAN	BT575755(F1) NH_MGC_71 Homo sapiens cDNA clone IMAGE3905265.5
2881	16039	28802	0.82	4.0E-11	AL162847.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
4649	17070	30557	1.24	4.0E-11	P40568.1	EST_HUMAN	HUMSLP1059 Human brain cDNA Homo sapiens cDNA clone 089
5021	19979	32457	3.27	4.0E-11	P20295	SWISSPROT	PRE-MIRNA SPLICING FACTOR RHA HELICASE PRP2
7197	20221	33552	0.54	4.0E-11	A4442630.1	EST_HUMAN	zsf6910.7 Soares, testis, NHT Homo sapiens cDNA clone IMAGE757965.5 similar to TR-G1055250
7900	20561		3.87	4.0E-11	AJ224659.1	NT	G1055250 P1-HEROMONE RECEPTOR VM4.1
9720	22891		1.86	4.0E-11	BE109425.1	EST_HUMAN	Homo sapiens mammodioid, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) gene, complete cds
10020	22947	38415	0.86	4.0E-11	AJ609759.1	EST_HUMAN	RC110258-210100-013-009 HT0255 Homo sapiens cDNA
12745	25360	31750	1.56	4.0E-11	11545732	NT	Hb2g12.x1 NCI, COA2_Bm23 Homo sapiens cDNA clone IMAGE2109530.3 similar to WP-2K353.1 CE00845
1488	14321	27404	2.55	3.0E-11	6079077	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
4305	17334		1.37	3.0E-11	AJ309248.1	EST_HUMAN	Mus musculi expressed in non-neuronal cells 2, protein (NM228) (Nm22), mRNA
851	14014	26987	1.48	2.0E-11	AJ150502.1	EST_HUMAN	EST1180720 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
							qf82c04.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE1752102.3 similar to contains MER10.03
							MER10 repetitive element

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Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID: NO.	Expression Signal	Most Similar (BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1189	14239	27189	4.46	2.0E-11	R24807.1	EST_HUMAN	Y93612.71 Sources infant brain 1N1B Homo sapiens cDNA clone IMAGE:353144 5'
1189	14239	27187	4.46	2.0E-11	R24807.1	EST_HUMAN	Y93612.71 Sources infant brain 1N1B Homo sapiens cDNA clone IMAGE:353144 5'
1617	14646	27624	5.86	2.0E-11	117432.1	NT	Gallus gallus rhu-globin, beta-4' globin, beta-A' globin, epsilon-globin, and epsilon' receptor-like protein
1617	14646	27624	5.86	2.0E-11	117432.1	NT	Gallus gallus rhu-globin, beta-4' globin, beta-A' globin, epsilon-globin, and epsilon' receptor-like protein
1620	14683	27629	1.25	2.0E-11	A1126371.1	EST_HUMAN	gq51010.1 Sources pregnant uterus NHPRU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gq1126322 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN) contains L1, L1
3211	18266	28186	8.4	2.0E-11	AF083913.1	SW SPSPROT	Human endogenous retrovirus HERV-P/147D
3337	18398	28095	1	2.0E-11	A478617.1	EST_HUMAN	IMP400241 NCI, CGAP, K411 Homo sapiens cDNA clone IMAGE:2161068 3'
3375	18405	28350	0.71	2.0E-11	Q10473	SW SPSPROT	POLYPEPTIDE NACETYLGLUTOSAMINYLTRANSFERASE (UDP-GALNACT-6-ACETYLGLUTOSAMINYLTRANSFERASE) (UDP-GALNACT-6-ACETYLGLUTOSAMINYLTRANSFERASE) (GALNACT-6-ACETYLGLUTOSAMINYLTRANSFERASE)
3508	18554	1	1.09	2.0E-11	AF252653.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene exon 5
4427	17028	32537	1.39	2.0E-11	AF263573.1	EST_HUMAN	RC3-37105-11-0230-0114-0518 B10318 Homo sapiens cDNA
4656	17658	32537	0.96	2.0E-11	AF263573.1	EST_HUMAN	RC3-37105-11-0230-0114-0518 B10318 Homo sapiens cDNA
4656	17658	32537	0.96	2.0E-11	BE263565.1	EST_HUMAN	C12-210707-280303-100439 B10318 Homo sapiens cDNA
6266	19331	32592	2.36	2.0E-11	A10776563.1	EST_HUMAN	h83839.1 NCI, CGAP, CG1 Homo sapiens cDNA clone IMAGE:377403 5' similar to SW19410 YEAST
8443	18928	32758	1.71	2.0E-11	AF4891028.1	EST_HUMAN	P16358 PRE-RNA SPLICING FACTOR RNA RELEASE PR16
9471	20309	33722	0.82	2.0E-11	B692944.1	EST_HUMAN	761263 NCI, NCI, CGAP, G538 Homo sapiens cDNA clone IMAGE:5442356 3'
8214	21183	33722	0.51	2.0E-11	P33702	SW SPSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN CORE6
9578	22540	37065	1.31	2.0E-11	AQ202008.1	NT	Homo sapiens chromosome 5 duplication of the T cell receptor beta locus and tyrosinogen gene families
9814	23559	37065	4.42	2.0E-11	F19026.1	SW SPSPROT	OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN QLF1)
10882	19854	37305	0.85	2.0E-11	AF883974.1	EST_HUMAN	RC4-OT0072-175400-913-411 OT0072 Homo sapiens cDNA
10882	19854	37305	0.85	2.0E-11	AF883974.1	EST_HUMAN	RC4-OT0072-175400-913-411 OT0072 Homo sapiens cDNA
11446	24391	37363	1.54	2.0E-11	AA035368.1	EST_HUMAN	327702.1 Sources pregnant uterus NHPRU Homo sapiens cDNA clone IMAGE:471794 3'
11446	24391	37363	1.54	2.0E-11	AA035368.1	EST_HUMAN	327702.1 Sources pregnant uterus NHPRU Homo sapiens cDNA clone IMAGE:471794 3'
14148	23761	37638	1.54	2.0E-11	AA035368.1	EST_HUMAN	327702.1 Sources pregnant uterus NHPRU Homo sapiens cDNA clone IMAGE:471794 3'
17127	24420	37669	4.14	2.0E-11	AA281956.1	EST_HUMAN	RC18504.1 NCI, CGAP, G281 Homo sapiens cDNA clone IMAGE:683519 5'
17127	24420	37669	4.14	2.0E-11	AA281956.1	EST_HUMAN	RC18504.1 NCI, CGAP, G281 Homo sapiens cDNA clone IMAGE:683519 5'
12336	25128	37681	2.12	2.0E-11	W4824748.1	EST_HUMAN	RC3-37105-11-0230-0114-0518 B10318 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit E-Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12354	25143	31854	2.14	2.0E-11	BF377859.1	EST_HUMAN	OM2-TN0140-07000-372-g01 TN0140 Homo sapiens cDNA
12367	25148		1.49	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIA0027 protein, partial cds
12754	25390		1.69	2.0E-11	P06847	SWISSPROT	LINE1 REVERSE TRANSCRIPTASE HOMOLOG
13070	25904		3.69	2.0E-11	11417069	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
677	13740	20667	0.83	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
784	13844	29789	1.89	1.0E-11	HA163209.2	NT	Homo sapiens chromosome 21 segment HS21C039
1221	14339	27216	4.66	1.0E-11	HA163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1468	14531		2.95	1.0E-11	AF110914.1	NT	Homo sapiens PRK379 mRNA, complete cds
2053	15072	28091	1.41	1.0E-11	P16259	SWISSPROT	OXY1 TERG-BINDING PROTEIN
2130	15153	28168	3.16	1.0E-11	AF005673.1	NT	Homo sapiens nanogentide 12-oxoglutarate, complete cds
2170	15186	29207	1.16	1.0E-11	AJ309316.1	EST_HUMAN	EST181168 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3510	16556	29480	0.83	1.0E-11	BE004315.1	EST_HUMAN	OM2-BN0105-10300-262-d12 BN0105 Homo sapiens cDNA
4960	17075	30368	1.01	1.0E-11	AF168261.1	EST_HUMAN	356505.31 Source: NIMHNP; ST1 Homo sapiens cDNA clone IMAGE:1661243 3'
5493	18095	31395	14.43	1.0E-11	AF16247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5591	19017	32212	0.77	1.0E-11	BF22646.1	EST_HUMAN	7067101.11 NC1 CGAP P218 Homo sapiens cDNA clone IMAGE:3849948 3' similar to contains MER10.33
6712	21040		0.51	1.0E-11	AB042297.1	NT	MER10, repetitive element
8543	21911	34928	3.26	1.0E-11	4893246	NT	Homo sapiens P15 gene for 5-pyruvatekinase-dependent synthase, complete cds
8543	21911	34928	3.26	1.0E-11	4893246	NT	Homo sapiens PHO finger protein 2 (PHF2) mRNA
8543	21911	34928	3.26	1.0E-11	4893246	NT	77308.11 Source: infant brain; 1N18 Homo sapiens cDNA clone IMAGE:23166 5'
8543	21911	34928	3.26	1.0E-11	BF265119.1	EST_HUMAN	OV4NN1146-25000-428-403 NN1146 Homo sapiens cDNA
8543	21911	34928	3.26	1.0E-11	BF265119.1	EST_HUMAN	OV4NN1146-25000-428-403 NN1146 Homo sapiens cDNA
1510	24857	38120	1.18	1.0E-11	BF290078.1	EST_HUMAN	60214507F1 NIH MG6. 83 Homo sapiens cDNA clone IMAGE:426977 5'
2543	19021	28946	0.83	1.0E-12	AJ212074.2	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10157	23063	36556	1.02	1.0E-12	AL163300.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
10157	23063	36556	1.02	1.0E-12	AL163300.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
12075	24847	38542	2.85	1.0E-12	AL046930.1	NT	DKFZ560141.1 J. 686 (synonym: hula1) Homo sapiens cDNA clone DKFZ560141.1 5'
9983	22848		0.92	1.0E-12	BE074720.1	EST_HUMAN	IL2-BT07679-130200-036-G12 BT07679 Homo sapiens cDNA
12407	25180		3.22	1.0E-12	AJ217126.1	NT	Homo sapiens Xq pseudautosomal region, segment 22
4690	17711	30965	1.46	7.0E-12	OJ05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11677	24643	38220	7.41	7.0E-12	AF104735.1	EST_HUMAN	423901.31 Source: fetal liver; spleen; NIH-LS ST1 Homo sapiens cDNA clone IMAGE:451162 3'
3558	16904		0.55	6.0E-12	AF173054.1	EST_HUMAN	AF170554 HIT Homo sapiens cDNA clone HTFAFW6 5'
4375	17403	32083	0.29	6.0E-12	AY22516.1	EST_HUMAN	n38711.31 NC1 CGAP CG81 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Expn SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mod Similar (Top) HI BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6828	15691	33851	0.65	6.0E-12	AF020503.1	NT	Homo sapiens FRA38 common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
8447	22312	35766	0.88	6.0E-12	AF003248.1	NT	Macaca mulatta myosin heavy chain FM3A (FM3A) mRNA, complete cds
9829	22678	27043	1.66	6.0E-12	AA847688.1	EST_HUMAN	MER29 repetitive element
1044	14090	27043	3.57	5.0E-12	T06573.1	EST_HUMAN	EST04462 Fetal brain, Striatum (cat683206) Homo sapiens cDNA clone HBDY33
3401	18450	25078	1.17	5.0E-12	BC647795.1	EST_HUMAN	bc42055.Y1 NC1_QGAP_QCB1 Homo sapiens cDNA clone IMAGE:2291217 5'
3740	19782	25694	6.8	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudobulbous region, segment 22
6137	10214	32441	4.59	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6137	10214	32441	4.59	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6539	19697	32973	9.52	5.0E-12	AL097490.1	EST_HUMAN	EST1306800 IMAGE Insequens, MAGN Homo sapiens cDNA
7232	19977	33274	1	5.0E-12	AL040739.1	EST_HUMAN	DKFZP434B1615.51 434 (phenonym: hies3) Homo sapiens cDNA clone DKFZP434B1615 3'
7242	19977	33274	1.03	5.0E-12	AL040739.1	EST_HUMAN	DKFZP434B1615.51 434 (phenonym: hies3) Homo sapiens cDNA clone DKFZP434B1615 3'
8571	21539	34060	1.14	5.0E-12	AA033745.1	EST_HUMAN	z01912.51 Sorensen, Juel, NGRH18W Homo sapiens cDNA clone IMAGE:3379718 3' similar to contains L1.9.1 repetitive element
9015	21981	34060	0.7	5.0E-12	AA033745.1	EST_HUMAN	EST010085-220305-01-1307 O10088 Homo sapiens cDNA
9548	22311	34060	0.64	5.0E-12	AL079881.1	EST_HUMAN	DKFZP434B1615.51 434 (phenonym: hies3) Homo sapiens cDNA clone DKFZP434B1615 3'
9454	22438	35897	2.78	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudobulbous region, segment 102
9778	22719	36173	1.38	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR 102 (OLFACTORY RECEPTOR-LIKE PROTEIN HOMP07E) (OLFACTORY RECEPTOR 1-4) (OR1-4)
10838	25690	37144	4.14	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C03
10729	25951	37144	0.81	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C03
244	13342	25267	4.17	4.0E-12	AY700268.1	EST_HUMAN	244T111 Sorensen, Juel, NGRH18W Homo sapiens cDNA clone IMAGE:465976 3'
245	13342	25267	5.51	4.0E-12	AY700268.1	EST_HUMAN	244T111 Sorensen, Juel, NGRH18W Homo sapiens cDNA clone IMAGE:465976 3'
4530	19771	30556	0.74	4.0E-12	A080984.1	EST_HUMAN	244T111 Sorensen, Juel, NGRH18W Homo sapiens cDNA clone IMAGE:2270745 3' similar to TRC13539 Q13539
7891	20825	37144	0.72	4.0E-12	BF449140.1	EST_HUMAN	MARINER TRANSPOSASE
8595	21553	35422	2.92	4.0E-12	AF109007.1	NT	merf103.41 NC1_QGAP_Luc14 Homo sapiens cDNA clone IMAGE:3369077 3' similar to contains MER7.2
9035	22001	35422	0.75	4.0E-12	AF109007.1	NT	MER7 repetitive element
11410	24933	37698	3.26	4.0E-12	AJ226431.1	NT	Homo sapiens S164 gene, partial cds; PSI and hypothetical protein genes, complete cds, and S171 gene, partial cds
12556	25338	37698	2.82	4.0E-12	U78027.1	NT	Bos taurus Miaz2164 gene for mitochondrial carrier homolog 2, complete cds
							Homo sapiens 650 to 651 contig between AM11 and CBR1 on chromosome 21:22, segment 3/3
							Homo sapiens Brd4a1a yodine kinase (BTK), alpha-D-galactosidase A (GLA), L44-line ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	OFF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
618	15693	26500	3.06	3.0E-12	AW341683.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA clone IMAGE36093773 similar to TR-O4817
618	15693	26501	3.06	3.0E-12	AW341683.1	EST_HUMAN	O1457 SWMP. ;
6211	18220	31096	0.73	3.0E-12	AL165268.2	NT	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA clone IMAGE36093773 similar to TR-O4817
5527	18626	31662	0.96	3.0E-12	AF111168.2	NT	Homo sapiens serine peptidyl transferase, subtilisin gene, complete cds, and unknown genes
7559	20819	31662	0.64	3.0E-12	AB041297.1	NT	Homo sapiens P1S gene for 6-pyruvoylhistidinol synthase, complete cds
8603	20867	31114	0.65	3.0E-12	AB041298.1	EST_HUMAN	RC3-C10255-C61089-011402 C10255 Homo sapiens cDNA
8718	21686	35114	0.49	3.0E-12	CS3543	SWISSPROT	SERINE PROTEASE PEPSIN
8462	22426	33664	0.64	3.0E-12	CS3543	SWISSPROT	Human prostate specific antigen gene, 5' flanking region
11016	23691	37507	2.71	3.0E-12	U57972.1	NT	Human prostate specific antigen gene, 5' flanking region
1691	14593	27848	2.41	2.0E-12	AW802131.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
3490	16526	28451	0.95	2.0E-12	6754495	NT	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
4141	17172	30050	1.09	2.0E-12	J01864.1	NT	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
4451	17477	30051	1.97	2.0E-12	BE065593.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
5321	18427	31177	0.71	2.0E-12	P11589	SWISSPROT	RETROVIRUS RELATED POLYPROTEIN (CONTAINS REVERSE TRANSCRIPTASE ;
5622	19690	33702	1.83	2.0E-12	AF1067165.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
7381	20351	33702	3.22	2.0E-12	J08169.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
7597	20530	33669	1.18	2.0E-12	U5617305.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
7716	20731	34253	0.57	2.0E-12	AF074278.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
7922	20965	34253	2.1	2.0E-12	U102220	NT	Homo sapiens Actin (transposable element) (ALTE), mRNA
8077	22043	35466	0.43	2.0E-12	C10473	SWISSPROT	POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (PROTEIN LUDP
5983	22620	35466	1.68	2.0E-12	AF106884.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
10346	23259	37504	14.41	2.0E-12	BE165690.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
10881	23691	37504	0.8	2.0E-12	A334130.1	EST_HUMAN	hT3401.X1 Soares, NF κ B, T κ GBC, S1 Homo sapiens cDNA
12346	25119	37504	3.11	2.0E-12	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C883
12346	25119	37504	1.68	2.0E-12	U118248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORT SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
123	12321	26159	2.83	1.0E-12	AW82874.1	EST_HUMAN	Higuchi.X1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:287040 3' similar to contains MER18.11
2004	15925						MER18 repetitive element;
3085	18142	26053	1.48	1.0E-12	AB87126.1	EST_HUMAN	wn5107.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:269403 3' similar to contains L1.83 L1
3085	18142	26054	0.78	1.0E-12	AF000891.1	NT	repetitive element;
3838	18928	26054	0.78	1.0E-12	AF000891.1	NT	Homo sapiens testis-specific Testis Transcription Y2 (TTY2) mRNA, partial cds
3838	18928	26058	31.8	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcription Y2 (TTY2) mRNA, partial cds
3838	18928	26057	31.8	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2P93 Homo sapiens cDNA clone NT2P9304070 5'
6078	10158		2.05	1.0E-12	U6828.1	NT	AU132248 NT2P93 Homo sapiens cDNA clone NT2P9304070 5'
6150	10234		1.65	1.0E-12	Q97267.1	SWISSPROT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
8277	18349	32862	0.97	1.0E-12	BF42800.1	EST_HUMAN	HYPOPHYSAL ZINC FINGER PROTEIN KIA0081
8277	18349	32863	0.97	1.0E-12	BF42800.1	EST_HUMAN	EST100008 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1847669 5'
8277	18349	32863	0.97	1.0E-12	BF42800.1	EST_HUMAN	EST100008 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1847669 5'
6893	19729	33014	0.76	1.0E-12	AF226843.1	NT	Myo musculosa WNT-2 gene, partial cds; putative enhyrin-related protein and cyclic fibroblast transmembrane
7223	20294	33537	1.9	1.0E-12	AF198884.1	NT	conducance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7357	20327	33676	11.35	1.0E-12	AJ249333.1	EST_HUMAN	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7357	20327	33676	11.35	1.0E-12	AJ249333.1	EST_HUMAN	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
7357	20327	33676	11.35	1.0E-12	AJ249333.1	EST_HUMAN	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
7357	20327	33676	11.35	1.0E-12	AJ249333.1	EST_HUMAN	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
7357	20327	33676	11.35	1.0E-12	AJ249333.1	EST_HUMAN	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
8834	21801	35220	0.48	1.0E-12	U66056.1	NT	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
8903	22019	35444	1.16	1.0E-12	AA782223.1	EST_HUMAN	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
1213	22952	36628	2.92	1.0E-12	AW962164.1	EST_HUMAN	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
12434	25200		2.54	1.0E-12	U738592.1	EST_HUMAN	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
12582	25881		2.51	1.0E-12	AL183286.2	NT	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
1054	14400	27050	0.7	9.0E-13	AW682714.1	EST_HUMAN	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
9843	16886		1.01	8.0E-13	AJ271735.1	NT	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to
3897	17007	26623	0.95	8.0E-13	AB026000.1	NT	956604.x1 Soares_Testis_spleen_INF.S_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID No.	Exon ID No.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9995	22897		2.59	9.0E-13	N95933.1	EST_HUMAN	z62906.at1 Soares fetal liver spleen NHL5 Homo sapiens cDNA clone IMAGE:283551.3
716	13760	28714	8.78	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
718	13760	20715	8.78	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1855	14881	27877	3.1	8.0E-13	U80071.1	NT	Homo sapiens basic transcription factor 2 p4 (102544) gene, partial cds, neuronal epithelial inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8449	21418	34832	0.75	8.0E-13	A1884398.1	EST_HUMAN	wm31109.at1 NC1 CGAP: U01 Homo sapiens cDNA clone IMAGE:243780.3
10505	23427		0.75	8.0E-13	A1884398.1	EST_HUMAN	wm31109.at1 NC1 CGAP: U01 Homo sapiens cDNA clone IMAGE:243780.3
8127	21064	34462	0.58	7.0E-13	A1884398.1	EST_HUMAN	wm31109.at1 NC1 CGAP: U01 Homo sapiens cDNA clone IMAGE:243780.3
8127	21064	34463	0.58	7.0E-13	A1884398.1	EST_HUMAN	wm31109.at1 NC1 CGAP: U01 Homo sapiens cDNA clone IMAGE:243780.3
8678	21544		0.49	7.0E-13	Q95185	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN (OLF)
12682	25550		5.59	7.0E-13	BE78229.1	EST_HUMAN	09482398f.NHL1 JGCG: C2 Homo sapiens cDNA clone IMAGE:366813.5
2111	15128	28148	3.58	6.0E-13	AL165207.2	NT	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
3333	18384		0.74	5.0E-13	RT9338.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
3408	18457		1.39	5.0E-13	AA435773.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
7050	20082	33390	0.7	5.0E-13	P03685	SWISSPROT	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
11209	24103	37693	2.07	5.0E-13	P07313	SWISSPROT	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
1883	14908		8.02	4.0E-13	A193134.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
2487	15171		2.44	4.0E-13	A193134.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
4778	17798		0.86	4.0E-13	A193134.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
5887	18782	31621	4.36	4.0E-13	BE10931.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
7413	20390	33751	1.03	4.0E-13	A3037780.1	NT	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
7970	20814	34192	0.98	4.0E-13	AA431528.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
7965	20928		1.47	4.0E-13	N44291.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
0193	22169	35587	1.2	4.0E-13	AL043810.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
9565	22796	38246	0.56	4.0E-13	AA078607.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
10360	23303	39779	5.26	4.0E-13	A128983.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
11562	24443	37895	1.9	4.0E-13	AA435819.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3
11802	24443	37895	1.9	4.0E-13	AA435819.1	EST_HUMAN	z62906.at1 Soares testis, NHL1 Homo sapiens cDNA clone IMAGE:243780.3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
181	13281		5.91	3.0E-13	AF003528.1	NT	Homo sapiens X-linked arylsulphatase-deficient gene (EDA), exon 2 and flanking repeat regions
886	13922		3.35	3.0E-13	AA400310.1	EST_HUMAN	zsv8908.1 Soares_teste_NHT Homo sapiens cDNA clone IMAGE:781409.6
2378	15386	28410	1.05	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2457	15491		2.11	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2673	15970	28986	2.5	3.0E-13	BF572802.1	EST_HUMAN	GM-PT0100-14700-242-108 F10100 Homo sapiens cDNA
3201	16258		2.19	3.0E-13	AA749844.1	EST_HUMAN	ab18405.1 NC1_DGAP_K048 Homo sapiens cDNA clone IMAGE:1324035.3
3314	16550	28464	0.9	3.0E-13	P18816	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3314	16550	28465	0.9	3.0E-13	P18816	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5618	18714	31972	0.64	3.0E-13	AA134017.1	EST_HUMAN	z88810.1 Sturge-Ling carcinoma 697218 Homo sapiens cDNA clone IMAGE:568315.5 similar to contains THR12 THR repetitive element
5618	18714	31973	0.64	3.0E-13	AA134017.1	EST_HUMAN	z88810.1 Sturge-Ling carcinoma 697218 Homo sapiens cDNA clone IMAGE:568315.5 similar to contains THR12 THR repetitive element
9108	19185	32404	0.71	3.0E-13	AW005939.1	EST_HUMAN	028502.X1 NC1_DGAP_Bm25 Homo sapiens cDNA clone IMAGE:395890.3 similar to TR-075139 075139 KIAA0874 PROTEIN...
8215	21184	34594	8.24	3.0E-13	U52111.2	NT	Homo sapiens X2d region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca ²⁺ /calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CD4 protein (CD4), nucleoside triphosphate phosphatase 1 (NTPase1) and reactive factor
8412	21381	34787	0.51	3.0E-13	AA332487.1	EST_HUMAN	EST160487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to testine protease P100, Ras-reactive factor
8412	21381	34788	0.51	3.0E-13	AA332487.1	EST_HUMAN	EST160487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to testine protease P100, Ras-reactive factor
10558	23480	36675	0.46	3.0E-13	AW925487.1	EST_HUMAN	RC2-DT0007.110100-014-10 DT0007 Homo sapiens cDNA
11038	24000		2.68	3.0E-13	AA047188.1	EST_HUMAN	HA0358 Human fetal liver cDNA library Homo sapiens cDNA
11385	24332	37881	3.32	3.0E-13	BE063509.1	EST_HUMAN	GM0-BT0281-331186-287-403 BT0281 Homo sapiens cDNA
11924	24805	38398	1.54	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
							Homo sapiens X2d region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca ²⁺ /calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CD4 protein (CD4), atretinoleukodystrophy protein >
151	13254	26183	3.93	2.0E-13	U52111.2	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
1275	14310	27271	7.14	2.0E-13	AF298710.1	NT	hnb7805.X1 Soares_NSF_3W_OT_PA_3_ST Homo sapiens cDNA clone IMAGE:3
3254	16347	29257	1.08	2.0E-13	BF431899.1	EST_HUMAN	Homo sapiens S104 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
3516	16554	29439	1.26	2.0E-13	AF108607.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4135	17107		1.81	2.0E-13	AL103278.2	NT	Homo sapiens chromosome 21 segment 1HSIC028
6245	18918	32548	4.71	2.0E-13	Q08832	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1)
6937	20210	33538	6.49	2.0E-13	X16912.1	NT	Human PKL gene for liver-type 5-phosphoribosyltransferase (EC 2.7.1.1) exon 2
7265	19920	33267	0.59	2.0E-13	10885072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1); mRNA
7265	19920	33268	0.59	2.0E-13	10885072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1); mRNA
7265	19920	33268	0.59	2.0E-13	10885072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1); mRNA
10824	23745	37246	4.33	2.0E-13	5931886	NT	Homo sapiens mihi-21 (C. elegans) Rha 1 (MAB21L1) mRNA
12347	23105		5.43	2.0E-13	AW882155.1	EST_HUMAN	CHG-NM001-10300-274-611 NM001 Homo sapiens cDNA
291	13395	26312	1.49	1.0E-13	S74729.1	NT	FGF-1 fibroblast growth factor 1 (human, kidney, placenta, 3' end, segment 2 of 2)
869	13344	26012	4.85	1.0E-13	AJ007973.1	NT	Homo sapiens LGM252 gene
1339	14373	27343	1.39	1.0E-13	X8734.1	NT	H. sapiens DNA, DMB, HLA-C1, IP22, LUP2, TAP2, DOB, DOB2 and RINGA 9, 13 and 14 genes
2037	15055	28074	2.43	1.0E-13	AA720574.1	EST_HUMAN	hw21p02.s1 NCI CGAP CG50 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR 3
4623	17644	30532	2.2	1.0E-13	BF340987.1	EST_HUMAN	h0233002BF1 NCI CGAP Bmi1 Homo sapiens cDNA clone IMAGE:118559 5'
6580	18648	33515	0.61	1.0E-13	AJ097321.1	EST_HUMAN	Y1555.spc F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 3'
8242	21211	34616	0.79	1.0E-13	AA577612.1	EST_HUMAN	nc24801.s1 NCI CGAP Gsta1 Homo sapiens cDNA clone IMAGE:1094801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
8242	21211	34617	0.79	1.0E-13	AA577612.1	EST_HUMAN	nc24801.s1 NCI CGAP Gsta1 Homo sapiens cDNA clone IMAGE:1094801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
10450	23572		0.82	1.0E-13	Q15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (IMAGE-B4 ANTIGEN);
10684	23580	37084	0.40	1.0E-13	AF300701.1	NT	Mus musculus osteocalcin-related protein tyrosine phosphatase mRNA, complete cds
11707	24072	38249	10.33	1.0E-13	BF108755.1	EST_HUMAN	contains MER28.b2 MER29 repetitive element;
12205	25046		2.34	1.0E-13	AV116377.1	EST_HUMAN	AV116377 DOB Homo sapiens cDNA clone DOBAE03 5'
12244	25054		3.21	1.0E-13	AJ271755.1	NT	Homo sapiens Xq pseudocentromeric region; segment 1/2
333	13422	28345	3.14	9.0E-14	AA781159.1	EST_HUMAN	4f2c01.s1 Soares, Jentsch, NHT Homo sapiens cDNA clone 191232 3' similar to contains MER1011 MER19 repetitive element;
344	13423	28346	2.37	9.0E-14	AA781159.1	EST_HUMAN	4f2c01.s1 Soares, Jentsch, NHT Homo sapiens cDNA clone 191232 3' similar to contains MER1011 MER19 repetitive element;
2508	15611		4.8	9.0E-14	AA781577.1	EST_HUMAN	RC1-CT10322-200100-015-039 CT10322 Homo sapiens cDNA
2507	15568	28617	1.03	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter 1 (SGLT2 gene)
2507	15568	28618	1.03	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter 1 (SGLT2 gene)
2764	15758	28777	6.94	9.0E-14	AJ030492.1	NT	Homo sapiens TFR gene cluster (a T cell factor, complete cds)

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3126	18195	20094	6.43	0.0E-14	AJW513296.1	EST_HUMAN	x554365.x1 NC1 CGAP_UH Homo sapiens cDNA clone IMAGE:2707833 3'
3282	13422	28345	0.87	0.0E-14	AA781169.1	EST_HUMAN	954041.1 Soares_testis_NHT Homo sapiens cDNA clone 1397232 3' similar to contains MER181 MER19 repetitive element.
3811	10861	29759	7.16	9.0E-14	D14547.1	NT	-Human DNA, SINE repetitive element
4789	17807	30599	1.08	0.0E-14	AJ029153.1	EST_HUMAN	Sapiens odinus gene for animal vesicle secreted protein semenogelin 1
3009	19585		1.44	8.0E-14	BEE48269.1	EST_HUMAN	H7T093.x1 NC1 CGAP_LY24 Homo sapiens cDNA clone IMAGE:321424 3'
3078	17018		3.48	8.0E-14	R76269.1	EST_HUMAN	H76269.x1 Soares placenta NQ24 Homo sapiens cDNA clone IMAGE:14793 3'
8633	27138	34339	21.45	8.0E-14	X09271.1	NT	H sapiens DNA for endogenous retroviral like element
8918	22738	36162	3.11	8.0E-14	AJ210819.1	EST_HUMAN	ZV7270.1 ST Strategene fetal refina B97202 Homo sapiens cDNA
12738	19585	31783	1.52	8.0E-14	AB58516.1	EST_HUMAN	QV2310238.X27036-074-BT1 B10258 Homo sapiens cDNA
12350	23294		3.1783	8.0E-14	BA088178.1	EST_HUMAN	W62303.x1 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:262643 3'
1533	15873		3.99	7.0E-14	AW151973.1	EST_HUMAN	MER181.H1 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER1012
9272	22238		0.51	7.0E-14	AF13286.2	NT	Homo sapiens chromosome 21 segment HS21C085
337	12493	26381	16.94	0.0E-14	AFD2503.1	NT	Homo sapiens FR43B common fragile region, diadenosine triphosphate hydrolases (FHT) gene, exon 5
10181	23105	36587	2.54	0.0E-14	AFD2503.1	NT	Homo sapiens FR43B common fragile region, diadenosine triphosphate hydrolases (FHT) gene, exon 5
10181	23105	39386	2.54	0.0E-14	AFD2503.1	NT	Homo sapiens FR43B common fragile region, diadenosine triphosphate hydrolases (FHT) gene, exon 5
520	13988	26003	5.23	5.0E-14	O65120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (FHIT) gene, exon 5
3683	10720		0.95	5.0E-14	AF103247.2	NT	ASSOCIATED PROTEIN 2(CANAUCAL MULTIDRUG RESISTANCE-RELATED PROTEIN)
500	18103	30970	1.39	5.0E-14	U07379.1	EST_HUMAN	H403005.x1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2675186 3' similar to contains L1L2.L1
6511	17133	31854	4.84	5.0E-14	P08347	SWISSPROT	LINC1PREDIGE TRANSCRIPTASE HOMOLOG
1895	14602	27916	1.92	4.0E-14	X09273.1	SWISSPROT	SANTENIERE TRANSCRIPTION PRECURSOR
3795	18907		1	4.0E-14	AA465021.1	EST_HUMAN	3877682.T1 Soares testis tissue NHHRU Homo sapiens cDNA clone IMAGE:487658 5'
4320	17349	30233	0.96	4.0E-14	FA46328.1	EST_HUMAN	N77612.3 Soares multiple sequence_2NHANSP Homo sapiens cDNA clone IMAGE:279160 3' similar to contains L1L3.L1 repetitive element:
8291	21260		0.6	4.0E-14	X67344.1	NT	1 sapiens DNA, DMB, ALA-Z1, IPPZ, LUMP2, TAP1, LUMP7, PAB2, DOB2 and RINGA, 9, 13 and 14 genes

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12055	25988		6.35	4.0E-14	AI80224.1	EST_HUMAN	Wt08003.x1 NCL CGAP_H10 Homo sapiens cDNA clone IMAGE:2453332 3' similar to contains AU repetitive element
950	14003	26055	4.59	3.0E-14	X92466.1	NT	R.norvegicus mRNA for CP62 protein
4963	17978	30869	1.16	3.0E-14	7698644	NT	Human sapiens a diaphanin and metalloproteinase domain 29 (ADAM29) mRNA
							961c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2394070 3' similar to FR-00619 000519 FATTY ACID AMIDE HYDROLASE.1
6868	19650	33246	0.96	3.0E-14	AIJ20786.1	EST_HUMAN	961c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2394070 3' similar to FR-00619 000519 FATTY ACID AMIDE HYDROLASE.1
6868	19650	33247	0.96	3.0E-14	AIJ20786.1	EST_HUMAN	961c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2394070 3' similar to FR-00619 000519 FATTY ACID AMIDE HYDROLASE.1
7021	25675		0.51	3.0E-14	AI165246.2	NT	Homo sapiens chromosome 21 segment HS21C048
7229	20231	33585	0.57	3.0E-14	AA38831.1	EST_HUMAN	EST16030.1 B100 N1 Homo sapiens cDNA clone IMAGE:2701523 5'
9139	22105	33531	0.83	3.0E-14	NI2165.1	EST_HUMAN	961c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2394070 3' similar to FR-00619 000519 FATTY ACID AMIDE HYDROLASE.1
11337	24287	37811	2.83	3.0E-14	BE386018.1	EST_HUMAN	961c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2394070 3' similar to FR-00619 000519 FATTY ACID AMIDE HYDROLASE.1
11658	18347	31293	8.06	3.0E-14	AV25334.1	EST_HUMAN	961c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2394070 3' similar to FR-00619 000519 FATTY ACID AMIDE HYDROLASE.1
12624	25654		1.68	3.0E-14	AI165246.2	NT	Homo sapiens chromosome 21 segment HS21C048
360	13465	26395	2.76	2.0E-14	AI165246.2	NT	Homo sapiens Xq pseudautosomal region; segment 22
360	13465	26396	2.76	2.0E-14	AI165246.2	NT	Homo sapiens Xq pseudautosomal region; segment 22
991	18347	26652	9.86	2.0E-14	AI165246.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
2597	15504		1.91	2.0E-14	AV137268.1	EST_HUMAN	RC5-B1037.091289-031.012 B10377 Homo sapiens cDNA
2472	15476		1.91	2.0E-14	7457626	NT	Homo sapiens madrid tumor deletion region protein 1 (RTDR1) mRNA
2531	15534	28554	2.2	2.0E-14	AI165246.2	NT	Homo sapiens chromosome 21 segment HS21C069
2531	15534		1.03	2.0E-14	BE22432.1	EST_HUMAN	h00g10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains AU repetitive element
2683	15570		1.48	2.0E-14	P08548	SWISSPROT	repetitive element contains ORF 11 ORF repetitive element
5622	18586	31669	0.91	2.0E-14	BE386061.1	EST_HUMAN	LINE1 REVERSE TRANSCRIPTASE HOMOLOG
							repetitive element
5702	18707	31972	0.81	2.0E-14	AI312351.1	EST_HUMAN	Human beta globin region on chromosome 11
5966	18566	32062	3.16	2.0E-14	U001317.1	NT	RC3-BN007.240200-011-409 BN0072 Homo sapiens cDNA
7067	20080		0.92	2.0E-14	BE005590.1	EST_HUMAN	Homo sapiens e diaphanin and metalloproteinase domain 11 (ADAM11) mRNA
7260	20462	33396	0.57	2.0E-14	4585709	NT	ZINC-FINGER PROTEIN NEURO-D4
7502	20467	33328	0.87	2.0E-14	P356163	SWISSPROT	IG-TD397.077289-024-004 HT0397 Homo sapiens cDNA
7751	20704	34072	21.51	2.0E-14	BE189781.1	EST_HUMAN	IG-TD397.077289-024-004 HT0397 Homo sapiens cDNA
7751	20704		21.51	2.0E-14	BE189781.1	EST_HUMAN	IG-TD397.077289-024-004 HT0397 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal ID NO:	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
410	13483	28418	5.24	5.0E-16	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
2771	15763	28794	2.05	5.0E-16	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRd gene, and sodium phosphate transporter (NPT3) gene, complete cds
3482	16528		1.06	5.0E-16	AW29817.1	EST_HUMAN	UHHBVO-ep-g-10-GU-11-1 NCI CGAP Subd Homo sapiens cDNA clone IMAGE2731219.3
11056	23660		2.27	5.0E-16	AV750066.1	EST_HUMAN	AY50056 HTF Homo sapiens cDNA clone HTFAVE06.6
427	13122	28020	3.54	4.0E-16	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6822	18076	33165	0.86	4.0E-16	AB507870.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript U4A0501
11401	21088	34487	1.79	4.0E-16	AJ130864.1	NT	Homo sapiens mRNA for transcription factor
11401	21088	34489	1.79	4.0E-16	AJ130864.1	NT	Homo sapiens mRNA for transcription factor
4245	17274		6.54	3.0E-16	N89452.1	EST_HUMAN	LY1142F Human fetal testis, LaminA ZNP Express Homo sapiens cDNA clone LY1142.5 similar to
5097	18077	30958	0.67	3.0E-16	AA078097.1	EST_HUMAN	APR1CADOX1A1 Human testis, Pseudoviral cDNA library Homo sapiens cDNA clone 7P01F03
5097	18077	30959	0.67	3.0E-16	AA078097.1	EST_HUMAN	7P01F03 Human testis, Pseudoviral cDNA library Homo sapiens cDNA clone 7P01F03
6996	20205		1.27	3.0E-16	Q34625	SWISSPROT	GLUTATHIONE PEROXIDASE RYD1 PRECURSOR (GOORANT-METABOLIZING PROTEIN RYD21)
7495	20460	33916	3.06	3.0E-16	N27085.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7495	20460	33920	3.06	3.0E-16	N27085.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
10295	23210		2.66	3.0E-16	AA807128.1	EST_HUMAN	nc82a07 nt NCI CGAP CG31 Homo sapiens cDNA clone IMAGE1351704.3 similar to contains MER19.H
11146	24106	37933	3.42	3.0E-16	AB023693.1	NT	Homo sapiens DNA, DLEC1 is ORC1L4 gene region, exon 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
250	13347	28273	4.45	2.0E-16	AF223391.1	NT	Homo sapiens cadherin channel alpha1E subunit (CA1NA1E) gene, exons 7-49, and partial cds, alternatively spliced
368	13454	29382	4.01	2.0E-16	AF223391.1	NT	Homo sapiens cadherin channel alpha1E subunit (CA1NA1E) gene, exons 7-49, and partial cds, alternatively spliced
368	13454	29393	4.01	2.0E-16	AF223391.1	NT	Homo sapiens cadherin channel alpha1E subunit (CA1NA1E) gene, exons 7-49, and partial cds, alternatively spliced
2381	15389	28413	1.02	2.0E-16	BE340127.1	EST_HUMAN	H09001 nt NCI CGAP JMR13 Homo sapiens cDNA clone IMAGE3140256.3 similar to contains MER29.b3
2381	15389	28414	1.02	2.0E-16	BE340127.1	EST_HUMAN	H09001 nt NCI CGAP JMR13 Homo sapiens cDNA clone IMAGE3140256.3 similar to contains MER29.b3
4096	17129	30023	1.21	2.0E-16	AW236495.1	EST_HUMAN	nc26001 nt NCI CGAP JMR10 Homo sapiens cDNA clone IMAGE2741921.3 similar to contains L13.L1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) HIT BUST E Value	Top HIT Assession No.	Top HIT Database Source	Top HIT Descriptor
4683	17674		2.73	2.0E-15	AB09335.1	EST_HUMAN	w0700.x1 Scores, NFL1, CGBP, S1 Homo sapiens cDNA clone IMAGE:234623.3 similar to TRQ61043
8308	19377	32619	1.02	2.0E-15	BE62362.1	EST_HUMAN	Q1004333F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3977268.5
8308	19377	32617	1.02	2.0E-15	BE62362.1	EST_HUMAN	Q1004333F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3977268.5
7321	20282		1.42	2.0E-15	AJ400897.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C1orf14 gene, C1orf16 gene and C1orf17 gene
7486	20461	33610	2.64	2.0E-15	AJ704105.1	EST_HUMAN	Z77633.1 Scores, fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:469824.3
7625	20585	33548	4.76	2.0E-15	U05004.1	EST_HUMAN	Z67810.1 Scores, fetal lung, NHL1, 16W Homo sapiens cDNA clone IMAGE:298975.6 similar to WP:FA4F4.8 C020227 TRANSPOSASE ;
8117	21054	34151	0.67	2.0E-15	AL18347.2	NT	Homo sapiens chromosome 21 segment HS21C047
8297	22223	35653	2.73	2.0E-15	D1547.1	NT	Human DNA, SINE, repetitive element
8427	22391	35620	0.74	2.0E-15	AJ39778.1	EST_HUMAN	Z77633.1 Scores, testis, NIH Homo sapiens cDNA clone IMAGE:728414.5
8427	22391	35630	0.74	2.0E-15	AJ39778.1	EST_HUMAN	Z77633.1 Scores, testis, NIH Homo sapiens cDNA clone IMAGE:728414.5
8427	22391	35157	1.19	2.0E-15	AW37485.1	EST_HUMAN	CA0410244-201695078-s12 H1024 Homo sapiens cDNA
8427	22391	35157	1.19	2.0E-15	AW37485.1	EST_HUMAN	CA0410244-201695078-s12 H1024 Homo sapiens cDNA
8427	22391	35157	1.19	2.0E-15	AJ71735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
11187	24143		4.15	2.0E-15	AJ71735.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exon 7-49, and partial cds, alternatively spliced
12834	18339	31288	3.19	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exon 7-49, and partial cds, alternatively spliced
12834	18339	31289	3.19	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exon 7-49, and partial cds, alternatively spliced
2785	15777		2.05	1.0E-15	A085084.1	EST_HUMAN	W2695.x1 NCI, CGAP, L24 Homo sapiens cDNA clone IMAGE:2270745.3 similar to TRQ13339 Q13339
3025	16982	26005	1.53	1.0E-15	BE04384.1	EST_HUMAN	W2695.x1 NCI, CGAP, L24 Homo sapiens cDNA clone IMAGE:2270745.3 similar to TRQ13339 Q13339
3169	18214	29126	1.2	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOX10G
6189	18198	31071	1.11	1.0E-15	A084028.1	EST_HUMAN	W2695.x1 NCI, CGAP, L24 Homo sapiens cDNA clone IMAGE:2270745.3 similar to TRQ13339 Q13339
6508	19572	33225	1.83	1.0E-15	D51783.1	EST_HUMAN	W2695.x1 NCI, CGAP, L24 Homo sapiens cDNA clone IMAGE:2270745.3 similar to TRQ13339 Q13339
7205	20229	33272	1.93	1.0E-15	BE074217.1	EST_HUMAN	W2695.x1 NCI, CGAP, L24 Homo sapiens cDNA clone IMAGE:2270745.3 similar to TRQ13339 Q13339
7205	20229	33272	1.93	1.0E-15	P08507	SWISSPROT	TYNIN BETA CHAIN, CYLARY
8574	21542	34682	1.04	1.0E-15	AL162360.2	NT	Homo sapiens chromosome 21 segment HS21C080
8763	21730	35152	4.51	1.0E-15	AJ209778.1	EST_HUMAN	Q78805.x1 Scores, testis, NIH Homo sapiens cDNA clone IMAGE:1765227.3
8763	21730	35153	4.51	1.0E-15	AJ209778.1	EST_HUMAN	Q78805.x1 Scores, testis, NIH Homo sapiens cDNA clone IMAGE:1765227.3
9394	22969	35789	0.49	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9397	22982	35790	1.5	1.0E-15	4507208	NT	Homo sapiens spermidin synthase (SRM) mRNA

Table 4

Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8502	22606	36055	0.70	1.0E-15	Q35975	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9020	22017	36033	0.95	1.0E-15	A48844933.1	EST_HUMAN	ql37cd3 at NC1_GGAP_K048 Homo sapiens cDNA clone IMAGE:1468972 3' similar to contains L13 L1 repetitive element;
11106	24127	37657	4.18	1.0E-13	AF04003.1	NT	Homo sapiens major histocompatibility locus class II region
13008	25720	31612	9.25	1.0E-15	A178344.1	EST_HUMAN	Homo sapiens cut (proteasome)-like 1 (CSAAT displacement protein) (CUTL1) mRNA
4532	17555	30443	1.15	9.0E-16	4503168	NT	HSC29F08 (normalised infant brain cDNA Homo sapiens cDNA clone c2203)
11338	24288	37612	1.94	9.0E-16	F0608.1	EST_HUMAN	Homo sapiens chromone (C-met) receptor 8 (CCKBR) mRNA
5706	18878	32000	0.76	7.0E-16	4685120	NT	PROTEIN-ARGININE DEIMINASE TYPE ALPHA
7594	20527	33885	1.45	7.0E-16	O08907	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7594	20527	33886	1.45	7.0E-16	O08907	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
12957	25509		1.88	7.0E-16	T81169.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE ALPHA
2161	16187		7.77	8.0E-16	AAV07261.1	EST_HUMAN	EST:12171 Synovial fibro (6837210) Homo sapiens cDNA clone IMAGE:119652 5'
1489	14622	27495	1.28	5.0E-16	AJ25154.1	NT	EST:184702 IMAGE resequences, MAGI, Homo sapiens cDNA
2689	15685	28702	2.62	5.0E-16	A492178.1	EST_HUMAN	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
10414	23335	36821	2.65	6.0E-16	AL182945.2	NT	68624 at Sscera, total fetus, N2H2F8_3w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element;
11849	24732	38319	2.65	5.0E-16	BF21768.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
13044	25583		10.66	5.0E-15	11418127	NT	60186734F1 NIH, MGCC 37 Homo sapiens cDNA clone IMAGE:1104129 5'
22481	12558	28421	1.84	4.0E-16	AB001182.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2388	13268	28421	2.21	4.0E-16	AAV797168.1	EST_HUMAN	Homo sapiens gene for TME4 and PWP2 complete and partial cds
11836	13368	29422	3.94	4.0E-16	AB036376.1	SWISSPROT	QV1-LJM0338-200300-115-g02 UM0039 Homo sapiens cDNA
5271	16517	29436	3.94	4.0E-16	BE036376.1	SWISSPROT	QV1-LJM0338-200300-115-g02 UM0039 Homo sapiens cDNA
4165	17197	30083	4.74	4.0E-16	BE036376.1	EST_HUMAN	MYELIN OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
17901	20916	34310	37.37	4.0E-16	AL163284.2	EST_HUMAN	PMA-E10950-010400-002-g05 B10950 Homo sapiens cDNA
9550	23584	35042	0.97	4.0E-16	P03548	SWISSPROT	PMA-E10950-010400-002-g05 B10950 Homo sapiens cDNA
12300	25103		2.41	4.0E-16	P03548	SWISSPROT	Homo sapiens hypodermal protein FLJ10224 (FLJ10224) mRNA
12392	25160	31816	2.11	4.0E-16	6972456	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12550	25340		1.36	4.0E-16	RT1899.1	EST_HUMAN	Homo sapiens Gb2-associated binder 2 (K040571), mRNA
133	13288	29169	1.24	3.0E-16	AAV022882.1	EST_HUMAN	9f6b11.17 Sarcos infant brain INB Homo sapiens cDNA clone IMAGE:30485 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar EST/Ref E Value	Top Hit Database No.	Top Hit Source	Top Hit Descriptor
133	13238	26170	1.24	3.0E-16	AW022862.1	EST_HUMAN	d4560.1 y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2463376 5'
469	13539		1.91	3.0E-16	AL048446.1	EST_HUMAN	DNF2P-03-007_11 334 (synonym: Nlas3) Homo sapiens cDNA clone DNFP2-03-037 5'
478	13548		3.08	3.0E-16	AF133446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1448	14470	27455	1.53	3.0E-16	Q20993	SWISSPROT	ZONADHESIN PRECURSOR
2848	18046	28095	3.94	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3953	19953	28097	0.98	3.0E-16	T08106.1	EST_HUMAN	EST10680 Infant Brain, Bonto Scanes Homo sapiens cDNA clone HIBB413 5' and
3980	17020		0.77	3.0E-16	AF20593.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (HIT) gene, exon 5
3981	17021		1.06	3.0E-16	U03387.1	NT	Human BX220 gene
5350	18455		1.11	3.0E-16	AA077226.1	EST_HUMAN	7B10P02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10P02
5988	18703	31598	1.12	3.0E-16	AF03326.1	NT	Homo sapiens glycocalyx 3 (FGL3) gene, partial cds and flanking repeat regions
6005	21671	33592	4.92	3.0E-16	AF003395.1	EST_HUMAN	arid3b0.5.1 Stragelens schizo brain S11 Homo sapiens cDNA clone IMAGE:1984183 3' similar to contains
10250	23175		0.91	3.0E-16	AF003395.1	EST_HUMAN	arid3b0.5.1 Stragelens schizo brain S11 Homo sapiens cDNA clone IMAGE:1984183 3' similar to contains
10478	23400	36897	5.77	3.0E-16	U03387.1	NT	Human BX220 gene
13079	23661	31517	1.44	3.0E-16	U03387.1	EST_HUMAN	arid3b0.5.1 Stragelens schizo brain S11 Homo sapiens cDNA clone IMAGE:1984183 3' similar to contains
973	14025		1.04	2.0E-16	AL183279.2	NT	Human BX220 gene
2355	15402		1.32	2.0E-16	U03387.1	EST_HUMAN	arid3b0.5.1 Stragelens schizo brain S11 Homo sapiens cDNA clone IMAGE:1984183 3' similar to contains
2999	15955		1.25	2.0E-16	U03387.1	EST_HUMAN	arid3b0.5.1 Stragelens schizo brain S11 Homo sapiens cDNA clone IMAGE:1984183 3' similar to contains
4207	17239	30123	1.14	2.0E-16	U03387.1	NT	Human BX220 gene
6905	19657	33254	0.83	2.0E-16	Q31126	SWISSPROT	HIS10NE-RICH PROTEIN KE4
7084	20023	34316	1.4	2.0E-16	AF107023.1	EST_HUMAN	HIS10NE-RICH PROTEIN KE4
8300	21265	34681	1.85	2.0E-16	AF107023.1	EST_HUMAN	HIS10NE-RICH PROTEIN KE4
8498	21484	34682	0.73	2.0E-16	BE680628.1	EST_HUMAN	HYPO705.5 NCL CGAP P12 Homo sapiens cDNA clone IMAGE:120947 similar to TRC05460 05460
8498	21484	34683	0.73	2.0E-16	BE680628.1	EST_HUMAN	HYPO705.5 NCL CGAP P12 Homo sapiens cDNA clone IMAGE:120947 similar to TRC05460 05460
8872	21930	35291	0.75	2.0E-16	AF107714.1	EST_HUMAN	7B2B09.x1 NCL CGAP P12B Homo sapiens cDNA clone IMAGE:3303521 3'
8872	21930	35292	0.75	2.0E-16	AF107714.1	EST_HUMAN	7B2B09.x1 NCL CGAP P12B Homo sapiens cDNA clone IMAGE:3303521 3'
11274	24228	37762	1.58	2.0E-16	AF107714.1	EST_HUMAN	7B2B09.x1 NCL CGAP P12B Homo sapiens cDNA clone IMAGE:3303521 3'
198	13265	28210	2.57	1.0E-16	AF200718.1	NT	Human sapiens tubulin carrier protein E2-c (UBCH10), mRNA

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Definite Source	Top Hit Descriptor
392	13495		37.96	1.0E-16 AA628592.1	EST_HUMAN		af39111.1 Soares, fetal, fetus, N2H2F8, 5w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OPR12 ORF repetitive element:
1098	15209	28014	2.22	1.0E-16 BF327942.1	EST_HUMAN		QVQ-BN0148-07700-293-410 BN0148 Homo sapiens cDNA
8510	18400	32083	0.88	1.0E-16 AF103942.1	EST_HUMAN		Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
8574	18634		25.8	1.0E-16 U45933.1	NT		Homo sapiens CCR8 chemokine receptor (CCR8) gene, complete cds
8728	18782	33061	3.08	1.0E-16 Q02779	SWISSPROT		MITOCHONDRIAL PROTEIN KINASE 19 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7802	19534		6.75	1.0E-16 U45933.1	NT		Homo sapiens CCR8 chemokine receptor (CCR8) gene, complete cds
9838	22532	33031	1.06	1.0E-16 AW87985.1	EST_HUMAN		QV2P1002104040-124-603 P100210 Homo sapiens cDNA
3751	16793	25704	2.77	9.0E-17 AW500048.1	EST_HUMAN		CMH-NN1003-200900-103-401 NN1003 Homo sapiens cDNA
6886	19039		2.35	9.0E-17 A192994.1	EST_HUMAN		g22c11.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2100524 3' similar to contains MER28.12 MER28 repetitive element:
8445	21414		5.47	9.0E-17 AW15027.1	EST_HUMAN		tg49t12x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2300560 3' similar to contains OPR12 ORF repetitive element:
10584	23509		2.3	9.0E-17 AF200718.1	NT		Homo sapiens p53 tumor transforming gene protein (PTT16) gene, complete cds
1020	14089		2.01	9.0E-17 AW880791.1	EST_HUMAN		h9p0032.089305-355-401 O10932 Homo sapiens cDNA
3907	16947		0.88	9.0E-17 AL162802.2	NT		Homo sapiens chromosome 21 segment HS21C380
5983	25842	31927	3.24	9.0E-17 BE17261.1	EST_HUMAN		NR34-T0559-959300-503-624 H10559 Homo sapiens cDNA
7460	20455		1.82	9.0E-17 AW730759.1	EST_HUMAN		AV730759 HTF Homo sapiens cDNA clone HTFACB07.6
8019	20556	34349	0.94	9.0E-17 G133835	EST_HUMAN		Mus musculus dyx19c, exon, heavy chain 11 (Dyach11), mRNA
1452	14485		2.03	9.0E-17 G733027	NT		Mus musculus scolobocarin 3, coding complex 2 (Acolbac2), mRNA
5398	18459		3.14	7.0E-17 AE219590.1	NT		Homo sapiens putative MAP (MAP) mRNA, partial cds, alternatively spliced
6845	19808	32193	7.34	7.0E-17 AF229843.1	NT		Mus musculus WNT-2 gene, partial cds, putative ankyrin-related protein and cyclic fibroblast tetramembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
284	13305	26234	6.62	6.0E-17 AW683890.1	EST_HUMAN		RC1-HN003-220300-021-501 HN003 Homo sapiens cDNA
6448	19511	32781	1.9	8.0E-17 AW56272.1	EST_HUMAN		h9t1d4.x1 Soares, INF1, _GBC, S1 Homo sapiens cDNA clone IMAGE:2978955 3' similar to contains L1.12 L1 repetitive element:
10955	23577	37074	0.54	6.0E-17 P20138	SWISSPROT		MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (P8P7)
10026	23448		0.48	6.0E-17 W92331.1	EST_HUMAN		zefB93.8.1 Soares, fetal, heart, M8H18W Homo sapiens cDNA clone IMAGE:559893 3'
421	13118	28014	3.22	5.0E-17 T64110.1	EST_HUMAN		Y05H08.11 Stratiogene lung (6837210) Homo sapiens cDNA clone IMAGE:78689 3'
7840	20787	34162	1.76	5.0E-17 T91043.1	EST_HUMAN		Y05H08.11 Stratiogene liver spleen INF15 Homo sapiens cDNA clone IMAGE:109327 5'
9717	22746	38195	1.24	4.0E-17 AW128165.1	EST_HUMAN		Y05H08.11 NCL CGAP_K08 Homo sapiens cDNA clone IMAGE:2919322 3' similar to contains ALU repetitive element:contains MER19.11 MER19 repetitive element:

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11821	24704	38288	1.96	4.0E-17	AL183247.2	NT	Human sapiens chromosome 21 segment HS21C047
12003	28114		2.02	4.0E-17	A073546.1	EST_HUMAN	ov550Lx1 Score: 1618.181 Homo sapiens cDNA clone IMAGE:1840288 3' similar to TR-Q 18530
1460	14522		1.72	3.0E-17	D1547.1	NT	Q18830 PHMS1 mRNA, contains MER10.2 MER10 repetitive element;
2108	15125	28144	1.22	3.0E-17	AW110725.1	EST_HUMAN	Human DNA, SINE repetitive element
3208	18263		1.66	3.0E-17	P33410	SWISSPROT	IMAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3556	16989	29614	1.33	3.0E-17	BE28522.1	EST_HUMAN	hw65004Lx1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3181669 3'
3556	16989	29615	1.33	3.0E-17	BE28522.1	EST_HUMAN	hw65004Lx1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3181669 3'
5008	18078		1.17	3.0E-17	BF511268.1	EST_HUMAN	UH-BH49-c38-03-01.1 NCI CGAP S088 Homo sapiens cDNA clone IMAGE:3085043 3'
8611	21579	34958	1.16	3.0E-17	M8455.1	EST_HUMAN	z214602.1 Score: 1618.181 Homo sapiens cDNA clone IMAGE:262491 3' similar to contains PTB3.3 P1 H3 repetitive element;
10580	22887	36455	4.64	3.0E-17	A802688.1	NT	Human sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
10746	22888	37164	0.73	3.0E-17	A802688.1	EST_HUMAN	Q13580001-720700-283-412 BNC637 Homo sapiens cDNA
10746	22888	37165	0.73	3.0E-17	BF527012.1	EST_HUMAN	Q13580001-720700-283-412 BNC637 Homo sapiens cDNA
12268	25089		3.31	3.0E-17	11477068	NT	Human sapiens cDNA, SECY (S. cerevisiae) (SECY), mRNA
333	13442	26367	3.4	2.0E-17	A1270380.1	EST_HUMAN	Q82463Lx1 NCI CGAP_E202 Homo sapiens cDNA clone IMAGE:1836022 3' similar to contains Alu repetitive element;
354	13442	26367	3.97	2.0E-17	A1270380.1	EST_HUMAN	Q82463Lx1 NCI CGAP_E202 Homo sapiens cDNA clone IMAGE:1836022 3' similar to contains Alu repetitive element;
590	14042		2.04	2.0E-17	A4722832.1	EST_HUMAN	z081904.1 Score: 1618.181 Homo sapiens cDNA clone IMAGE:340751 3'
2453	15458	28479	2.3	2.0E-17	Q26983	SWISSPROT	ZONADHESIN PRECURSOR
2453	15458	28480	2.3	2.0E-17	Q26983	SWISSPROT	ZONADHESIN PRECURSOR
2341	15969	28622	8.23	2.0E-17	P12039	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 XOA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5440	18542	31452	1.8	2.0E-17	A27086.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5440	18542	31453	1.8	2.0E-17	A27086.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6309	19463		1.99	2.0E-17	A045088.1	NT	Human sapiens MHC class 1 region
6309	19463		1.66	2.0E-17	A045088.1	EST_HUMAN	DKFZ57623010.11162 (synonym: hmc2) Homo sapiens cDNA clone DKFZ57623010.5
8133	21070		0.85	2.0E-17	A8037839.1	NT	Human sapiens mRNA for KIAA1418 protein, partial cds
8420	21389	34769	1.47	2.0E-17	Q69158	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLFR3
8908	21767	35011	1.29	2.0E-17	A430040.1	EST_HUMAN	EST13304 Testis tumor Homo sapiens cDNA 5' and similar to similar to glycophorin
10228	23153	36943	2.35	2.0E-17	BE29488.1	EST_HUMAN	60944480P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:286016 5'
10294	23189	38873	2.83	2.0E-17	AL183247.2	NT	Human sapiens chromosome 21 segment HS21C047

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Single Exon Probe Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10294	20169	36674	2.83	2.0E-17	AL103247.2	NT	Homo sapiens chromosome 21 segment HS210047
10422	21544	37044	5.23	2.0E-17	D13391.1	NT	Human CYP18 gene for arylidase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10748	23697	37162	0.66	2.0E-17	P68003	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10748	23697	37163	0.66	2.0E-17	P68003	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10772	23693	37190	0.57	2.0E-17	A176902.1	EST_HUMAN	w84404.x1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719.3
10772	23693	37191	0.57	2.0E-17	A176902.1	EST_HUMAN	w84404.x1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719.3
12366	25153		1.31	2.0E-17	AF219894.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
751	13512	26755	3.24	1.0E-17	P03183	SWISSPROT	MULTIDrug RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1721	14751		1.35	1.0E-17	AJ271796.1	NT	Homo sapiens Xq pseudochromosomal region; segment 22
1782	14851	27797	4.54	1.0E-17	AI193207.2	NT	Homo sapiens chromosome 21 segment HS210307
2124	15141	28198	1.95	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2343	15353	28374	2.43	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene 1 (exon 1) region and exons 1A and 1B
3591	16026		1.06	1.0E-17	AF224899.1	NT	Homo sapiens mannitolase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4162	17153		6.83	1.0E-17	R05942.1	EST_HUMAN	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
6900	19990		0.86	1.0E-17	AW468463.1	EST_HUMAN	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
6959	19993	33151	1.73	1.0E-17	AI168942.1	EST_HUMAN	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
6959	19993	33152	1.73	1.0E-17	AI168942.1	EST_HUMAN	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
7265	20268	33303	0.95	1.0E-17	AI168931	SWISSPROT	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
8393	21955	33326	0.87	1.0E-17	BE502744.1	EST_HUMAN	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
10365	22383	35766	0.87	1.0E-17	AW46833.1	EST_HUMAN	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
11747	24632	38212	1.04	1.0E-17	Q12824	SWISSPROT	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
13104	25915		1.83	1.0E-17	BE221470.1	EST_HUMAN	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
3569	27292		2.96	8.0E-18	AI472107.1	EST_HUMAN	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5
3900	16540	20747	1.87	8.0E-18	4759377	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1)mRNA
3996	16536	20850	3.75	8.0E-19	Q07537	SWISSPROT	POLYPEPTIDE NACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc-POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAc-T1)
349	13438	26391	23.15	7.0E-19	AW316676.1	EST_HUMAN	h25272.1 Scores: fetal liver system INFLS Homo sapiens cDNA clone IMAGE:128338.5

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
349	13438	26902	23.15	7.0E-18	AW318976.1	EST_HUMAN	xc10804.x1 NCL_GGAP_Pert1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl:20888 60S
7677	20855	33397	0.95	7.0E-18	AW387542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-OT0081-170000-01-103 OT0081 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl:20888 60S
12769	13438	26901	2.67	7.0E-18	AW318976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xc10804.x1 NCL_GGAP_Pert1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl:20888 60S
12769	13438	26902	2.67	7.0E-18	AW318976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xc10804.x1 NCL_GGAP_Pert1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl:20888 60S
3308	19359	29278	1.29	6.0E-18	X77761.2	NT	Rattus norvegicus partial GAPDH-1 gene for glia-derived neuroproliferation mod.1, enhancer region (TGASE C1) (TGC)
4777	17797		4.3	6.0E-18	P82181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSEU TRANSGLUTAMINASE) Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83446), mRNA
8593	21561		2.64	6.0E-18	11428105	NT	Homo sapiens chromosomes 21 segment 1621C10
8691	21659	35882	0.67	6.0E-18	AL163210.2	NT	Homo sapiens chromosomes 21 segment 1621C10-6
11469	24412	37681	1.34	6.0E-18	AL163248.2	NT	H. sapiens DNA, DMB, HJ421, 1P2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RN/G8, 9, 13 and 14 genes
11657	24583	38168	2.06	6.0E-18	X87344.1	NT	Human osteoblast cytosolic (G2D2) gene, exon 4
12527	25266	31605	2.95	6.0E-18	U67425.1	NT	Human osteoblast cytosolic (G2D2) gene, exon 4
1160	14192	27144	17.8	5.0E-18	A280214.1	EST_HUMAN	Human osteoblast cytosolic (G2D2) gene, exon 4
9326	13469	31231	0.99	5.0E-18	A280214.1	EST_HUMAN	Human osteoblast cytosolic (G2D2) gene, exon 4
9720	22030	35469	5.93	5.0E-18	BE143312.1	EST_HUMAN	Human osteoblast cytosolic (G2D2) gene, exon 4
11323	24273	37600	3.26	5.0E-18	10242378	NT	Human osteoblast cytosolic (G2D2) gene, exon 4
11323	24273	37601	3.26	5.0E-18	10242378	NT	Human osteoblast cytosolic (G2D2) gene, exon 4
12649	25332		6.39	5.0E-18	AW167168.1	EST_HUMAN	Human osteoblast cytosolic (G2D2) gene, exon 4
12680	25544		3.2	5.0E-18	AW165047.1	EST_HUMAN	Human osteoblast cytosolic (G2D2) gene, exon 4
125	13332	28160	1.04	4.0E-18	BE444076.1	EST_HUMAN	Human osteoblast cytosolic (G2D2) gene, exon 4
125	13332	28161	1.04	4.0E-18	BE444076.1	EST_HUMAN	Human osteoblast cytosolic (G2D2) gene, exon 4
1729	14759	27744	1.91	4.0E-18	AA021814.1	EST_HUMAN	Human osteoblast cytosolic (G2D2) gene, exon 4
1906	14930		0.95	4.0E-18	A1736392.1	EST_HUMAN	Human osteoblast cytosolic (G2D2) gene, exon 4
2211	15226	28547	1.1	4.0E-18	006430	SWISSPROT	Human osteoblast cytosolic (G2D2) gene, exon 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	OFF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2211	15228	28246		1.1	4.0E-18 Q08430	SWISSPROT	NAACETYLLACTOSAMINE BETA-1,6-NACETYLGALACTOSAMINYLTRANSFERASE (N-ACETYLLACTOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (GNT)
3095	16846	29753		0.76	4.0E-18 A181886.1	EST_HUMAN	est3406.x1 Barleasat codon HPLR87 Homo sapiens cDNA clone IMAGE:279338 3' similar to contains Alu repetitive element
5437	18530	31447		2.29	4.0E-18 A1017965.1	EST_HUMAN	ou23406.x1 Sources NF1_T1_GBC_S1 Homo sapiens cDNA clone IMAGE:1607138 3'
5437	18530	31448		2.29	4.0E-18 A1017965.1	EST_HUMAN	ou23406.x1 Sources NF1_T1_GBC_S1 Homo sapiens cDNA clone IMAGE:1607138 3'
8173	21148			0.67	4.0E-18 AAT46811.1	EST_HUMAN	nc44608.x1 NCI_GCAP_A1M1 Homo sapiens cDNA clone IMAGE:1269688 similar to contains L1.12 L1 repetitive element
11348	24288	37826		4.22	4.0E-18 AA371807.1	EST_HUMAN	EST180933 Pituitary gland, subtracted (proliferating hormone) II Homo sapiens cDNA 5' and similar to EST containing O family repeat
850	13066	26955		24.99	3.0E-18 AA814196.1	EST_HUMAN	ac23h11.x1 NCI_GCAP_H8d Homo sapiens cDNA clone IMAGE:1324581 3' similar to SV1955_HUMAN
930	13083	29036		3.54	3.0E-18 BC398524.1	EST_HUMAN	PA6762.463 MED303MAL PRO REF:161
9372	17012	29026		1.31	3.0E-18 AL16247.2	NT	CU-51 T0862-21 T0300-258-2 B T0303 Homo sapiens cDNA
7003	20720	33444		6.43	3.0E-18 BE507671.1	EST_HUMAN	Human cDNA clone 121 and H321G347
11271	24223	37748		1.79	3.0E-18 BE1218650.1	EST_HUMAN	PLV30003.1 T0300-201-1428 BV0081 Homo sapiens cDNA
12774	25412			5.18	3.0E-18 AV1022015.1	EST_HUMAN	671694885: NH1 XGC 37 Homo sapiens cDNA clone IMAGE:4103652 5'
251	13348	26274		5.97	2.0E-18 AV1636263.1	EST_HUMAN	451312.1 Marfan Field Cephias Homo sapiens cDNA clone IMAGE:2468128 5'
1155	14197			67.85	2.0E-18 BE235697.1	EST_HUMAN	OU14 T0595: 182026-07-40/1 T0058 Homo sapiens cDNA
3140	19197	29107		1.27	2.0E-18 Q38075	SWISSPROT	607114352: NH1 XGC 16 Homo sapiens cDNA clone IMAGE:3335044 5'
5485	18895			3.85	2.0E-18 AA89610.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5584	18890	31644		3.38	2.0E-18 D14547.1	EST_HUMAN	4153007 x1 Sources beta1, NHT1 Homo sapiens cDNA clone IMAGE:1406892 3' similar to TR.O14577
5584	18890	31645		3.38	2.0E-18 D14547.1	NT	O14577 BAC CLONE RG11A109 FROM 7031, COMPLETE SEQUENCE. ;
5978	19053			1.07	2.0E-18 BE347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6280	19351	33508		1.07	2.0E-18 BE347229.1	EST_HUMAN	602021148: NCI_GCAP_Bm67 Homo sapiens cDNA clone IMAGE:4158670 5'
6280	19351	33508		1.07	2.0E-18 BE347229.1	EST_HUMAN	Human INVAR gene for interferon alpha/beta receptor
6405	19471	32724		0.76	2.0E-18 BF032940.1	EST_HUMAN	Human INVAR gene for interferon alpha/beta receptor
6451	19516	32707		4.42	2.0E-18 AV1665553.1	EST_HUMAN	IL3H401.1 Sources NF1_T1_GBC_S1 Homo sapiens cDNA
7970	20929	33993		0.72	2.0E-18 AA487619.1	EST_HUMAN	MR191.2 MER19 repetitive element
8487	21455	34872		0.52	2.0E-18 BE439524.1	EST_HUMAN	est60011.1 Striatum field rdna 937202 Homo sapiens cDNA clone IMAGE:839485 5' similar to
							HTM1-10871 HTM1 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Med Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10407	23239	39813		1.31	2.0E-19 AW151673.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
10407	23239	39814		1.31	2.0E-19 AW151673.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
11319	24296	37797		3.07	2.0E-19 AW470791.1	EST_HUMAN	U183306.X1 NCI_CGAP_G612 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.L3
12039	24914	39508		2.88	2.0E-19 AW151690.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
12461	14197			3.97	2.0E-19 BE250097.1	EST_HUMAN	U183306.X1 NCI_CGAP_G612 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.L3
4445	17471			0.93	1.0E-18 U95406.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
5429	18532	31412		2.71	1.0E-19 AV53405.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
5560	18746	31914		1.87	1.0E-19 D00099.1	NT	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
5560	18746	31915		1.87	1.0E-19 D00099.1	NT	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
6907	19937	32829		1.33	1.0E-19 AL163290.2	NT	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
8765	21752	35174		1.13	1.0E-19 AF146298.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
10259	23184	39659		4.28	1.0E-18 U91323.1	NT	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
12412	25184	31821		6.49	1.0E-19 AF003520.1	NT	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
547	13919	29540		5.55	9.0E-19 AA291991.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
548	13918	29540		4.1	9.0E-19 AA291991.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
8181	21151			5.71	0.0E-19 F06988.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
9039	22002	35423		2.64	0.0E-19 AL163293.2	NT	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
9039	22002	39424		2.64	9.0E-19 AL163293.2	NT	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
11462	24065	37953		3.37	9.0E-19 AB032998.1	NT	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
12172	13918	29540		1.64	9.0E-19 AA291991.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
10950	14096			1.31	9.0E-19 AF071402.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
4433	17460			0.96	9.0E-19 F06848	SWISSPROT	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
8488	21456	34873		1.04	9.0E-19 BE198906.1	EST_HUMAN	X87610.X1 NCI_CGAP_G644 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12

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Single Exon Probes Expressed in Bone Marrow

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6172	16247	32450	0.51	2.0E-19	AV731332.1	EST_HUMAN	AV731332 HTF Homo sapiens cDNA clone HTFAZ006 5'
7851	20524	33592	0.72	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8673	21641	33596	0.35	2.0E-19	AA072854.1	EST_HUMAN	2634209.1 Scores retina N26-HR Homo sapiens cDNA clone IMAGE:303890 5'
10289	23194	35692	0.69	2.0E-19	Q95755	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLFP2
432	13555		2.11	1.0E-19	BE40811.1	EST_HUMAN	601304125F1 NH_LAC0_21 Homo sapiens cDNA clone IMAGE:363310 5'
2174	15190	28211	1.65	1.0E-19	U30765.1	EST_HUMAN	X57927.1 Scores adult brain N26-HR85Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2729	15723		2.48	1.0E-19	Q35044.1	NT	Human gene for Ah-receptor, exon 7-9
2890	19920		4.26	1.0E-19	4748077	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3412	16460	23581	1.18	1.0E-19	AA654987.1	EST_HUMAN	MER37 repetitive element;
5166	18195		0.9	1.0E-19	AA171737.1	EST_HUMAN	XB8810.x1 Scores NF_L1_GBC_S1 Homo sapiens cDNA clone IMAGE:2904789 3' similar to contains MER37.2
1937	19277	32502	2.73	1.0E-19	U12188.1	NT	L1.32.L1.1 repetitive element;
6333	26895		0.83	1.0E-19	AA65527.1	EST_HUMAN	Cytosolic carboxyl sodiumdicarboxylate cotransporter mRNA, partial cds
7990	20534	34213	0.89	1.0E-19	U08513.1	NT	hK2403.s1 NO_CGAP_P1 Homo sapiens cDNA clone IMAGE:393093 similar to contains L1.11.L1 repetitive element;
7990	20534	34214	0.99	1.0E-19	U08513.1	NT	Cytosolic carboxyl Nucleoside cotransporter-related protein mRNA, complete cds
8355	23594		0.71	1.0E-19	U200718.1	NT	Homo sapiens putative tumor transforming gene protein (PTTG) gene, complete cds
8793	21760	35182	1.72	1.0E-19	AA4657.1	NT	Putative phosphatase kinase beta subunit mRNA, complete cds
9093	22559		2.74	1.0E-19	U65200.1	EST_HUMAN	hK2402.2 Scores full liver open 1NF1.5 Homo sapiens cDNA clone IMAGE:12543 5' similar to contains OTR repetitive element;
10106	23032		0.97	1.0E-19	U65200.1	NT	Human galactose 4-epimerase (GAL) gene, exons 7, 8 and 9, and partial cds
10547	23469	39864	27.33	1.0E-19	U1312269.1	EST_HUMAN	XC131071.4 B1069-031-505 ST0174 Homo sapiens cDNA clone IMAGE:272672 5'
10557	23470	39874	2.11	1.0E-19	AA4493.1	EST_HUMAN	X31409.1 Scores melanocyte 28NH.H Homo sapiens cDNA clone IMAGE:272672 5'
11659	24904		3.69	1.0E-20	AA123137.1	EST_HUMAN	df4901.v1 Norton First Cochlea Homo sapiens cDNA clone IMAGE:2487050 5'
6803	18857	33145	2.48	1.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6903	18917	33144	2.45	1.0E-20	AA22137.1	EST_HUMAN	qq85909.x1 Scores NF_L1_GBC_S1 Homo sapiens cDNA clone IMAGE:1842689 3'
7781	20714	34085	1.31	1.0E-20	AA22137.1	EST_HUMAN	qq85909.x1 Scores NF_L1_GBC_S1 Homo sapiens cDNA clone IMAGE:1842689 3'
3289	16342	29293	0.72	7.0E-20	BF32845.1	EST_HUMAN	PM4-AN0086-009002-003-404 AN0086 Homo sapiens cDNA
7189	18419	31220	5.55	7.0E-20	AA119120.1	EST_HUMAN	DKF254J10092.J1 547 (synonym: h5r1) Homo sapiens cDNA clone DKF254J0992 5'
8841	21606	35227	9.11	7.0E-20	AA567597.1	EST_HUMAN	hK6204.s1 NC1_CGAP_P1 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28.2

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	21808	36228	8.11	7.0E-20	AA557597.1	EST_HUMAN	145604.s1 NCI_GGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28.52
12023	24859		6.31	7.0E-20	9972033	NT	MER29 repetitive element:
3056	18013	29535	3.93	6.0E-20	P9188	SW/ISSPROT	Homo sapiens ribosomal protein, L13a (RPL13A), mRNA
4301	17330	30210	2.98	6.0E-20	BE522434.1	EST_HUMAN	ALU SUBFAMILY J SEQUENCE CONTAINING WARNING ENTRY
4626	17547		1.05	5.0E-20	AV725128.1	EST_HUMAN	801441231F11 NH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
7322	20293	33936	1.19	5.0E-20	AF075901.1	EST_HUMAN	AV720323 HTO Homo sapiens cDNA clone HTCBTA01 5'
8277	21249	34657	5	5.0E-20	W00525.1	EST_HUMAN	AF075931 Homo fetal liver cDNA library Homo sapiens cDNA clone H40286
8277	21249	34657	5	5.0E-20	W00525.1	EST_HUMAN	277608.s1 Soares_fetal_liver_spleen_NFLS_31 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element:
8440	21609	34822	0.79	5.0E-20	BE165950.1	EST_HUMAN	277608.s1 Soares_fetal_liver_spleen_NFLS_31 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element:
9187	22153	35682	1.24	5.0E-20	AB028174.1	NT	1453-H10457-10200-388-001 D10043 Homo sapiens cDNA
9187	22153	35683	1.24	5.0E-20	AB028174.1	NT	Mus musculus MYAN-3 mRNA, complete cds
9800	2123		0.83	5.0E-20	CG0699	SW/ISSPROT	MYOTHECAL PROTEIN, DUB45024.1
1024	14857	27635	1.73	4.0E-20	AL15247.2	SW/ISSPROT	Homo sapiens chromosome 21 segment H5210247
9732	18820		0.89	4.0E-20	CG0699	SW/ISSPROT	H52ONE H2B C (H2BQ)
8258	21227		5.27	4.0E-20	AB028174.1	EST_HUMAN	294503.s1 NCI_GGAP_Oxas Homo sapiens cDNA clone IMAGE:405433 5'
10655	22765	37298	1.9	3.0E-20	BF18249.1	EST_HUMAN	Q13-Q1094502000-088-001 D10043 Homo sapiens cDNA
2149	15165	28181	0.81	3.0E-20	U03848.1	NT	Human BXP21 gene
4237	17265	30183	1.53	3.0E-20	P23273	SW/ISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4556	17576	30562	1.43	3.0E-20	AA037618.1	EST_HUMAN	2495012.s1 Soares_pregnant_fetus_NHRU Homo sapiens cDNA clone IMAGE:494895 3' similar to contains L1_9 L1 repetitive element:
5297	22253	34597	3.32	3.0E-20	D14647.1	NT	Human DNA, SINE repetitive element
10684	22665	37059	0.86	3.0E-20	BF18249.1	EST_HUMAN	80184350F11 NH_MGC_84 Homo sapiens cDNA clone IMAGE:405433 5'
11024	23989		1.59	3.0E-20	F11359	SW/ISSPROT	RETROVIRUS-RELATED POLYPROTEIN CONTAINS: REVERSE TRANSCRIPTASE ; ENDOINUCLEASE
11840	24723	38308	8.22	3.0E-20	A128424.1	EST_HUMAN	q70402.s1 NCI_GGAP_K43 Homo sapiens cDNA clone IMAGE:1864903 3' similar to contains Alu repetitive element:
11840	24723	38309	8.22	3.0E-20	A128424.1	EST_HUMAN	q70402.s1 NCI_GGAP_K43 Homo sapiens cDNA clone IMAGE:1864903 3' similar to contains Alu repetitive element:
12029	25130	31849	4.15	3.0E-20	BE688422.1	EST_HUMAN	80151410F11 NH_MGC_71 Homo sapiens cDNA clone IMAGE:3916232 5'
831	13988		33.91	2.0E-20	AW303888.1	EST_HUMAN	W24160.s1 NCI_GGAP_UH4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to 3W_RS0_MOUSE P97441 40S RIBOSOMAL PROTEIN S6 ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (10p) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1113	14157	27107	3.88	2.0E-20	AA916335.1	EST_HUMAN	ng5b06.at NCL CGAP Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TRG1224068
1113	14157	27108	3.88	2.0E-20	AA916335.1	EST_HUMAN	G1224068 ORF2: FUNCTION UNKNOWN. ; ng5b06.at NCL CGAP Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TRG1224068
2828	13888		15.97	2.0E-20	AW030966.1	EST_HUMAN	x24410.1 NCL CGAP Lip2 Homo sapiens cDNA clone IMAGE:2761068 3' similar to SW_R85_MOUSE
4883	17698	30680	4.76	2.0E-20	C28693	SWISSPROT	P97481.40S RIBOSOMAL PROTEIN S8. ;
4883	17698	30687	4.76	2.0E-20	C28693	SWISSPROT	ZONARHESIN PRECURSOR
8485	21424	34540	0.9	2.0E-20	A339457.1	EST_HUMAN	EST180238 Liver II Homo sapiens cDNA 5' and
9445	25503	35557	7.85	2.0E-20	D10383.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
9445	25508	35559	7.85	2.0E-20	D10383.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12703	25714	31611	3.98	2.8E-20	H55371.1	EST_HUMAN	CHR22B370 Chromosome 22 zen Homo sapiens cDNA clone C22_391 5'
2029	18622	28083	4.32	1.0E-20	AA291693.1	EST_HUMAN	Z11681.1 NCL CGAP GC31 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER16.2 MER16 repetitive element;
4467	17493	30380	1.04	1.0E-20	BF115158.1	EST_HUMAN	784800.X1 NCL CGAP XG11 Homo sapiens cDNA clone IMAGE:335155 5' similar to contains L12 L1
7079	20100	33411	1.04	1.0E-20	KF46867.1	EST_HUMAN	AF09597 Homo sapiens cDNA clone IMAGE:2994714 5' similar to SW_NIAM_HUMAN
6518	22481	35526	2.24	1.0E-20	11181847	NT	AF09597 Homo sapiens cDNA clone IMAGE:2994714 5' similar to SW_NIAM_HUMAN Homo sapiens autocrine High/Concentrated Protein (ACHP) mRNA
11879	24761	38346	2.11	1.0E-20	AF223891.1	NT	Homo sapiens cationic channel alpha1E subunit (CACNA1E) gene, exon 7-49, and partial cda, alternatively spliced
12458	25215		3.09	1.0E-20	AA420453.1	EST_HUMAN	ng5b06.at NCL CGAP F11 Homo sapiens cDNA clone IMAGE:745694 similar to contains L13 L1 repetitive element;
2923	15891		1	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MIP1H12-8J21
12175	25023		3.77	9.0E-21	AW898186.1	EST_HUMAN	RC3-NN0068-90/900-021-1503 NN0068 Homo sapiens cDNA
9163	22129		1.13	8.0E-21	AW674891.1	EST_HUMAN	B330602.1 NH_MGC_10 Homo sapiens cDNA clone IMAGE:2994714 5' similar to SW_NIAM_HUMAN
11896	24748	38330	4.39	8.0E-21	AA90411.1	EST_HUMAN	O95169 NADH-UBIQUINONE OXIDOREDUCTASE ASH SUBUNIT PRECURSOR ;
12342	25140		2.94	8.0E-21	D21330	SWISSPROT	0871068.at NCL CGAP GC31 Homo sapiens cDNA clone IMAGE:1936833 3'
2032	15099	28115	1.59	7.0E-21	P16900	SWISSPROT	A TP SYNTHASE A CHAIN (PROTEIN 6)
2032	15099	28116	1.59	7.0E-21	P16900	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (LAMININ CHAIN B3)
3716	16759	28671	0.63	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (LAMININ CHAIN B3)
4283	17633		9.22	7.0E-21	AA04592.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
6573	19312	32000	0.81	7.0E-21	AL163218.2	NT	z687606.r1 Boreas_pigment_uarru_NDRPU Homo sapiens cDNA clone IMAGE:487688 5'
							Homo sapiens chromosome 21 segment HS21C018

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8751	21696	35124	1.42	7.0E-21	AJ27557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxyribonucleotides (dNT-2 gene), exons 1-5
9024	21690	35411	11.21	7.0E-21	D14716.1	NT	Human chromosomal protein HMG1 related gene
10472	23394	38891	0.82	7.0E-21	AJ659022.1	EST_HUMAN	RC3-OT1601-271169-031-03 OT1601 Homo sapiens cDNA
11954	24017	37540	1.09	7.0E-21	AA72464.1	EST_HUMAN	4275003.01 Source, fetal, heart, NBH1819W Homo sapiens cDNA clone IMAGE398981 3' similar to gox14398 VITAMIN K-DEPENDENT PROTEIN 5 PRECURSOR (HUMAN) contains THR13 OPR repetitive element;
11998	24837	38004	1.87	7.0E-21	7796888	NT	Homo sapiens PTD19 protein (PTD19), mRNA
4100	17103	30052	1.08	6.0E-21	BE408911.1	EST_HUMAN	60730412P1 NHR130C-21 Homo sapiens cDNA clone IMAGE393510 5'
9491	22985	30052	0.99	6.0E-21	BE162737.1	EST_HUMAN	PM114355-1 NHR130C-21 Homo sapiens cDNA clone IMAGE393510 5'
4390	17418	30322	3.16	6.0E-21	BE564838.1	EST_HUMAN	PM114355-1 NHR130C-21 Homo sapiens cDNA clone IMAGE393510 5'
4639	17860	30753	0.18	6.0E-21	4686474	EST_HUMAN	PM114355-1 NHR130C-21 Homo sapiens cDNA clone IMAGE393510 5'
9271	20151		0.82	6.0E-21	AW40894.1	EST_HUMAN	1655410.01 NC1 CGAP DNA1 Homo sapiens cDNA clone IMAGE2618184 3'
7713	20268	33570	0.96	6.0E-21	BE565955.1	EST_HUMAN	7782411.01 NC1 CGAP P228 Homo sapiens cDNA clone IMAGE3305573 3' similar to contains OPR11 OPR repetitive element;
10310	23669	37374	0.43	6.0E-21	Q91060	SWISSPROT	ZINC FINGER PROTEIN GLT1 (GL1)
10390	23669	37375	0.43	6.0E-21	Q91060	SWISSPROT	ZINC FINGER PROTEIN GLT1 (GL1)
12255	25981		5.98	6.0E-21	AA343574.1	EST_HUMAN	0096408.01 NC1 CGAP X48 Homo sapiens cDNA clone IMAGE727978 5'
1748	14777	27792	1.05	4.0E-21	AA070713.1	EST_HUMAN	PM55 MRNA, contains OPR11 OPR repetitive element;
7055	20077	33396	3.35	6.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for TIM, complete cds
10139	23065	39541	0.59	4.0E-21	U91928.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-H) gene, Rhesus, and sodium phosphate transporter (NPT3) gene, complete cds
1854	14980	27876	1.05	3.0E-21	AA218891.1	EST_HUMAN	2015003.01 Stradegene fetal retina S91702 Homo sapiens cDNA clone IMAGE529771 3'
2282	15295	28319	1.48	3.0E-21	AL193201.2	NT	Homo sapiens chromosome 21 segment H821C001
3090	16153	29065	4.17	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5577	18973	31636	0.93	3.0E-21	AJ27557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxyribonucleotides (dNT-2 gene), exons 1-5
5677	18973	31637	0.93	3.0E-21	AJ27557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'3'-deoxyribonucleotides (dNT-2 gene), exons 1-5
5928	18916		0.74	3.0E-21	AJ661044.1	EST_HUMAN	AJ661044.1 GLT Homo sapiens cDNA clone GLC004.10 3'
6903	19374		1.86	3.0E-21	BF164736.1	EST_HUMAN	RC104466F1 NHR130C-21 Homo sapiens cDNA clone IMAGE366948 5'
7271	20006	33306	7.16	3.0E-21	BF561093.1	EST_HUMAN	RC1-07088-10860-018-g08 OT1088 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10031	23078	36446	0.77	3.0E-21	AW1897760.1	EST_HUMAN	GM-HN0085-260405-265405-H08.N0083 Homo sapiens cDNA
147	14250	28145	28.45	2.0E-21	BE163247.1	EST_HUMAN	Q153-H10469-170300-090-312.H10468 Homo sapiens cDNA
1219	14237	28145	3.29	2.0E-21	BE094410.1	EST_HUMAN	RC4-BT0311-147186-011-H08.BT0311 Homo sapiens cDNA
2848	16543	28867	2.28	2.0E-21	Q26883	SWISSPROT	ZONADHESIN PRECURSOR
2346	15043	28866	2.26	2.0E-21	Q26883	SWISSPROT	ZONADHESIN PRECURSOR
5681	19539	31604	1.64	2.0E-21	A624582.1	EST_HUMAN	163003.x1 NCL CGAP P41 Kent Homo sapiens cDNA clone IMAGE2200109.3 similar to TR.Q16984.Q16984
5688	19732	31610	0.81	2.0E-21	A624582.1	EST_HUMAN	HYPOPHYSAL 511 KD PROTEIN
5688	19732	31610	0.81	2.0E-21	A624582.1	EST_HUMAN	28078121 Scores: 1611.NM1.NM118787 Homo sapiens cDNA clone IMAGE36870.3
5688	19732	31610	0.81	2.0E-21	A624582.1	EST_HUMAN	28078121 Scores: 1611.NM1.NM118787 Homo sapiens cDNA clone IMAGE36870.3
8149	10224	32654	0.81	2.0E-21	AV14545	EST_HUMAN	22828211 Scores: 1611.NM1.NM118787 Homo sapiens cDNA clone IMAGE36870.3
8615	21563	34060	0.48	2.0E-21	Q101070.1	EST_HUMAN	22828211 Scores: 1611.NM1.NM118787 Homo sapiens cDNA clone IMAGE36870.3
8708	21874	34058	0.64	2.0E-21	BE141768.1	EST_HUMAN	Q1010703-291705-59111.H1010703 Homo sapiens cDNA
8775	22141	35667	3.66	2.0E-21	AL135770.1	EST_HUMAN	AUT38770.P1.6211.H08.83 Homo sapiens cDNA clone IMAGE36870.3
11847	24564	38152	1.72	2.0E-21	BE073920.1	EST_HUMAN	601800365F1.NM1.MG.83 Homo sapiens cDNA clone IMAGE36870.3
11647	24604	38153	1.72	2.0E-21	BE073920.1	EST_HUMAN	601800365F1.NM1.MG.83 Homo sapiens cDNA clone IMAGE36870.3
12560	23279	17611	17.61	2.0E-21	AF178916.1	NT	Homo sapiens putative 5-hydroxytryptophan DNA glycoprotein, complete cds
1260	14256	27359	2.06	1.0E-21	A4557657.1	EST_HUMAN	M48204.x1 NCL CGAP P41 Kent Homo sapiens cDNA clone IMAGE1043718 similar to contig ME28.52
1402	14435	17611	7.17	1.0E-21	A651284.1	EST_HUMAN	ME28.52
6634	19652	17611	2.6	1.0E-21	AL076792.1	EST_HUMAN	163003.x1 NCL CGAP P41 Kent Homo sapiens cDNA clone IMAGE1043718 similar to contig ME28.52
7398	20366	33719	4.83	1.0E-21	A223104.1	EST_HUMAN	163003.x1 NCL CGAP P41 Kent Homo sapiens cDNA clone IMAGE1043718 similar to contig ME28.52
10603	23525	37021	0.46	1.0E-21	AL163203.2	NT	NEUTRAL PROTEASE LARGE SUBUNIT
10603	23525	37022	0.46	1.0E-21	AL163203.2	NT	NEUTRAL PROTEASE LARGE SUBUNIT
10949	23869	17611	1.67	1.0E-21	5780038	NT	Homo sapiens chromosome 21 segment HS21C003
12032	28514	17611	1.32	1.0E-21	AF046133.1	NT	Homo sapiens chromosome 21 segment HS21C003
4439	17485	30355	2.03	0.0E-22	A1702498.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
8961	21917	35411	1.29	0.0E-22	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C001
8951	21917	35411	1.29	0.0E-22	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C001
11144	24104	37031	3.13	0.0E-22	AV161974.1	EST_HUMAN	AV161974 MDS Homo sapiens cDNA clone MDS0005.6
949	14002	17611	7.03	0.0E-22	BE144748.1	EST_HUMAN	CMO-H10179-281059-076-H05.H10179 Homo sapiens cDNA
8238	21917	17611	3.82	0.0E-22	A404602.1	EST_HUMAN	28078121 Scores: 1611.NM1.NM118787 Homo sapiens cDNA clone IMAGE36870.3
660	13731	26056	6.76	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4312	17341	30221	2.96	7.0E-22	U94538	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5076	16096	32966	0.97	7.0E-22	U90986.1	EST	Homo sapiens gene for actinin receptor type IIB, complete cds
6038	22004		2.48	7.0E-22	AF151054.1	NT	Homo sapiens HSPC229 mRNA, complete cds
6184	22150	35376	3.88	7.0E-22	AF178500.1	EST	EST 007348 Fatal brain, <i>Stratagene</i> (c1895209) Homo sapiens cDNA clone HF6P07
6961	22698	35349	1.98	7.0E-22	AF100660.1	NT	Homo sapiens T cell receptor beta locus, TORB1/TSX/212 TORB1/TSX/252 region
8384	21532		1.68	6.0E-22	AF102973.1	EST	W45507.71 NC1 CGAP_Gas4 Homo sapiens cDNA clone IMAGE 3540812 3'
8385	16351		0.72	5.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
8385	16351		0.72	5.0E-22	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C103
8695	19723	32968	3.05	5.0E-22	AL18303.2	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10026	23094	37098	7.82	5.0E-22	U63622.1	NT	naa27D05.x1 NC1 CGAP_P728 Homo sapiens cDNA clone IMAGE 3265698 3' similar to contains AU repetitive element
12765	25413		2.76	5.0E-22	BF478511.1	EST	Homo sapiens Xq pseudobuccal region, segment 1/2
9650	16993		0.83	4.0E-22	AJ27735.1	NT	AV703223 A05 Homo sapiens cDNA clone IMAGE1512 5'
8443	21411	34824	0.42	4.0E-22	AV703223.1	EST	Homo sapiens chromosome 21 segment HS12C002
8765	25008		3.36	4.0E-22	AF163202.2	NT	0918828T01 NT1_MGC_2170 Homo sapiens cDNA clone IMAGE 4095434 5'
11077	24039	37863	2.15	4.0E-22	BF218030.1	EST	Homo sapiens chromosome 21 segment HS21C009
12838	25518		2.74	4.0E-22	AF163200.2	NT	in 14H10.x1 NC1 CGAP_Gas4 Homo sapiens cDNA clone IMAGE 2186611 3' similar to gbL119593 HIGH AFFINITY NCI CELLULAR RECEPTOR B(HUMAN) contains L1 L1 repetitive element
990	14013		1.00	3.0E-22	AJ498676.1	EST	W6396 NC1 CGAP_Bn28 Homo sapiens cDNA clone IMAGE 2429839 3' similar to SW RL21_HUMAN
2576	15877	28596	2.15	3.0E-22	A850308.1	EST	P4078 3' non-coding protein IMG1 related gene
3686	18726		1.35	3.0E-22	D14718.1	NT	W6397.x1 Sarcos, unpaired, alpha, NHRPU Homo sapiens cDNA clone IMAGE 1097860 3' similar to contains NER12.42 MER12 repetitive element
4838	17855	30782	2.88	3.0E-22	AJ060125.1	EST	OV9-H10368-20020-058472 H10368 Homo sapiens cDNA
8972	21540		1.21	3.0E-22	U51195.1	EST	RG5-H10707-1-53300-321-H10707 Homo sapiens cDNA
8703	21871	35093	3.4	3.0E-22	U60950.1	EST	R status RY253 mRNA for a potential ligand-binding protein
8703	21871	35094	0.77	3.0E-22	X60950.1	NT	R status RY253 mRNA for a potential ligand-binding protein
1970	14891		4.79	2.0E-22	X60950.1	EST	X73205.31 Sarcos malaricopey RNHM Homo sapiens cDNA clone IMAGE 287709 3'
2528	15031	28582	1.82	2.0E-22	P24616	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3431	16478	28598	4.78	2.0E-22	839443.1	EST	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKG3), mRNA
4233	17882	30163	1.28	2.0E-22	AF117764.1	NT	PM1-371025-291109-001-df1 371025 Homo sapiens cDNA
5991	25646	32232	1.34	2.0E-22	V39458.1	EST	222001.11 Sarcos, senescent, fibroblasts, NHR5F Homo sapiens cDNA clone IMAGE 322873 5' similar to gb-X72908 MONOCYTE CHEMOATRACTIC PROTEIN 3 PRECURSOR (HUMAN);
5991	18372	32611	3.57	2.0E-22	BF022116.1	EST	RCO-NT0075-150900-023-H12 NT0079 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10091	22886	36456	1.61	2.0E-22	AJ278322.1	EST_HUMAN	q77603.x1 Soares, NIH/NIH, S1 Homo sapiens cDNA clone IMAGE:187829.3 similar to contains MER29.13 MER29 repetitive element;
10158	23081	36557	0.65	2.0E-22	AJ715315.1	EST_HUMAN	nc04111.1 NC_003617 Homo sapiens cDNA clone IMAGE:1216269.3
10391	23081	36557	0.65	2.0E-22	AJ715315.1	EST_HUMAN	nc04111.1 NC_003617 Homo sapiens cDNA clone IMAGE:1216269.3
10391	23081	36557	0.65	2.0E-22	AJ715315.1	EST_HUMAN	nc04111.1 NC_003617 Homo sapiens cDNA clone IMAGE:1216269.3
12054	24227	36525	1.88	2.0E-22	AW16900.1	EST_HUMAN	Y18620.1 Soares Infant brain T1NB Homo sapiens cDNA clone IMAGE:29740.5
12139	24504	31705	1.92	2.0E-22	AW16900.1	EST_HUMAN	nc04111.1 NC_003617 Homo sapiens cDNA clone IMAGE:29740.5
1895	14621	27917	1.78	1.0E-22	AW66517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2588	15599	28000	1.82	1.0E-22	U05071.1	NT	PMAS-SN0023-070400-009-H2 SN020 Homo sapiens cDNA
3422	16470	26590	1.49	1.0E-22	D14547.1	NT	Human DNA, SNE repetitive element
5235	18300		1.5	1.0E-22	AF03628.1	EST_HUMAN	Homo sapiens X-linked arylsulfatase ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
8015	20553	34547	0.95	1.0E-22	B5024697.1	EST_HUMAN	MR0310685-22030-002-H07 B10659 Homo sapiens cDNA
10916	23683	37854	0.8	1.0E-22	AJ35455.1	EST_HUMAN	q36307.x1 NC_003617 Homo sapiens cDNA clone IMAGE:2020081.3 similar to contains MER29.13 MER29 repetitive element;
10916	23683	37854	0.8	1.0E-22	AJ35455.1	EST_HUMAN	q36307.x1 NC_003617 Homo sapiens cDNA clone IMAGE:2020081.3 similar to contains MER29.13 MER29 repetitive element;
12081	25654	37855	0.05	6.0E-23	AF193280.1	EST_HUMAN	q36307.x1 NC_003617 Homo sapiens cDNA clone IMAGE:2020081.3 similar to contains MER29.13 MER29 repetitive element;
12081	25654	37855	0.05	6.0E-23	AF193280.1	EST_HUMAN	q36307.x1 NC_003617 Homo sapiens cDNA clone IMAGE:2020081.3 similar to contains MER29.13 MER29 repetitive element;
3322	16373	37842	1.99	7.0E-23	AF193280.1	EST_HUMAN	q36307.x1 NC_003617 Homo sapiens cDNA clone IMAGE:2020081.3 similar to contains MER29.13 MER29 repetitive element;
11376	24523	37842	4.11	7.0E-23	AF193280.1	EST_HUMAN	q36307.x1 NC_003617 Homo sapiens cDNA clone IMAGE:2020081.3 similar to contains MER29.13 MER29 repetitive element;
3447	16194		1.88	6.0E-23	AF193280.1	NT	Human DNA, SNE repetitive element
4297	17326	30208	1.13	6.0E-23	AF193280.1	NT	Homo sapiens chromosome 21 segment HS21C049
12281	25099	31834	4.64	6.0E-23	AF224693.1	NT	Homo sapiens menadione, beta A, lysozyme (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12281	25099	31835	4.64	6.0E-23	AF224693.1	NT	Homo sapiens menadione, beta A, lysozyme (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12480	25228	31795	3.03	6.0E-23	AJ209130.1	EST_HUMAN	q36307.x1 NC_003617 Homo sapiens cDNA clone IMAGE:1839480.3 similar to
5910	18918	31562	4	5.0E-23	U02871.2	NT	SW-610, MOUSE P2349 PROTEIN MOV-10.1
5937	20590	32676	3.55	5.0E-23	AF170818.1	NT	Homo sapiens chromosome Xc28 melanoma antigen family A2c (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calreticulin (CAL), NAD(P)H dehydrogenase-like protein (NDHL), and Lp
7671	25550	32679	3.25	5.0E-23	AF170818.1	NT	Pongo pygmaeus olfactory receptor (PPY118) gene, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	19640	32026	1.07	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8550	19640	32607	1.07	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8171	21141	34547	4.18	3.0E-23	AA130165.1	EST_HUMAN	235909.1 Soares_piguan_10000_Homo sapiens cDNA clone IMAGE:503066 5' similar to contains MER29.12 MER29.12 repetitive element;
9604	22608	35038	2.74	3.0E-23	Z70654.1	NT	Human endogenous retroviral element HC2
9604	22608	35039	2.74	3.0E-23	Z70654.1	NT	Human endogenous retroviral element HC2
10680	23602	36727	1.27	3.0E-23	AI186727.1	EST_HUMAN	Homo sapiens KIA0081 gene (partial), X13 gene and 12/17L1 gene
667	17322	26657	3.75	2.0E-23	AJ268860.1	NT	Homo sapiens KIA0081 gene (partial), X13 gene and 12/17L1 gene
1145	15917		3.02	2.0E-23	M55270.1	NT	Human matrix cell protein (MCP) gene, complete cds
2807	15796	28917	2.08	2.0E-23	P21105	SWISSPROT	TENASCIN PRECURSOR (TNX) (HEXADECAHON-LIKE)
2807	15796	28918	2.08	2.0E-23	P21105	SWISSPROT	TENASCIN PRECURSOR (TNX) (HEXADECAHON-LIKE)
3384	16433		1.15	2.0E-23	AI201458.1	EST_HUMAN	98731.1 Soares_piguan_10000_Homo sapiens cDNA clone IMAGE:194357 3' similar to TR-01337 Q1337
3729	16771		2.97	2.0E-23	AF103600.1	EST_HUMAN	98731.1 Soares_piguan_10000_Homo sapiens cDNA clone IMAGE:194357 3' similar to TR-01337 Q1337
4051	17040	26647	2.80	2.0E-23	U03693.1	EST_HUMAN	98731.1 Soares_piguan_10000_Homo sapiens cDNA clone IMAGE:194357 3' similar to TR-01337 Q1337
4051	17040	26648	2.80	2.0E-23	U03693.1	EST_HUMAN	98731.1 Soares_piguan_10000_Homo sapiens cDNA clone IMAGE:194357 3' similar to TR-01337 Q1337
5023	19672	30952	8.49	2.0E-23	D14547.1	NT	Human DNA, SINE repetitive element
5205	21175		4.26	2.0E-23	AF280107.1	NT	Homo sapiens cyclochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cyclochrome P450 polypeptide 43 (CYP3A43) gene, partial cds
9165	22161	35589	1.12	2.0E-23	AI163032.2	NT	polypeptide 5 (CYP3A5) gene, partial cds
12362	25069		3.91	2.0E-23	M32658.1	NT	Homo sapiens chromosome 21 segment HS21C103
12787	25419		2.55	2.0E-23	AF209600.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
4559	17581	30472	1.44	1.0E-23	AI163292.2	NT	Human alpha 1 cell receptor beta locus, TCRB/783A2 to TCRB/7252 region
4709	17516		4.76	1.0E-23	AI163210.2	NT	Homo sapiens chromosome 21 segment HS21C082
6882	19684		3.11	1.0E-23	BC578471.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
8969	21807	35090	4.73	1.0E-23	AA448007.1	EST_HUMAN	601234455F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:369865 5' zw62030.1 Soares_10000_Homo sapiens cDNA clone IMAGE:792698 5' similar to contains PTR6.2 PTR6 repetitive element;
554	13824		3.05	9.0E-24	AA668313.1	EST_HUMAN	ab7508.41 Stragane fetal retina 297202 Homo sapiens cDNA clone IMAGE:852758 3' similar to
4978	17866	30586	1.15	8.0E-24	P21289	SWISSPROT	TRE 19822 E19822 CA PROTEIN, ;
4978	17866	30587	1.15	8.0E-24	P21289	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 18
6951	19051	32922	1.34	8.0E-24		SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 18
8155	21063	34492	0.77	8.0E-24		NT	Homo sapiens capping protein (actin filament) muscle 2 line, alpha 2 (CAP2A2), mRNA
							Homo sapiens capping protein (actin filament) muscle 2 line, alpha 2 (CAP2A2), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Exon Signal	Most Similar (Top) HIT BLAST E Value	Top HIT Accession No.	Top HIT Database Source	Top HIT Description	
3886	16926		1.36	7.0E-24	AIW67984.1	EST_HUMAN	Q1074047.1:10200-122406 D70047 Homo sapiens cDNA	
707	13769		2.31	6.0E-24	AB071125.1	NT	Muscle laccase mRNA for Tests-Specific Protein Y (TSPY), complete cds	
639	13896		15.66	6.0E-24	AIJ163240.1	EST_HUMAN	Human telomerase chromosome 21 segment H821C049	
3884	17094		8.31	5.0E-24	AJ220043.1	NT	Human sapiens 959 to contig between AML1 and CBRT on chromosome 21q22, segment 3/3	
8034	20371		1.34	5.0E-24	AF225991.1	NT	Human sapiens calcium channel alpha1E subunit (CAV1A1E) gene, exons 7-49, and partial cds, alternatively spliced	
6039	19121		3.2328	4.0E-24	AI4584178.1	EST_HUMAN	h11065 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:1085625 3' similar to SW:POL_MLVK	
9020	21856		3.63	4.0E-24	AF163711.1	EST_HUMAN	PC3-3T97/33010244:PROTEIN 5'1597 Homo sapiens cDNA	
11514	24356		3.9002	4.0E-24	AF163711.1	EST_HUMAN	PC3-3T97/33010244:PROTEIN 5'1597 Homo sapiens cDNA	
12644	23528		3.1769	4.0E-24	AB028076.1	NT	Human sapiens mRNA for h1041035 protein, partial cds	
12607	25713		3.6160	4.0E-24	M20707.1	NT	Human sapiens Lysine-immunoglobulin germline pseudogene (Ch-22.4) variable region (subgroup V kappa II)	
12676	26509		3.1709	4.0E-24	11418318	NT	Human sapiens G-2 and S-phase associated 1 (G2SE1), mRNA	
7285	20092		33398	3.0E-24	U60691.1	NT	Human germline T-cell receptor beta chain TCORBV1751A1T, TCORBV1751A1T, TCORBV1051P, TCORBV2851P, TCORBV1851P, TCORBV1451T, TCORBV1151A1T, HVJ beta, TCORBV2851P, TCORBV2451, TCORBV1451, TCORBV351, TCORBV51A1T, TRV4, TRV5, TRV7, TRV9, TCORBD1, TCORBJ151, TCORBJ152.2	
7285	20092		33399	3.0E-24	U60691.1	NT	Human germline T-cell receptor beta chain TCORBV1751A1T, TCORBV1751A1T, TCORBV1051P, TCORBV2851P, TCORBV1851P, TCORBV1451T, TCORBV1151A1T, HVJ beta, TRV7, TRV9, TCORBD1, TCORBJ151, TCORBJ152.2	
8795	21723		2.85	3.0E-24	AIW61487.1	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32	
8522	21769		2.7529	3.0E-24	AF163703.1	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32	
8620	22659		36126	3.0E-24	AF163703.1	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32	
17121	26309		31772	2.16	3.0E-24	BF12765.1	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32
2354	145739		26395	2.0E-24	AI457389.1	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32	
3512	16652		0.86	2.0E-24	U6068106.1	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32	
7593	20092		34031	2.0E-24	AIJ163203.2	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32	
7715	20672		34039	2.0E-24	AF036824.1	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32	
7720	20672		34042	2.0E-24	AF036824.1	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32	
0002	22048		35484	0.95	2.0E-24	AI119158.1	EST_HUMAN	h10802 at NCI_GGAP_Gart Homo sapiens cDNA clone IMAGE:2607660 3' similar to contains M2628.32

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Toe Hit Descriptor
6130	22066		0.96	2.0E-24	H0214.1	EST_HUMAN	YB2008.T1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element:
10213	23138	39928	0.98	2.0E-24	A1927156.1	EST_HUMAN	1774003.X1 NCI_GGAP_KG11 Homo sapiens cDNA clone IMAGE:2138008 3'
10213	23138	39927	0.98	2.0E-24	A1927156.1	EST_HUMAN	1774003.X1 NCI_GGAP_KG11 Homo sapiens cDNA clone IMAGE:2138008 3'
12588	25947		10.03	2.0E-24	M3837.1	NT	Human O family duplicated repeat element
1705	14735	27717	2.83	1.0E-24	T708340	NT	Homo sapiens CGI-127 protein (LOC51048). mRNA
2681	19677		1.82	1.0E-24	AW820184.1	EST_HUMAN	QV051034-100400-165-510 5'10284 Homo sapiens cDNA
3033	18061	28009	0.78	1.0E-24	D68423.1	EST_HUMAN	Homo sapiens PTEIN (PTEN) gene, exon 2
4250	17328		2	1.0E-24	AF14318.1	NT	Homo sapiens keratin complex-1, gene C28 (Krt-28). mRNA
8541	18603	32955	0.68	1.0E-24	T106306	NT	Homo sapiens chromosome 21 region RS21103
7760	20748	34123	3.95	1.0E-24	AL163003.2	NT	Homo sapiens chromosome 21 region RS21103
8002	20941	34334	0.68	1.0E-24	BE144528.1	EST_HUMAN	MBCH10765-17189-505-309 5'118103 Homo sapiens cDNA
8276	21243	34636	1.81	1.0E-24	AW901164.1	EST_HUMAN	CHCH-NT1012-13300-281-13011 Homo sapiens cDNA
6625	19683	32951	0.52	1.420402		NT	Homo sapiens nuclear pore complex (NPC) protein (NUP133). mRNA
12008	24885	38480	1.53	9.0E-26	T709707	NT	Homo sapiens nuclear pore complex protein (NUP133). mRNA
5031	18045		2.85	7.0E-25	A4463944.1	EST_HUMAN	1076508.X1 NCI_GGAP_KG11 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.32
8861	21528	34949	6.83	7.0E-25	A4463944.1	EST_HUMAN	1076508.X1 NCI_GGAP_KG11 Homo sapiens cDNA clone IMAGE:911754 similar to contains THR32 THR repetitive element:
12012	24886	38498	3.24	7.0E-25	A4593540.1	EST_HUMAN	H25908.X1 NCI_GGAP_P11 Homo sapiens cDNA clone IMAGE:914843 similar to SWR14A_YEAST
7184	19315		10.38	6.0E-25	AW87033.1	EST_HUMAN	P38105 PROBABLE 60S RIBOSOMAL PROTEIN L4EA.1
7882	24951		10.38	6.0E-25	Z938360	NT	2059507.1 Scores. fetal. liver. spleen. 1N1LS 5'11 Homo sapiens cDNA clone IMAGE:418889 5'
1659	14981	27897	1.87	5.0E-25	AW850271.1	EST_HUMAN	Mus musculus dogapin (Dogap). mRNA
5183	18182		0.82	5.0E-25	A4984228.1	EST_HUMAN	L3-C10219-18189-031-004 C10219 Homo sapiens cDNA
11525	20382	39150	3.16	5.0E-25	AW87907.1	EST_HUMAN	048801.X1 NCI_GGAP_B12 Homo sapiens cDNA clone IMAGE:183161 3' similar to contains Alu repetitive element:
1141	14974	27451	2.3	4.0E-25	T88107.1	EST_HUMAN	ES1391717 IMAGE:183161 3' similar to contains Alu repetitive element:
3413	19461		2.68	4.0E-25	AW837671.1	EST_HUMAN	YB6804.X1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:121785 5'
3225	19983	28876	0.83	4.0E-25	AW700368.1	NT	PM2-OT1008-280200-207-g07 OT10083 Homo sapiens cDNA
4945	17372		3.13	4.0E-25	BE170957.1	EST_HUMAN	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
3331	18382	28003	2.77	3.0E-25		NT	QV3-OT10543-14000-148-471 OT10543 Homo sapiens cDNA
3331	18382	28004	2.77	3.0E-25		NT	Homo sapiens hypothetical protein FL20344 (FL20344). mRNA
5977	18966	32157	0.64	3.0E-25	U35312.1	NT	Human degenerate channel MOEG mRNA, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Annotation No.	Top Hit Database Source	Top Hit Description
6769	19824	33107	0.66	3.0E-25	AA63590.1	EST_HUMAN	nc27502.s1 NCI GAP P222 Homo sapiens cDNA clone IMAGE:1177615 similar to p5461668 ZINC
6890	19448	35070	4.08	3.0E-25	AL163210.2	NT	FINGER PROTEIN 66 (HUMAN);
1350	14365	27584	2.0	2.0E-25	5632196	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
2317	15328	26581	7.52	2.0E-25	BE68601.6.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2042	15551	26572	3.35	2.0E-25	P17008	SWISSPROT	403 RIBOSOMAL PROTEIN S16
4216	17247	30131	1.96	2.0E-25	P17008	SWISSPROT	403 RIBOSOMAL PROTEIN S16
4216	17247	30132	1.96	2.0E-25	P17008	SWISSPROT	403 RIBOSOMAL PROTEIN S16
10123	23049	36528	2.03	2.0E-25	AL146973.1	EST_HUMAN	AL146973 Homo sapiens Testis (Stanford GS) Homo sapiens cDNA
304	13450	26578	1.4	1.0E-25	AL140220.1	EST_HUMAN	DKFZP334H0313.J1 434 (synonym: Hec3) Homo sapiens cDNA clone DKFZP334H0313.6
1253	14289		1.34	1.0E-25	6933467	NT	Human endogenous retrovirus, complete genome
2441	15446	26466	1.04	1.0E-25	Q00055	SWISSPROT	ATP SYNTHASE LIPID-BINDING-DOMAIN P2PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4695	17912	30002	2.33	1.0E-25	BE192737.1	EST_HUMAN	PMT-HT048-08070-002-106 HT0454 Homo sapiens cDNA
6719	19776		0.63	1.0E-25	AA189080.1	EST_HUMAN	z44506.s1 Striatum INT neuron (853723) Homo sapiens cDNA clone IMAGE:633267.3 similar to confilins A19 repetitive element
6955	25978	33516	3.22	1.0E-25	AA592890.1	EST_HUMAN	nn5411.s1 NCI CGAP K068 Homo sapiens cDNA clone IMAGE:1087749.3
6246	21215	34623	4.38	1.0E-25	AA709579.1	EST_HUMAN	ZR6904.s1 Soares, fetal heart NDRH16W Homo sapiens cDNA clone IMAGE:394422.3 similar to contains PTRS 3' PTR repetitive element
9904	22858	36317	0.89	1.0E-25	X09900.1	NT	R. rattus RY235 mRNA for a potential ligand-binding protein
9904	22859	36316	0.89	1.0E-25	X09900.1	NT	R. rattus RY235 mRNA for a potential ligand-binding protein
11316	24286	37794	2.91	1.0E-25	U51163.1	NT	Homo sapiens IMAGE:92 (IMAGE-92), IMAGE-85 (IMAGE-85), IMAGE-84 (IMAGE-84), and IMAGE-81 (IMAGE-81) genes, complete cds
12278	25097	39180	1.47	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12278	25097	39181	1.47	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
13053	25301		1.63	1.0E-25	D14755.1	NT	Human histone H3b, constant region complex (gamma)
2451	15494	26519	1.47	3.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5776	16970		1.36	6.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
1560	14619	27565	2.88	7.0E-26	AF03526.1	NT	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4005	17044	26552	1.21	7.0E-26	692211.1	NT	H. sapiens DNA for endogenous retroviral like element
4168	17217	30103	1.69	7.0E-26	AA746158.1	EST_HUMAN	h02612.s1 Soares, NF1, C5C, S1 Homo sapiens cDNA clone IMAGE:2658389.3
5721	18616	31994	0.72	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11978	24895		6.08	7.0E-26	AA115996.1	EST_HUMAN	z43006.s1 Striatum, neocortex, human NT 26AM1 82724 Homo sapiens cDNA clone IMAGE:548943.5 similar to p54M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2234	12248	28272	2.25	6.0E-26	AF028008.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and lymphocyte gene families
3367	18407	29329	3.91	6.0E-26	AA020131.1	EST_HUMAN	cd28/24.7 Strategic neuroepithelium (8637231) Homo sapiens cDNA clone IMAGE:543271 5'
11920	24887	35482	1.91	6.0E-26	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21CH10
1181	14222	27176	1.88	5.0E-26	AI108235.1	EST_HUMAN	as39h08.2 Barista acta HPLR88 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WPF4C12.11 CE03371.
1181	14222	27176	1.88	5.0E-26	AI108235.1	EST_HUMAN	as39h08.2 Barista acta HPLR88 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WPF4C12.11 CE03371.
1546	14579	19546	0.98	4.0E-26	AA329546.1	EST_HUMAN	EST33446 Embryo, 12 week, 11 Homo sapiens cDNA 5' and
9767	22703	37514	3.71	4.0E-26	7657970	NT	Homo sapiens upstream coding transcript303 (cancer RNA polymerase (UB TF) mRNA
11022	23687	37514	2.63	4.0E-26	BE266197.1	EST_HUMAN	601918459F1 SHC1 Homo sapiens cDNA clone IMAGE:535210 5'
11773	14802	27767	2.15	3.0E-26	D14547.1	NT	Human D14547.1 SHC1 Homo sapiens cDNA clone IMAGE:535210 5'
2019	15040	28051	1.27	3.0E-26	AI048552.2	EST_HUMAN	DNF22434.1 Strategic neuroepithelium NT/PRAM1 887234 Homo sapiens cDNA clone DNF2434069 5'
2047	15068		3.59	3.0E-26	AA115805.1	EST_HUMAN	DNF22434.1 Strategic neuroepithelium NT/PRAM1 887234 Homo sapiens cDNA clone IMAGE:548949 5'
3791	16632	29748	1.12	3.0E-26	AA152464.1	EST_HUMAN	Similar to p3-M14338 VITAMIN K-DEPENDENT PROTEIN 5 PRECURSOR (HUMAN);
3791	16632	29748	1.12	3.0E-26	AA152464.1	EST_HUMAN	Similar to p3-M14338 VITAMIN K-DEPENDENT PROTEIN 5 PRECURSOR (HUMAN);
7096	20590	33334	1.22	3.0E-26	BE24548.1	EST_HUMAN	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
11894	24775	35391	2.03	3.0E-26	AI087586.1	EST_HUMAN	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
11894	24775	35392	2.03	3.0E-26	AI087586.1	EST_HUMAN	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
11228	24930	38404	4.91	3.0E-26	AA583173.1	EST_HUMAN	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
13101	25924	31576	1.37	3.0E-26	AF16520.1	NT	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
13101	25924	31576	1.37	3.0E-26	AF16520.1	NT	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
852	14301	28872	10.68	2.0E-26	AL103262.2	EST_HUMAN	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
11022	14302	28872	3.68	2.0E-26	AI038069.2	EST_HUMAN	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
3245	16500	29226	4.92	2.0E-26	X69694.1	NT	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
11105	24935		2.38	2.0E-26	D37675.1	NT	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
11553	24409	38049	2.55	2.0E-26	AB01412.1	EST_HUMAN	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
11745	24633		1.76	2.0E-26	AF050586.1	NT	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
12097	24683	38565	1.84	2.0E-26	AF03786.1	NT	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374
12338	25168		1.7	2.0E-26	AB037892.1	NT	cd39f10.4 Strategic colon (8637204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TRG98374

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
137	13242	26172	37.48	1.0E-28	BE170371.1	EST_HUMAN	Q14HT0538-020300-129-a02 HT0538 Homo sapiens cDNA
2093	13001	26100	1.33	1.0E-26	AL030933.2	EST_HUMAN	DKFZ-33411610_1134 (synonym: hras) Homo sapiens cDNA clone DKFZ-33411610 5'
2597	15953		11.4	1.0E-26	AF281085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds
7018	20142		2.79	1.0E-26	BE185980.1	EST_HUMAN	MR3-HT0497-150200-119-g01 HT0487 Homo sapiens cDNA
11239	24192		2.12	1.0E-26	AL030487.1	EST_HUMAN	DKFZ-39602148_11361 (synonym: hlk25) Homo sapiens cDNA clone DKFZ-39602148 5'
12830	26964		2.85	1.0E-26	H60064.1	EST_HUMAN	CHR22032 Chromosome 22 exon Homo sapiens cDNA clone C22_46 5'
7837	20764		1.24	9.0E-27	BF31727.1	EST_HUMAN	RC3-FN0138-10800-022-a02 FN0138 Homo sapiens cDNA
8888	22815		4.34	9.0E-27	U93163.1	NT	Homo sapiens IMAGE-382 (IMAGE-83), IMAGE-83 (IMAGE-83), and IMAGE-81 (IMAGE-81) genes, complete cds
12142	26008		5.95	9.0E-27	BF445696.1	EST_HUMAN	na0307.X1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE3328944 3' similar to contains OFR-11
11	13131	26029	4.71	8.0E-27	A681462.1	EST_HUMAN	W49004.X1 NCL CGAP_L1618 Homo sapiens cDNA clone IMAGE2408150 3' similar to contains THR-12
859	13028		4.81	8.0E-27	AL163272.2	NT	THR repetitive element 1
1414	14447	27419	30.06	8.0E-27	AV162737.1	EST_HUMAN	ad07H03.X1 Schindler fetal brain 10004 Homo sapiens cDNA clone IMAGE2783295 3' similar to gb:K00598
1414	14437	27420	30.06	8.0E-27	AV162737.1	EST_HUMAN	ad07H03.X1 Schindler fetal brain 10004 Homo sapiens cDNA clone IMAGE2783295 3' similar to gb:K00598
2177	15162	26714	1.1	8.0E-27	AV164761.1	EST_HUMAN	TUBULIN ALP-PA1 CHAIN HUMAN
3189	16284	29174	1.17	8.0E-27	P12236	SWISSPROT	P0253001.5-220303-029-027 N3017 Homo sapiens cDNA
3394	16414	29039	0.94	8.0E-27	A4F61897.1	NT	ADP-ATP CARRIER PROTEIN, LIVER (SCP-ORF172 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3))
5779	18871	32053	0.97	8.0E-27	AV722314.1	EST_HUMAN	Homo sapiens UBR1 (UBR1) gene, complete cds
7170	18401		2.12	8.0E-27	BE026560.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB08 5'
7248	19983	33290	2.41	8.0E-27	U64970.1	EST_HUMAN	MR4-BT0389-26200-204-098 BT0389 Homo sapiens cDNA
8564	23528	33976	1.41	8.0E-27	AV163756.1	EST_HUMAN	J751F Human fetal heart, Umbilical 24F Express Homo sapiens cDNA clone J751 5' similar to
8564	23528	33976	1.41	8.0E-27	AV163756.1	EST_HUMAN	REPETITIVE ELEMENT L1
8564	23528	33976	1.41	8.0E-27	AV163756.1	EST_HUMAN	CM1-CT0315-591256-065-067 CT0315 Homo sapiens cDNA
884	13747		1.85	7.0E-27	T0684.1	NT	CM1-CT0315-591256-065-067 CT0315 Homo sapiens cDNA
5126	18135		2.05	7.0E-27	AW629172.1	EST_HUMAN	Human endogenous retroviral element H2
6209	22178		0.98	7.0E-27	U68084.1	NT	h51H12.x1 Scars, NFL, T, OBC, S1 Homo sapiens cDNA clone IMAGE-2675876 3' similar to TRC076040
11011	24001		3.24	7.0E-27	A1217195.1	NT	OT6040 ORF2: FUNCTION UNKNOWN ;
12759	25402		1.54	7.0E-27	AV1723395.1	EST_HUMAN	Homo mRNA for KIA03231 gene, partial cds
						NT	Homo sapiens Xq pseudautosomal region, segment 1/2
						EST_HUMAN	AV723395 HTB Homo sapiens cDNA clone HTBAHB02 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11080	24042	37595	10.71	6.0E-27	M08997.1	NT	Human nucleolar protein (622) mRNA, complete cds
8055	20992		0.79	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C03
10597	23519	37010	3.37	5.0E-27	BF606914.1	EST_HUMAN	592121467F11 NH_ MGC_36 Homo sapiens cDNA clone IMAGE:4278527 5'
10597	23519	37011	3.37	5.0E-27	BF606914.1	EST_HUMAN	592121467F11 NH_ MGC_36 Homo sapiens cDNA clone IMAGE:4278527 5'
6509	19900	33258	1.72	4.0E-27	9910599	NT	Mus musculus sperm tail associated protein (Stap) mRNA
8271	21240		1.22	4.0E-27	AL163269.2	NT	Homo sapiens chromosome 21 segment HS21C09
8316	21285		1.25	4.0E-27	AF578779.1	NT	Human nucleolar protein (622) mRNA, complete cds
10101	23027	39504	0.72	4.0E-27	AF578779.1	EST_HUMAN	Q10-070033-207300-153110 OT003 Homo sapiens cDNA
11029	24810	38405	1.98	4.0E-27	X82211.1	NT	Homo sapiens cDNA for ectoparasitoid nuclear line element
2057	15078	28068	4.38	3.0E-27	X82333.3	NT	Human RYX3 mRNA for a potential ligand-binding protein
4300	17529	30259	1.08	3.0E-27	U62076.4	EST_HUMAN	P10-87037-090100-091-d11 B7037 Homo sapiens cDNA
5419	18222	31400	0.86	3.0E-27	AF577703.1	EST_HUMAN	7B4C028 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B4C08
8089	21025	34424	0.37	3.0E-27	AF577703.1	EST_HUMAN	7B4C028 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone IMAGE:3281283 3'
9880	22917	36271	0.48	3.0E-27	BF603391.1	EST_HUMAN	801486321F11 NH_ MGC_36 Homo sapiens cDNA clone IMAGE:3882088 5'
43	13163	28068	9.25	2.0E-27	AF594197.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1011	14935		24.32	2.0E-27	AA595345.1	EST_HUMAN	h01b10.31 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:1000669 similar to gb:U17880 605
3128	46183		10.81	2.0E-27	AF626172.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); h01b112.4 Soares, NFL, L, GBC, S1 Homo sapiens cDNA clone IMAGE:2078579 3' similar to TR:07840 OT6040 ORF2: FUNCTION UNKNOWN. ;
3238	48330	29218	1.81	2.0E-27	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cdc gene, complete cds; and unknown gene
3238	48330	29216	1.61	2.0E-27	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cdc gene, complete cds; and unknown gene
6933	19866	33176	0.72	2.0E-27	H02695.1	EST_HUMAN	y89601.4 Soares plasmid Nbz2IP Homo sapiens cDNA clone IMAGE:159340 5' similar to SP-HMGC, MOUSE Q02891 HOMEDBOX PROTEIN ;
8427	21098	34807	1.44	2.0E-27	A860347.1	EST_HUMAN	w89607.21 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:236268 3'
9824	22668	36562	2.81	2.0E-27	AA594527.1	EST_HUMAN	h01b005.51 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:9493737 similar to contains L1 B L1 repetitive element ;
10151	23078	39552	0.78	2.0E-27	X60958.1	NT	Kratius RYX3 mRNA for a potential ligand-binding protein
10395	23317	39797	1.32	2.0E-27	U78990.1	EST_HUMAN	EST100738 Fetal brain, Striatum (callosal223) Homo sapiens cDNA clone HBC6707
10395	23317	39798	1.32	2.0E-27	U78990.1	EST_HUMAN	EST100738 Fetal brain, Striatum (callosal223) Homo sapiens cDNA clone HBC6707
11302	24232	37778	2.97	2.0E-27	AUT1885.1	EST_HUMAN	AUT17683 HUMAN1 Homo sapiens cDNA clone IMAGE:1200748 5'
11818	14634		19.93	2.0E-27	AA595345.1	EST_HUMAN	h01b10.31 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:1000669 similar to gb:U17880 605 ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe Seq ID NO.	Exon Seq ID NO.	ORF Seq ID NO.	Expression Signal	Most Similar (Top) Htt BLAST E Value	Top Hit Accesion No.	Top Hit Database Source	Top Hit Description
435	13510		2.28	1.0E-27	AB183242.1	NT	Homo sapiens chromosome 21 segment H521 C046
998	14049	27002	1.68	1.0E-27	AB028698.1	NT	Homo sapiens DNA, DLEC1 to ORG1L4 gene region, section 1/2 (DLEC1, ORG1L3, ORG1L4 genes, complete cds)
1707	14738	27720	0.95	1.0E-27	cd876309	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
4108	14741		5.21	1.0E-27	BE36127.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
6694	19751	33028	1.08	1.0E-27	60068353	EST	Homo sapiens Retinoid-derived POU-domain factor-1 (RPF1), mRNA
7054	20076	33394	2.01	1.0E-27	F30158.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
7054	20076	33395	2.01	1.0E-27	F30158.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
8957	21923	33351	1.0E-27	1.0E-27	BE079292.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
9337	22302	33201	2.33	1.0E-27	BE079292.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
10090	23007	35478	1.9E-27	1.0E-27	D87446.1	NT	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
12018	24689	39490	3.73	1.0E-27	DA111063.1	NT	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
143	13245		2.16	9.0E-28	BE348398.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
311	13403	26329	2.84	9.0E-28	AU126260.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
4817	17834	30732	1.06	9.0E-28	F60447	SWISSPROT	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
12222	20599		3.71	9.0E-28	BF371658.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
12593	23817		1.9	8.0E-28	AU157971.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
11955	14226	27182	8.98	7.0E-28	AU142750.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
11230	24451	38072	2.43	7.0E-28	11417869.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
12191	22033		2.38	7.0E-28	AU735344.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
9271	20257		1.09	6.0E-28	AF016522.1	NT	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
12606	24543		3.82	6.0E-28	AA505462.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
318	13410		3.1	5.0E-28	AU21003.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
4035	17073	28973	1.32	5.0E-28	AF76762.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
2653	16532	28857	1.46	4.0E-28	AU190068.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
2869	16047	28967	1.18	4.0E-28	4403316	NT	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
3126	16162	26092	1.93	4.0E-28	BE40100.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
1705	16162	26092	1.93	4.0E-28	BE40100.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
12606	24543		3.82	6.0E-28	AA505462.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
318	13410		3.1	5.0E-28	AU21003.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
4035	17073	28973	1.32	5.0E-28	AF76762.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
2653	16532	28857	1.46	4.0E-28	AU190068.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
2869	16047	28967	1.18	4.0E-28	4403316	NT	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
3126	16162	26092	1.93	4.0E-28	BE40100.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
1705	16162	26092	1.93	4.0E-28	BE40100.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
12606	24543		3.82	6.0E-28	AA505462.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
318	13410		3.1	5.0E-28	AU21003.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
4035	17073	28973	1.32	5.0E-28	AF76762.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
2653	16532	28857	1.46	4.0E-28	AU190068.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
2869	16047	28967	1.18	4.0E-28	4403316	NT	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
3126	16162	26092	1.93	4.0E-28	BE40100.1	EST	Homo sapiens X-chromosome (H. influenzae) homolog (XLYB) mRNA
1705	16162	26092	1.93	4.0E-28</			

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7551	25514	33872	2.46	4.0E-28	A118894.1	EST_HUMAN	q66f10.x1 Srcrns_testc_NHT Homo sapiens cDNA clone IMAGE:1758019 3' similar to g6M16603 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN):
11213	24166		3.51	4.0E-28	AF228306.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinase gene families
11349	24299		38.65	4.0E-28	AB033241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
11394	25514	33872	3.87	4.0E-28	A118894.1	EST_HUMAN	q66f10.x1 Srcrns_testc_NHT Homo sapiens cDNA clone IMAGE:1758019 3' similar to g6M16603 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN):
12599	25301		1.85	4.0E-28	AI554244.1	EST_HUMAN	RC3-CT0254-260405-270-472 CT0254 Homo sapiens cDNA Homo sapiens metalloproteinase-like, disintegrin-like, cysteine-rich protein 2 option (ADAM22) mRNA, complete cds
1288	14323		2.61	3.0E-28	AF153382.1	NT	MF3-CT0712-285505-315-409 CT0713 Homo sapiens cDNA
8179	22146	35572	1.94	3.0E-28	BF354030.1	EST_HUMAN	Homo sapiens MHC class I region
11382	24232	37758	2.14	3.0E-28	U63588.1	NT	Y68007.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410865 3' similar to contains Alu repeats
12828	25316		2.52	3.0E-28	AI831891.1	EST_HUMAN	RC1-CT0565-230330-319-035 CT0564 Homo sapiens cDNA Homo sapiens disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
89	13205	28129	11.64	2.0E-28	BE092197.1	EST_HUMAN	Homo sapiens CTG84 gene for integrin beta 4 subunit, exon 3-41
1047	14083	27045	4.14	2.0E-28	4851972	NT	Homo sapiens CTG84 gene for integrin beta 4 subunit, exon 3-41
1189	14210	27164	12.37	2.0E-28	Y11107.3	NT	RC58068.x1 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2.L1 repetitive element:
2485	15489	28513	2.27	2.0E-28	AI346934.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21 C009
3373	18423	29348	0.76	2.0E-28	AL103062	NT	Y17603.x1 NCL CGAP_K08T Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element:
8440	19005	32756	1.46	2.0E-28	BF224402.1	EST_HUMAN	601814196T NIH_MGC_51 Homo sapiens cDNA clone IMAGE:4048751 5'
8464	19239		0.46	2.0E-28	BF212865.1	EST_HUMAN	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
8578	21343	34780	8.68	2.0E-28	AF503373.1	NT	EST1384394 IMAGE: ressequencs, MKG1 Homo sapiens cDNA
9943	22570		8.68	2.0E-28	AIW22305.1	EST_HUMAN	Homo sapiens nematode-like, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
11306	24817	38414	1.92	2.0E-28	AF246893.1	NT	Y75629.T1 Sones infant trant. 1N18 Homo sapiens cDNA clone IMAGE:44300 9
12309	25003		2.05	2.0E-28	BF06076.1	EST_HUMAN	Human gene for A1h-receptor, exon 1-9
12309	25003		3.15	1.0E-28	AB0944.1	NT	QV1-1710821-120000-300-503 T10821 Homo sapiens cDNA
2235	15243	24368	1.84	1.0E-28	BF333238.1	EST_HUMAN	Homo sapiens ubiquitin TPR motif, Y150form (UTY) mRNA, alternative transcript 2, complete cds
2235	15243	24368	0.92	1.0E-28	AF500095.1	NT	Y752104.HTF Homo sapiens cDNA clone H1769493 3' (LOC30091), mRNA
4685	18200	30989	0.64	1.0E-28	AI732194.1	EST_HUMAN	Homo sapiens similar to fibronectin protein C12 (H. sapiens) (LOC30091), mRNA
8193	21163		8.03	1.0E-28	11428983	NT	Homo sapiens hypothetical protein FL10888 (FL10888), mRNA
8332	21321		3.37	1.0E-28	8622778	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9633	22577	39027	4.47	1.0E-26	AA308744.1	EST_HUMAN	EST178618 HCC cell line (relatals to liver in mouse) II Homo sapiens cDNA 5' and similar to similar to retroviral LTR
10235	23160	39649	6.47	1.0E-26	4756431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A), mRNA
10235	23160	39649	6.47	1.0E-26	4756431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A), mRNA
12186	20333	39649	4.36	1.0E-26	AA054182.1	EST_HUMAN	2F5101.1 Scores refina N354HR Homo sapiens cDNA clone IMAGE:390448 5'
12931	22716	31302	2.88	1.0E-26	AL103247.2	NT	Homo sapiens chromosome 21 segment HS210047
13037	22819	31302	3.46	9.0E-26	AW66987.1	EST_HUMAN	H76506.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12713	22867	31302	3.12	8.0E-26	Q00130	SWISSPROT	HYPOPHYRETICAL GENE 50 PROTEIN
1008	14386	27615	1.04	7.0E-26	AW66947.1	EST_HUMAN	EST178621 IMAGE ressequenced, MAGI Homo sapiens cDNA
3564	13910	27615	0.9	7.0E-26	BE24708.1	EST_HUMAN	30114460.F1 NH.MGC.10 Homo sapiens cDNA clone IMAGE:335537 5'
13986	22816		9.37	7.0E-26	AL152352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
697	13664	26776	6.87	6.0E-26	AI535746.1	EST_HUMAN	W65601.x1 NH.MGC.19035 Homo sapiens cDNA clone IMAGE:346668 3' similar to TR-O1475
12488	22334		8.12	6.0E-26	BE44433.1	EST_HUMAN	Q15475 UNMANAGED PEROX-PROTEIN CONTAINS LTR.61 LTR repetitive element;
12488	22334		8.12	6.0E-26	BE44433.1	EST_HUMAN	Q15475 UNMANAGED PEROX-PROTEIN CONTAINS LTR.61 LTR repetitive element;
12488	22334		1.97	8.0E-26	BF66397.1	EST_HUMAN	Q2184052.1 NH.MGC.42 Homo sapiens cDNA clone IMAGE:430009 5'
5323	16047		8.35	8.0E-26	AI168124.1	EST_HUMAN	Human cDNA clone IMAGE:3621036
9368	22449		8.35	8.0E-26	AI168124.1	EST_HUMAN	RC3-OT009.1 T0003-0112 OT0091 Homo sapiens cDNA
3246	16301		1.33	4.0E-26	A1732067.1	EST_HUMAN	cn15602.x1 Normal Human Tubercular Bone Cells Homo sapiens cDNA clone NTGEC-cn15602 random
6126	12023		5.91	4.0E-26	BE146303.1	EST_HUMAN	QV110471.230300.121405147471 Homo sapiens cDNA
8417	21366	34764	0.02	4.0E-26	AI678101.1	EST_HUMAN	W35509.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element;
8417	21366	34764	0.02	4.0E-26	AI678101.1	EST_HUMAN	W35509.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element;
9097	22053	35466	2.97	4.0E-26	JA4698.1	NT	Human 50 kD heat shock protein gene, complete cds
2379	15387	28411	0.94	3.0E-26	U8747.1	NT	Human beta-galactoside alpha2,6-sialyltransferase (SAT1) mRNA, exon U
4444	17470	30359	1.81	3.0E-26	AB042267.1	NT	Homo sapiens PFS gene for 6-pyruvate/hydroxymethyl synthase, complete cds
4764	17784	30360	0.94	3.0E-26	BF33326.1	EST_HUMAN	QV110481.1-120003-360-503 BT0821 Homo sapiens cDNA
6040	19122	32327	0.77	3.0E-26	BE314018.1	EST_HUMAN	6Y1162657.1 NH.MGC.19 Homo sapiens cDNA clone IMAGE:350857 5'
9095	22051	35473	2.19	3.0E-26	D38044.1	NT	Human gene for A3-receptor, exon 7,9
9655	22508	38047	1.97	3.0E-26	AW303317.1	EST_HUMAN	xy1783.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains A3U repetitive element; contains MER19.12 MER19 repetitive element;
9989	22842		2.2	3.0E-26	AL163246.2	NT	Homo sapiens chromosome 21 segment HS210049

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10319	23242		0.73	3.0E-20	BE330127.1	EST_HUMAN	h09g01.x1 NCL CGAP_K4413 Homo sapiens cDNA clone IMAGE:2146250 3' similar to contains MER28.b3 MER29 repetitive element.
12365	25163		2.34	3.0E-20	D03882.1	NT	Human HLM15 mRNA for HLM15, complete cds
493	13465	28487	1.86	2.0E-20	A1934609.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
493	13465	28488	1.86	2.0E-20	A1934609.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
1355	14560	27638	7.19	2.0E-20	A1963904.1	EST_HUMAN	wf6610.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2492603 3' similar to TR015546 O15646 HERV-ENVELOPE GLYCOPROTEIN.
1355	14568	27639	7.19	2.0E-20	A1963904.1	EST_HUMAN	wf6610.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2492603 3' similar to TR015546 O15646 HERV-ENVELOPE GLYCOPROTEIN.
4308	17537	30215	2.4	2.0E-20	AI162368.2	NT	Homo sapiens chromosome 21 segment HS21C048
5251	18250	31128	0.96	2.0E-20	O54827	SWISSPROT	POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE VA
5924	19010	32253	1.06	2.0E-20	A082499.1	EST_HUMAN	cc71664.x1 NCL CGAP_C02 Homo sapiens cDNA clone IMAGE:161081.4 3' similar to contains L1.12.1 repetitive element.
6304	19375	32613	1.22	2.0E-20	A090416.1	EST_HUMAN	wf7207.x1 Soares_NHL_T_0802_S1 Homo sapiens cDNA clone IMAGE:2356660 3' similar to contains human MER20 repetitive element.
7608	19375	32613	1.18	2.0E-20	A090416.1	EST_HUMAN	wf7207.x1 Soares_NHL_T_0802_S1 Homo sapiens cDNA clone IMAGE:2356660 3' similar to contains human MER20 repetitive element.
8509	21778	34480	0.04	2.0E-20	U5267170.1	EST_HUMAN	60142229FT NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3949348 5'
8624	21980	35117	0.83	2.0E-20	U5267170.1	EST_HUMAN	60142229FT NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3949348 5'
8624	21980	35118	0.83	2.0E-20	U5267170.1	EST_HUMAN	60142229FT NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3949348 5'
8955	22852	36258	3.5	2.0E-20	AI193248.2	NT	Homo sapiens DNA-binding protein (LOC556242), mRNA
8955	22852	36259	3.5	2.0E-20	AI193248.2	NT	Homo sapiens DNA-binding protein (LOC556242), mRNA
10663	23521	37013	3.37	2.0E-20	AI193248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10663	23521	37014	3.37	2.0E-20	AI193248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11505	24892	37014	4.13	2.0E-20	AI193248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11505	24892	37014	4.13	2.0E-20	AI193248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11844	24727	35536	2.03	2.0E-20	AI186701.1	EST_HUMAN	Homo sapiens splicing factor similar to snai1 (SPF31), mRNA
11844	24727	35536	2.03	2.0E-20	AI186701.1	EST_HUMAN	Homo sapiens splicing factor similar to snai1 (SPF31), mRNA
10965	23603	37420	0.99	1.0E-20	X00695.1	EST_HUMAN	Q1071003-220300-021-504 HN0032 Homo sapiens cDNA RC1-HN0005-220300-021-504 HN0032 Homo sapiens cDNA R1 ratia RY43 mRNA for a potential ligand-binding protein
5734	18790	33070	3.29	9.0E-30	AA761215.1	EST_HUMAN	n22007.s1 NCL CGAP_C031 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element.
12263	25087	33070	2.14	9.0E-30	AA761215.1	EST_HUMAN	Homo sapiens shc10n regulated transporter-like (ZIRTL), mRNA
6462	16517		9.62	8.0E-30	F08688.1	EST_HUMAN	HCE22P051 Normalized infant brain cDNA Homo sapiens cDNA clone c-23005
8613	21093	34697	3.18	8.0E-30	AA338373.1	EST_HUMAN	ESTW3717 Thymus 1 Homo sapiens cDNA 5' and similar to EST containing O family repeat
9031	21997	35416	3.9	8.0E-30	AI155702.1	EST_HUMAN	PT2.1_19_311.7 tumor2 Homo sapiens cDNA 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1518	14530		1.02	7.0E-30	BE591133.1	EST_HUMAN	P14-87072-15040-204-411 B70724 Homo sapiens cDNA
1571	14634		1.4	6.0E-30	X57768.1	NT	Human lamda-immunoglobulin constant region complex (germline)
1583	14617	27802	1.8	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
1594	14617	27802	2.51	6.0E-30	BE503028.1	EST_HUMAN	QYC-BN0147-260406-274-412 BN0147 Homo sapiens cDNA
1605	14635	27178	1.02	6.0E-30	BE503028.1	EST_HUMAN	QYC-BN0147-260406-274-412 BN0147 Homo sapiens cDNA
1605	20835	27178	0.74	6.0E-30	AF177227.1	NT	Homo sapiens CTL tumor antigen s202-10 mRNA, partial cds
13054	14634		4.36	6.0E-30	X57768.1	NT	Human lamda-immunoglobulin constant region complex (germline)
4041	17079	26976	32.66	5.0E-30	A395992.1	EST_HUMAN	g94g03.x1 NOL CGAP CLL1 Homo sapiens cDNA clone IMAGE:216276 3' similar to contains Alu repetitive element
8310	25748		4.96	5.0E-30	U87031.1	NT	Human acylactyl hydrolase (ACD) gene, exon 7
11233	24186		2.21	5.0E-30	AL18379.2	NT	Homo sapiens chromosome 21 segment R521C079
11486	24432	37981	2.03	5.0E-30	AL18379.2	NT	Homo sapiens chromosome 21 segment R521C079
11486	24432	37982	2.03	5.0E-30	AL18379.2	NT	Homo sapiens chromosome 21 segment R521C079
2103	15169	28165	1.76	4.0E-30	AW93474.1	EST_HUMAN	QV3D-T0043-020203-080-03 D70043 Homo sapiens cDNA
2103	15169	28166	1.76	4.0E-30	AW93474.1	EST_HUMAN	QV3D-T0043-020203-080-03 D70043 Homo sapiens cDNA
7035	18397	31254	0.56	4.0E-30	P11360	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS REVERSE TRANSCRIPTASE);
9295	22222	35652	2.6	4.0E-30	AW812488.1	EST_HUMAN	GM1-ST0181-091182-035-08 S70181 Homo sapiens cDNA
1154	14196		4.51	3.0E-30	A338551.1	EST_HUMAN	q94503.x1 Ssmae, Jct. feat. N207F8. 8w Homo sapiens cDNA clone IMAGE:168820 3' similar to contains MER20.32 MER20 repetitive element
3770	19812	29721	1.03	3.0E-30	AF128593.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-3
7470	20435	33793	0.5	3.0E-30	P18622.1	EST_HUMAN	B120561 Tctex11 Homo sapiens cDNA clone 512056
8284	21243		0.52	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8831	21768		0.44	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10900	20721	37224	2.18	3.0E-30	BE350127.1	EST_HUMAN	h05901.x1 NOL CGAP X4113 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER20.33 MER20 repetitive element
10932	23952	37096	0.62	3.0E-30	AB032069.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
10932	23952	37097	0.62	3.0E-30	AB032069.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11541	24462	38334	5.89	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
878	13739	26669	1.67	2.0E-30	AW867316.1	EST_HUMAN	GM1-CT0307-31005-189-103 CT0307 Homo sapiens cDNA
1086	14130	27482	3.03	2.0E-30	BE70698.1	EST_HUMAN	HSC20701 normalized infant brain cDNA Homo sapiens cDNA clone c-2305
1476	14606	27482	5.36	2.0E-30	BE70698.1	EST_HUMAN	RCSH70682-110400-013-08 HT0582 Homo sapiens cDNA
2727	15721	26738	11.19	2.0E-30	BE766232.1	EST_HUMAN	IL2-NT0101-280700-118-504 NT0101 Homo sapiens cDNA
2830	13986	26049	6.11	2.0E-30	AF141561.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds

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Probe SEQ ID NO.	Bon SEQ ID NO.	Off SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8893	18845	28761	2.1	2.0E-30	AW20658.1	EST_HUMAN	U-H-B1-46-c-12-QUL1 NCI CGAP_5035 Homo sapiens cDNA clone IMAGE:272558.3
4812	17826	30728	1.76	2.0E-30	BE26894.1	EST_HUMAN	80T118860FT NIH MGIC_17 Homo sapiens cDNA clone IMAGE:302833.5
4812	17826	30727	1.76	2.0E-30	BE26894.1	EST_HUMAN	80T118860FT NIH MGIC_17 Homo sapiens cDNA clone IMAGE:302833.5
8820	19872	33269	0.71	2.0E-30	BF306337.1	EST_HUMAN	80T186220FT NIH MGIC_17 Homo sapiens cDNA clone IMAGE:413863.6
8820	21787	33211	0.98	2.0E-30	AAJ019103.1	EST_HUMAN	2658c10T1 Sources alpha N25-HRT Homo sapiens cDNA clone IMAGE:303185.5
8882	21849	33270	7.02	2.0E-30	C18839.1	EST_HUMAN	C18839 Human placenta cDNA (TfJuglone) Homo sapiens cDNA clone GEN:57001.5
8892	21848	33371	3.59	2.0E-30	BE57057.1	EST_HUMAN	7627c12X1 NCI CGAP_L024 Homo sapiens cDNA clone IMAGE:338492.3 similar to SW-DHSA, HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR.
8882	21848	35372	3.69	2.0E-30	BE57057.1	EST_HUMAN	7627c12X1 NCI CGAP_L024 Homo sapiens cDNA clone IMAGE:338492.3 similar to SW-DHSA, HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR.
10355	23280	38758	3.88	2.0E-30	AW671588.1	EST_HUMAN	EST_HUMAN
10442	23364	36854	8.55	2.0E-30	AW470791.1	EST_HUMAN	EST_HUMAN
280	13381	25099	18.55	1.0E-30	C18838.1	EST_HUMAN	EST_HUMAN
559	13810	26529	7.04	1.0E-30	AW48892.1	EST_HUMAN	EST_HUMAN
717	13779	26713	1.23	1.0E-30	AL10209.2	NT	EST_HUMAN
2223	15299	28200	3.82	1.0E-30	AF054371.1	EST_HUMAN	4c7H08.11 Stragelung lung (8697210) Homo sapiens cDNA clone IMAGE:588599.3
2689	15173	28496	4.19	1.0E-30	BS347728.1	EST_HUMAN	90202250FT NCI CGAP_Bim7 Homo sapiens cDNA clone IMAGE:417691.5
3057	15124	30121	4.19	1.0E-30	AA315045.1	EST_HUMAN	EST1168838 HPC cell line (metastasis to liver in mouse) [Homo sapiens cDNA 5' end
7595	20844	34328	2.08	1.0E-30	BF183290.1	EST_HUMAN	80T186092FT NIH MGIC_18 Homo sapiens cDNA clone IMAGE:404064.5
12852	23541		11.83	1.0E-30	H55593.1	EST_HUMAN	CFR22032 Chromosome 22 exon Homo sapiens cDNA clone C22_728.5
8897	21935	35046	0.82	9.0E-31	R18214.1	EST_HUMAN	YF8928.7 Sources infant brain 1N1B Homo sapiens cDNA clone IMAGE:30669.5 similar to g6X12658 RAS-RELATED PROTEIN RAS-2 (HUMAN)
8897	21935	35057	0.82	9.0E-31	R18214.1	EST_HUMAN	YF8928.7 Sources infant brain 1N1B Homo sapiens cDNA clone IMAGE:30669.5 similar to g6X12658 RAS-RELATED PROTEIN RAS-2 (HUMAN)
8871	21937	328293.1	1.79	9.0E-31	Z88293.1	EST_HUMAN	HS000303 normalized infant brain cDNA Homo sapiens cDNA clone c-0503.3
8873	21938	33534	0.46	9.0E-31	AF078776.1	NT	Rattus norvegicus putative four repeat on chemical mRNA, complete cds
1078	14123	27075	1.82	9.0E-31	AL103208.2	NT	Homo sapiens hypothetical protein T120420 (T120420), mRNA
2429	15430	5549	5.94	8.0E-31	AL103208.2	NT	Homo sapiens chromosome 21 segment HS210308
4955	17970	30850	1.12	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 16 (OR3)
4955	17970	30851	1.12	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
712	13774		1.89	7.0E-31/A4372637.1	EST_HUMAN	EST_HUMAN	EST_H4555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2678	18372	28891	2.38	7.0E-31/BE236517.1	EST_HUMAN	EST_HUMAN	hnc05611.x1 NC1 CGAP_L034 Homo sapiens cDNA clone IMAGE3182912.3
2678	18372	28892	2.38	7.0E-31/BE236517.1	EST_HUMAN	EST_HUMAN	hnc05611.x1 NC1 CGAP_L034 Homo sapiens cDNA clone IMAGE3182912.3
8744	21712	35133	0.99	7.0E-31/AF208441.1	NT	NT	Homo sapiens V1 vasculature vasopressin receptor (V1R) gene, promoter region and partial cds
8744	21712	35134	0.99	7.0E-31/AF208441.1	NT	NT	Homo sapiens V1 vasculature vasopressin receptor (V1R) gene, promoter region and partial cds
9821	22665		0.92	7.0E-31/BE408811.1	EST_HUMAN	EST_HUMAN	h01304125F1 NH1.M6C_21 Homo sapiens cDNA clone IMAGE3005510.9
12711	23065	31771	5.68	7.0E-31/X51755.1	NT	NT	Homo sapiens cDNA, complete cds
3891	16734		3.06	6.0E-31/AF223391.1	NT	NT	Homo sapiens sodium channel alpha1E subunit (SCN1A1E) gene, exon 7-49, and partial cds, alternatively spliced
8403	21461		7.57	6.0E-31/AF055008.1	NT	NT	Homo sapiens MHC class I region
8674	21642	35087	0.7	8.0E-31/BE350127.1	EST_HUMAN	EST_HUMAN	h009001.x1 NC1 CGAP_X0131 Homo sapiens cDNA clone IMAGE3146259.3 similar to contains MER20.33 MER229 repetitive element;
11090	24050	37573	1.86	8.0E-31/AU118103.1	EST_HUMAN	EST_HUMAN	AU118105 HEMBA1 Homo sapiens cDNA clone HEMBA1005650.5
12325	25127	31848	2.27	6.0E-31/AF372868.1	EST_HUMAN	EST_HUMAN	RC5-8T0377-491289-2031-D12 BT0337 Homo sapiens cDNA
12459	25764		2.08	8.0E-31/BE894488.1	EST_HUMAN	EST_HUMAN	601433037F1 NH1.M6C_72 Homo sapiens cDNA clone IMAGE3518524.9
1944	13295	28222	2.83	5.0E-31/M00894.1	NT	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
1944	13295	28223	2.83	5.0E-31/M00894.1	NT	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8788	21755		1.48	5.0E-31/BF06640.1	EST_HUMAN	EST_HUMAN	710580.4.x1 NC1 CGAP_G03 Homo sapiens cDNA clone IMAGE344478.3 similar to TRIC13537 Q13337
998	13965		3.45	4.0E-31/AJ271735.1	NT	NT	SIMILAR TO POGO ELEMENT, contains L11 L1 repetitive element;
1615	14647		1.01	4.0E-31/Q10473	SWISSPROT	SWISSPROT	POLYPEPTIDE N-ACETYLGLUCOSAMINYLTTRANSFERASE (PROTEIN-LDP ACETYLGLUCOSAMINYLTTRANSFERASE) (UDP-GALNAc-POLYPEPTIDE, N-ACETYLGLUCOSAMINYLTTRANSFERASE) (GALNAcT-1)
1534	14651		2.03	4.0E-31/AL163280.2	NT	NT	Homo sapiens chromosome 21 segment HS21C080
2800	15792		1.93	4.0E-31	57000380	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
10930	23620	37328	0.43	4.0E-31/AF64464.1	NT	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
2803	15903	28635	0.98	3.0E-31	6005971	NT	Homo sapiens SEC03, endoplasmic reticulum translocon component (S. cerevisiae) [kw] (SEC03L), mRNA
7592	20925	33883	6.73	3.0E-31	4826833	NT	Homo sapiens MDH dehydrogenase (ubiquitous) 1 beta subcomplex 8194D, ASH1 (NOUF8B) mRNA
7735	20891	34455	1.28	3.0E-31	11420320	NT	Homo sapiens "hypocretin" protein L11 (HCR2) (F010942), mRNA
8501	21469		2.35	3.0E-31/AL163280.2	NT	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
9309	22688	38328	4.80	3.0E-31/D14523.1	NT	NT	Homo mRNA for fibrin(ogen) degradation product 2, complete cds
10381	23881	37394	0.52	3.0E-31/A4431242.1	EST_HUMAN	EST_HUMAN	z006804.t1 Sorex_sorex_NHT Homo sapiens cDNA clone IMAGE371047.9

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Table 4
Abes Expressed In Bone Marrow[illegible]

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Table 4
Islet Expression in Bone Marrow

Probe Seq ID NO.	Exon Seq ID NO.	Q95 Seq ID NO.	Expression Signal	Mean Similarity (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12786	18336	31284	3.46	3.0E-33	5746741.NT	EST_HUMAN	Human sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11;22)(p15.5;p11.2) translocation) gene, translocated to 4 (MLL1) mRNA.
12837	25513	30821	4.33	3.0E-33	BE370088.1	EST_HUMAN	NR156283BF1.NI MGCC 21 Homo sapiens cDNA clone IMAGE:31387071 5'
4918	17987	30827	0.97	2.0E-33	BE296433.1	EST_HUMAN	NR171831F1.NI MGCC 17 Homo sapiens cDNA clone IMAGE:3529158 5'
6361	19448	32650	0.87	2.0E-33	BE34331.1	NT	Human cell 12-isoxygenase mRNA, complete cds
6024	19482	32058	0.88	2.0E-33	BE24333.1	NT	H. sapiens mRNA for myosin
5924	19682	32058	0.88	2.0E-33	BE24333.1	NT	H. sapiens mRNA for myosin
8621	21588	35007	2.19	2.0E-33	A114384.1	EST_HUMAN	276502B17.1 Stragelange HeLa cell c3 837216 Homo sapiens cDNA clone IMAGE:563150 5'
8621	21588	35007	2.19	2.0E-33	A114384.1	EST_HUMAN	276502B17.1 Stragelange HeLa cell c3 837216 Homo sapiens cDNA clone IMAGE:563150 5'
8621	21588	35007	2.19	2.0E-33	A114384.1	EST_HUMAN	276502B17.1 Stragelange HeLa cell c3 837216 Homo sapiens cDNA clone IMAGE:563150 5'
13049	24589	31894	4.17	2.0E-33	AV735446.1	EST_HUMAN	AV735448 CB Homo sapiens cDNA clone CBFB10A8 5'
13110	16781	31110	6.73	1.0E-32	BE143296.1	EST_HUMAN	NR1675320F1.NI MGCC 9 Homo sapiens cDNA clone CBFB10A8 5'
7258	18991	33239	6.73	1.0E-32	11437199.NT	EST_HUMAN	Homo sapiens chromosome 10 open reading frame 9 (CT10ORF9) mRNA
8043	21900	35334	6.78	1.0E-32	AA220874.1	EST_HUMAN	hwf1022.41 NCL CGAP CG27 Homo sapiens cDNA clone IMAGE:5318216 3' similar to TR-08839 088399
3493	18540		5.7	9.0E-33	BE327112.1	EST_HUMAN	hwf0603.41 NCL CGAP CG27 Homo sapiens cDNA clone IMAGE:5318216 3' similar to TR-08839 088399
6590	19820		3.43	9.0E-33	AF225391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
9140	22108	35532	1.82	9.0E-33	BF472251.1	EST_HUMAN	832024 (B4F1.NI) CGAP Bm67 Homo sapiens cDNA clone IMAGE:4156970 5'
11150	24110		4.08	9.0E-33	AL18262.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C030
33	13182	20068	2.4	7.0E-33	5531789.NT	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
63	13182	20068	2.4	7.0E-33	5531789.NT	EST_HUMAN	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2108	15185	28205	2.43	7.0E-33	A190115.1	EST_HUMAN	het1269.41 NCL CGAP U12 Homo sapiens cDNA clone IMAGE:4178906 3' similar to contains ORF h OPR
2857	15954		7.63	7.0E-33	AV735058.1	EST_HUMAN	repulsive element 1
2841	14730	27719	1.83	7.0E-33	AV735015.1	EST_HUMAN	AV735016 HIT Homo sapiens cDNA clone HTAFANF08 5'
3255	16510		1.83	7.0E-33	AV1971307.1	EST_HUMAN	AV735016 HIT Homo sapiens cDNA clone HTAFANF08 5'
9286	22264		1.07	7.0E-33	X54880.1	NT	Human NLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphatase) (EC 3.1.3.48)
11176	24134		2.89	7.0E-33	AF472262.1	EST_HUMAN	80202116F41 NCL CGAP Bm67 Homo sapiens cDNA clone IMAGE:4156970 5'
11578	24510	35071	2.45	7.0E-33	AV1971568.1	EST_HUMAN	EST1388587 MAGE sequences, MACL Homo sapiens cDNA
12409	25182	31819	3.85	7.0E-33	AA001416.1	EST_HUMAN	nr16901.31 NCL CGAP Phd1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1 H L1

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Ecom SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Seq Hit BLAST E Value	Top Hit Accession No.	Top Hit Description Source	Top Hit Descriptor
3749	10791		0.69	8.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6185	10290	32404	1.09	8.0E-33	F03083.1	EST_HUMAN	HS21D1201 HMB Homo sapiens cDNA clone A2001071468
6185	10290	32495	1.09	8.0E-33	F03083.1	EST_HUMAN	HS21D1201 HMB Homo sapiens cDNA clone A2001071468
8825	12819	33319	7.52	8.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
9050	22016	35440	3.18	8.0E-33	U14291.f08	EST_HUMAN	Human sequences similar to RAD23 (S. cerevisiae) homolog (H. sapiens) (LOC83277). mRNA
10371	23294	30769	0.97	8.0E-33	G75609.09	NT	Mus musculus SRV-3c containing gene 6 (Sox6), mRNA
10371	23294	30770	1.73	8.0E-33	G75609.09	NT	Mus musculus SRV-3c containing gene 6 (Sox6), mRNA
17082	14621	32724	1.73	8.0E-33	BF13551.1	EST_HUMAN	OV-F10165-100760-271-e2 F10166 Homo sapiens cDNA
1686	14621	32723	1.27	8.0E-33	BF13551.1	EST_HUMAN	OV-F10165-100760-271-e2 F10166 Homo sapiens cDNA
1894	14621	32722	1.31	8.0E-33	U111884.f08	EST_HUMAN	Human apolipoprotein B protein family 7 (ApoB), mRNA
1914	14938	27933	1.31	8.0E-33	N047208.1	EST_HUMAN	Human apolipoprotein B protein family 7 (ApoB), mRNA
1914	14938	27934	1.31	8.0E-33	N047208.1	EST_HUMAN	Human apolipoprotein B protein family 7 (ApoB), mRNA
2280	15083		1.46	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4087	11712	30015	1.28	5.0E-33	AB014596.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
8823	18877	33166	51.92	5.0E-33	AJ186080.1	EST_HUMAN	z55018.a1 Stralagene NT1 neuron (hs072203) Homo sapiens cDNA clone IMAGE:632627 ~ similar to contains Alu repetitive element
10010	23532	31027	0.85	5.0E-33	AW24967.1	EST_HUMAN	g83911.Lt NCI CGAP L228 Homo sapiens cDNA clone IMAGE:275246T.3
10010	23532	31028	0.85	5.0E-33	AW24967.1	EST_HUMAN	g83911.Lt NCI CGAP L228 Homo sapiens cDNA clone IMAGE:275246T.3
11330	14173		0.87	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2135	15152	28197	1.33	4.0E-33	476887.01	EST_HUMAN	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2428	16435		2.02	4.0E-33	AA088261.1	EST_HUMAN	ab51517.1 Stralagene lung carcinoma 892718 Homo sapiens cDNA clone IMAGE:844317 ~ similar to contains Alu repetitive element; contains MER28 negative element
2428	16435	28374	2.35	4.0E-33	AL163210.2	EST_HUMAN	ab51517.1 Stralagene lung carcinoma 892718 Homo sapiens cDNA clone IMAGE:844317 ~ similar to contains Alu repetitive element; contains MER28 negative element
2459	17354	33419	1.88	4.0E-33	AW249346.1	EST_HUMAN	UJH-84245-200-001-Lt NCI CGAP S341 Homo sapiens cDNA clone IMAGE:2727149.3
5477	18678	31487	21.95	4.0E-33	AA033053.1	EST_HUMAN	d716027.1 Stralagene colon (hs072603) Homo sapiens cDNA clone IMAGE:810038.9 ~ similar to contains POU domain, class 1, multiple type 1 (POU1F1) (HUMAN)
8333	19565	32857	2.14	4.0E-33	B63904.01	EST_HUMAN	Homo sapiens polyoma virus (YAC created), alpha (POLA), mRNA
9532	19565	32858	2.14	4.0E-33	B63904.01	EST_HUMAN	Homo sapiens polyoma virus (YAC created), alpha (POLA), mRNA
1001	14135		6.18	3.0E-33	BC550127.1	EST_HUMAN	hp0091.Lt NCI CGAP K413 Homo sapiens cDNA clone IMAGE:3146259.3 ~ similar to contains MER28 b3
1092	14135		4.81	3.0E-33	BC550127.1	EST_HUMAN	hp0091.Lt NCI CGAP K413 Homo sapiens cDNA clone IMAGE:3146259.3 ~ similar to contains MER28 b3
2459	18504		0.91	3.0E-33	BE550451.1	EST_HUMAN	AV847851 GLC Homo sapiens cDNA clone GLC5E506.3
98016	23127	37228	1.02	3.0E-33	AA861510.1	EST_HUMAN	a32612.e1 Soares, Iwate, NIH Homo sapiens cDNA clone IMAGE:1407847.3 ~ similar to TRQ134370 C13579 HUMAN TRANSPOSASE..

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
16	13138		0.63	2.0E-33	A180188.1	EST_HUMAN	q557g03.xt Soares_fetal_tissue_NCHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF11 ORF repetitive element;
105	13138		2.93	2.0E-33	A160189.1	EST_HUMAN	q557g03.xt Soares_fetal_tissue_NCHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF11 ORF repetitive element;
4448	17475		4.22	2.0E-33	BE156036.1	EST_HUMAN	q557g03.xt Soares_fetal_tissue_NCHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF11 ORF repetitive element;
6021	18035	33920	9.82	2.0E-33	AA626683.1	EST_HUMAN	IR6-01711.1 Stratigene lung carcinoma 92728 Homo sapiens cDNA clone IMAGE:844388 5' similar to
6120	18138	31015	2.85	2.0E-33	11421332	NT	ph200794_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
6120	18138	31018	2.68	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SRP-521 (SRP-52); mRNA
6583	19623	32388	1	2.0E-33	AJ277492.1	EST_HUMAN	Homo sapiens hypothetical protein SRP-521 (SRP-52); mRNA
9456	22420		2.29	2.0E-33	A052256.1	EST_HUMAN	q521d033.xt Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1890161 3'
10079	23859	37411	0.9	2.0E-33	11421332	NT	ph242639 TRANSLATIONAL INITIATION FACTOR 90 BETA SUBUNIT (HUMAN);
10079	23859	37412	0.9	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SRP-521 (SRP-52); mRNA
9	13120		2.05	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anticardiac endometrial dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6609	18764	31634	0.7	1.0E-33	AF003528.1	NT	Homo sapiens F-box protein FBXL4 (FBXL4) mRNA, complete cds
7637	20597	33901	1.48	1.0E-33	AF199420.1	NT	Homo sapiens protein kinase C beta-II type (PKCβ1) mRNA, complete cds
10381	20010		0.73	1.0E-33	U08822.1	NT	Homo sapiens cytochrome P-450 2D6 (CYP2D6) gene, exons 7, 8 and 9, and partial cds
11377	24324	37683	1.72	1.0E-33	AJ744220.1	EST_HUMAN	AY744220 C9 Homo sapiens cDNA clone G30AAAT1 6'
11550	24387	38167	1.79	1.0E-33	AJ744220.1	EST_HUMAN	QV3-BN047-230200-102-023 BN047 Homo sapiens cDNA
11973	24851	38448	2.58	1.0E-33	U08822.1	EST_HUMAN	Homo sapiens cytochrome P-450 2D6 (CYP2D6) gene, exons 7, 8 and 9, and partial cds
12686	25552		1.96	1.0E-33	AJ271797.1	EST_HUMAN	w588203.x1 NC1_C2AP_MG11 Homo sapiens cDNA clone IMAGE:2462101 3'
12852	13120		9.4	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anticardiac endometrial dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4648	17655		1.77	0.0E-34	BE156575.1	EST_HUMAN	PM4-HT0352-181199-201-D02 170932 Homo sapiens cDNA
13060	25053		3.44	0.0E-34	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2181	15190		0.83	8.0E-34	692276.1	NT	Homo sapiens hypothetical protein FL-10600 (FL10600); mRNA
8077	21014	28216	0.49	8.0E-34	BE068882.1	EST_HUMAN	MR4-BT0399-200100-201-H09 BT0399 Homo sapiens cDNA
1430	14473	27446	2.83	7.0E-34	170948.1	EST_HUMAN	yaf15005-r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:10820 5'
10359	20273	27446	0.6	7.0E-34	170948.1	EST_HUMAN	yaf15005-r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:10820 5'
12479	20273	27446	1.89	7.0E-34	U12989.1	EST_HUMAN	yf 402.1 Soares placenta N23pF Homo sapiens cDNA clone IMAGE:148722 5'
471	13845	28472	2.11	6.0E-34	U10991.1	NT	Human O2 protein mRNA, partial cds

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (100) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12287	25103	31636	1.86	8.0E-34	U08686.1	NT	Mus musculus DAB2J hind-specific (test-1) gene
1897	14822		2.36	5.0E-34	7709500.1	NT	Homo sapiens Npy3c-binding protein Npy3c (LOC51729), mRNA
5101	18111	30835	4.98	5.0E-34	U08686.1	NT	Human splicing factor SRSF5-7 (SRSF-5) mRNA, complete cds
8218	22184	35817	1.17	5.0E-34	AF078719.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11015	20860	37500	2.03	5.0E-34	AB037868.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
11983	24821		1.49	5.0E-34	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21008
2014	15035	28049	1.71	4.0E-34	AB04987.1	EST_HUMAN	IB94508.x1 NC1_OGAP_P-28 Homo sapiens cDNA clone IMAGE2249184.3
5223	19231	31705	0.64	4.0E-34	AW886252.1	EST_HUMAN	RC5-070078-263030-022-002.07078 Homo sapiens cDNA
5933	23258	33768	1.07	4.0E-34	BF209718.1	EST_HUMAN	651874902F1 NH1_MGC_54 Homo sapiens cDNA clone IMAGE4102213.6
5339	19428	32571	0.74	3.0E-34	M37277.1	NT	Human Ig gamma H-chain D-region genes, partial cds
11486	24428		3.18	3.0E-34	BF03527.1	EST_HUMAN	651748831F1 NH1_MGC_68 Homo sapiens cDNA clone IMAGE3962286.5
9303	22268	35866	1.90	2.0E-34	A678101.1	EST_HUMAN	W835903.x1 Soares_NF1_GBC_S1 Homo sapiens cDNA clone IMAGE2330170.3 similar to contains MER22 MER29 repetitive element
9303	22268	35866	1.90	2.0E-34	A678101.1	EST_HUMAN	W835903.x1 Soares_NF1_GBC_S1 Homo sapiens cDNA clone IMAGE2330170.3 similar to contains MER22 MER29 repetitive element
11498	24439	37897	1.87	2.0E-34	AF08303	SWISSPROT	PLEXA12 PRECURSOR (TRANSDUCIN-RELATED PROTEIN 5X)
11498	24439	37868	1.97	2.0E-34	P15035	SWISSPROT	PLEXA12 PRECURSOR (TRANSDUCIN-RELATED PROTEIN 5X)
1505	14638	27510	6.53	1.0E-34	P12238	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER (SODIUM IZ (ADP)ATP TRANSLUCASE 3) (ADENINE NUCLEOTIDE TRANSLUCATOR 3) (ANT 3)
3587	19730	20641	1.35	1.0E-34	AF033528.1	NT	Homo sapiens X-linked aniridia-related protein gene (EDA), exon 2 and flanking repeat regions
4098	17132	30025	0.81	1.0E-34	AY008907.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4098	17132	30026	0.81	1.0E-34	AY008907.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4098	17132	30026	0.81	1.0E-34	BE071144.1	EST_HUMAN	RC2-870506-240400-016-M08 BT0508 Homo sapiens cDNA
8281	19334	32565	1.98	1.0E-34	BE074052.1	EST_HUMAN	651484030F1 NH1_MGC_60 Homo sapiens cDNA clone IMAGE389569.5
8281	19334	32566	1.98	1.0E-34	BE074052.1	EST_HUMAN	651484030F1 NH1_MGC_60 Homo sapiens cDNA clone IMAGE389569.5
8881	22934	35630	0.49	1.0E-34	222366	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
10056	22862	35450	14.47	1.0E-34	AL038635.1	EST_HUMAN	DKFZ2684A1183.J1 6841 (pncvnt: Hb2) Homo sapiens cDNA clone DKFZ2684A1183.5
11618	24467	35007	1.71	1.0E-34	BE781780.1	EST_HUMAN	591470952F1 NH1_MGC_67 Homo sapiens cDNA clone IMAGE387478.5
11618	24467	35008	1.71	1.0E-34	BE781780.1	EST_HUMAN	591470952F1 NH1_MGC_67 Homo sapiens cDNA clone IMAGE387478.5
11530	24471	35022	3.22	1.0E-34		NT	Homo sapiens nucleolin 2 (NCL2), mRNA
12664	25021		1.4	1.0E-34	AA807087.1	EST_HUMAN	oc31611.1 NC1_OGAP_G081 Homo sapiens cDNA clone IMAGE351310.3 similar to gp-2684203
12874	25507		4.01	1.0E-34	AL183210.2	NT	TYROSIENE-PROTEIN KINASE RECEPTOR FL14 PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21010

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8696	18702	26617	1.26	9.0E-35	AW663032.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:286787.5
227	13326		13.21	8.0E-35	6031180	NT	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912
1761	14780	27765	4.47	8.0E-35	BF56937.1	EST_HUMAN	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912
1751	14780	27766	4.47	8.0E-35	BF56937.1	EST_HUMAN	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912
4802	17919	30811	2.91	8.0E-35	BF163196.1	EST_HUMAN	60180598FT NIH_MGC_78 Homo sapiens cDNA clone IMAGE:404324.5
11048	24012	37537	1.84	8.0E-35	BE374480.1	EST_HUMAN	60123648FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:308513.5
12402	25175		5.41	8.0E-35	BF569282.1	EST_HUMAN	60218482T1 NIH_MGC_32 Homo sapiens cDNA clone IMAGE:430560.3
6631	18689	32968	1.85	7.0E-35	11425417	NT	Homo sapiens pseudoviral vector (gamma herpes virus) gene 338 (GFP338) mRNA
1411	14444	27416	0.93	6.0E-35	AA757118.1	EST_HUMAN	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912
1985	15008	28009	2.83	6.0E-35	6006976	NT	Homo sapiens cDNA clone IMAGE:2731433.3
4083	17117	30012	0.76	6.0E-35	AW297181.1	EST_HUMAN	U18717-5 (p52-1) NCI CGAP_S268 Homo sapiens cDNA clone IMAGE:2731433.3
8259	21168	34605	3.66	6.0E-35	6009021	NT	Homo sapiens cDNA clone IMAGE:2731433.3
9058	22024	35447	0.51	6.0E-35	X04222.1	NT	Homo sapiens mRNA for novel T-cell activation protein
9059	22024	35448	0.51	6.0E-35	X04222.1	NT	Homo sapiens mRNA for KIAA0365 gene, partial cds
10025	22562	36420	0.68	6.0E-35	AB032384.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10283	23188	36672	3.04	6.0E-35	AB037786.1	NT	Homo sapiens immunoglobulin kappa light chain variable region L14
1722	14762	27737	61.8	5.0E-35	X03326.1	NT	Homo sapiens mRNA for KIAA0365 gene, partial cds
2755	15787	28605	0.9	5.0E-35	AB073693.2	NT	Homo sapiens RING1 and YYY binding protein (RYBP) mRNA
3021	16079	29000	1.47	5.0E-35	6012639	NT	Homo sapiens cDNA clone IMAGE:2731433.3
4498	17484	30354	2.05	5.0E-35	AF022388.1	NT	Homo sapiens cDNA clone IMAGE:2731433.3
4742	17762	30856	0.96	5.0E-35	BE246095.1	EST_HUMAN	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912
8628	21483		4.74	5.0E-35	BE660992.1	EST_HUMAN	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912
8652	21520	34939	2.2	5.0E-35	AJ209765.1	EST_HUMAN	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912
8652	21520	34940	2.2	5.0E-35	AJ209765.1	EST_HUMAN	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912
11512	24653		2.39	5.0E-35	AA001786.1	EST_HUMAN	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912
1426	14663	27440	10.86	4.0E-35	BE267907.1	EST_HUMAN	haid33063.x1 NCI CGAP_KRT18 Homo sapiens cDNA clone IMAGE:326104.3 similar to TRO75912

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Med Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1835	14882	27895	7.91	4.0E-35	AF01983.1	EST_HUMAN	y06607.1 Scores fetal liver spliced 1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTRR5 repetitive element;
4844	17861		0.63	4.0E-35	AF00328.1	NT	Homo sapiens X-linked arylsulfatase ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5145	18154		0.83	4.0E-35	BE43102.1	EST_HUMAN	001300706F1 NR1_MGC_21 Homo sapiens cDNA clone IMAGE:3835401 5'
7416	20383		1.81	4.0E-35	BE316027.1	EST_HUMAN	000991.XT NC1_OGAP_KG13 Homo sapiens cDNA clone IMAGE:34563 5' similar to contains MER20 b3 MER20 repetitive element;
8483	21830	35263	1.83	4.0E-35	BE316027.1	EST_HUMAN	DKF25844.148 t37.434 (synonym: hies3) Homo sapiens cDNA clone DKF2p-454L148 5'
1682	14615	27888	21.76	3.0E-35	BE316027.1	EST_HUMAN	001126201P1 NR1_MGC_9 Homo sapiens cDNA clone IMAGE:3346003 5'
2338	15346		3.36	3.0E-35	AF22492.1	NT	Homo sapiens phosphatidylesterase 1 gene, complete cds
5413	18516	31593	27.9	3.0E-35	BF433100.1	EST_HUMAN	Y06607.1 Scores fetal liver spliced 1NFLS Homo sapiens cDNA clone IMAGE:3695361 5' similar to TR0902H7 TR0902H7 F-box protein, partial cds
5413	18516	31594	27.9	3.0E-35	BF433100.1	EST_HUMAN	Y06607.1 Scores fetal liver spliced 1NFLS Homo sapiens cDNA clone IMAGE:3695361 5' similar to TR0902H7 TR0902H7 F-box protein, partial cds
9844	22760		1.71	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10355	23467	36854	0.93	3.0E-35	AW003083.1	EST_HUMAN	w03405.x1 NC1_OGAP_G09 Homo sapiens cDNA clone IMAGE:2480432 5' similar to SWI_P0L.4, HUMAN P10268 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
108	15832	26146	0.83	2.0E-35	U88905.1	EST_HUMAN	K8822F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K8822 5' similar to REPETITIVE ELEMENT
1182	14232	27188	1.39	2.0E-35	T11009.1	EST_HUMAN	A871F Heart Homo sapiens cDNA clone A871
2227	15241	28268	5.04	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gals2, complete cds
2695	16895	28706	1	2.0E-35	AW68006.1	EST_HUMAN	H86412.x1 Scores NF1_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2075168 5' similar to SWI_P0L.4, HUMAN Q14659 THYROID RECEPTOR INTERACTING PROTEIN 12;
3233	16374	29294	0.93	2.0E-35	6912469	NT	SWI_P0L.4, HUMAN Q14659 THYROID RECEPTOR INTERACTING PROTEIN 12;
3233	16374	29295	0.93	2.0E-35	6912469	NT	Homo sapiens GHR-associated binder 2 (KIAA0571), mRNA
3370	16913		1.08	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0565 protein, partial cds
3390	16970	29483	1.42	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E-4238 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project/T0BA Homo sapiens cDNA clone TCBAP-4328
3930	16970	29484	1.42	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E-4238 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project/T0BA Homo sapiens cDNA clone TCBAP-4328
4697	17718		2.65	2.0E-35	BE43102.1	EST_HUMAN	Y06607.1 Scores fetal liver spliced 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
5562	18768	31826	1.8	2.0E-35	BF332471.1	EST_HUMAN	Y06607.1 Scores fetal liver spliced 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7311	20522	33022	0.65	2.0E-35	BE33263.1	EST_HUMAN	Q12A1T0125-280700-297 G02 MT0126 Homo sapiens cDNA
7311	20522	33023	0.68	2.0E-35	BE33358.1	EST_HUMAN	Q12A1T0125-280700-297 G02 MT0126 Homo sapiens cDNA
1148	2106	32024	11.23	2.0E-35	X89417.1	NT	H sapiens PRDS-27 mRNA
12158	16374	20264	2.36	2.0E-35	6912459.NT	EST_HUMAN	Homo sapiens Gm2-associated binder 2 (KIA04067). mRNA
12158	16374	20265	2.36	2.0E-35	6912459.NT	EST_HUMAN	Homo sapiens Gm2-associated binder 2 (KIA04067). mRNA
12240	1638	31851	1.47	2.0E-35	BE204978.1	EST_HUMAN	801468774FT NIH JGCG 70 Homo sapiens cDNA clone IMAGE:385699.5
12240	1638	31852	1.47	2.0E-35	BE204978.1	EST_HUMAN	801468774FT NIH JGCG 70 Homo sapiens cDNA clone IMAGE:385699.5
12540	20398	31852	1.47	2.0E-35	BE204978.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS210210
12541	25432		7.86	2.0E-35	AL163210.2	NT	K6932F Human fetal heart; Lambda ZAP Express Homo sapiens cDNA clone K6932.5 similar to
12673	15832	26146	1.72	2.0E-35	N68085.1	EST_HUMAN	REPETITIVE ELEMENT
48	13108	20073	5.26	1.0E-33	AA631949.1	EST_HUMAN	Imr18 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12.1
48	13108	20074	5.26	1.0E-33	AA631949.1	EST_HUMAN	Imr18 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12.1
753	13314	20756	96.25	1.0E-35	AV3389473.1	EST_HUMAN	U2-S10182-13 G05-209-412 S10182 Homo sapiens cDNA
753	13314	20757	96.25	1.0E-35	AV3389473.1	EST_HUMAN	U2-S10182-13 G05-209-412 S10182 Homo sapiens cDNA
910	13965		0.99	1.0E-35	17947.1	EST_HUMAN	SP2A4382 44493 RE3 TROVIRUS-RELATED POL. POLYPROTEIN - HUMAN
2549	16550	28571	3.02	1.0E-35	7705694	NT	Homo sapiens hypothetical protein (LOC51233). mRNA
2778	15770	28760	1.85	1.0E-35	BE350127.1	EST_HUMAN	H92921 x1 NGI CGAP Kd13 Homo sapiens cDNA clone IMAGE:316226.3 similar to contains MER26.63
2778	15770	28761	1.85	1.0E-35	BE350127.1	EST_HUMAN	H92921 x1 NGI CGAP Kd13 Homo sapiens cDNA clone IMAGE:316226.3 similar to contains MER26.63
3177	16732	29148	3.44	1.0E-35	AV59422.1	EST_HUMAN	AV59422 GLO Homo sapiens cDNA clone GLOE08.3
3177	16732	29149	3.44	1.0E-35	AV59422.1	EST_HUMAN	AV59422 GLO Homo sapiens cDNA clone GLOE08.3
4482	17478	30365	1.04	1.0E-35	7656905.NT	EST_HUMAN	Mus musculus actin receptor interacting protein 1 (Arip1-pending). mRNA
4482	17478	30366	1.04	1.0E-35	7656905.NT	EST_HUMAN	Mus musculus actin receptor interacting protein 1 (Arip1-pending). mRNA
5358	16854	31321	1.54	1.0E-35	1152026.NT	EST_HUMAN	Homo sapiens chromatin assembly factor 1, subunit B (CAF1B). mRNA
7183	16854	31321	0.69	1.0E-35	AV59422.1	EST_HUMAN	MRI-S1011-111199-011-027 S1011 Homo sapiens cDNA
7183	16854	31321	0.69	1.0E-35	AV59422.1	EST_HUMAN	MRI-S1011-111199-011-027 S1011 Homo sapiens cDNA
7256	20862	34464	0.83	1.0E-35	AB033105.1	EST_HUMAN	Homo sapiens mRNA for KIAA1279 protein, partial cDNA
7503	20846	34531	0.94	1.0E-35	AB033105.1	EST_HUMAN	Homo sapiens mRNA for KIAA1279 protein, partial cDNA
9000	26669	36512	3.17	1.0E-35	AV158565.1	EST_HUMAN	AUT16895 PLUCB3 Homo sapiens cDNA clone PLUCB300382.3
9500	26669	36513	3.17	1.0E-35	AV158565.1	EST_HUMAN	AUT16895 PLUCB3 Homo sapiens cDNA clone PLUCB300382.3
10942	23832	37377	0.93	1.0E-35	BF489894.1	EST_HUMAN	hna06068 x1 NC1 CGAP Kd13 Homo sapiens cDNA clone IMAGE:3254051.7 similar to TR031341

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10942	24882	37376	0.83	1.0E-35	BF58694.1	EST_HUMAN	h263606.x1 NCL CGAP P.288 Homo sapiens cDNA clone IMAGE:325001 3' similar to TRC31341
12052	24926	38522	1.72	1.0E-35	AB22860.1	NT	O31341 BET-A-GALACTOSIDASE
12052	24926	38523	1.72	1.0E-35	AB22860.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12057	24930		1.59	1.0E-35	AI26119.1	EST_HUMAN	Homo sapiens mRNA for KIAA1057 protein, partial cds
12168	25057		1.71	1.0E-35	11418274	NT	promin-7 D01.7 bromin Homo sapiens cDNA 5'
12320	15550	28571	1.42	1.0E-35	7705954	NT	Homo sapiens insulin 1 (FBLN1), mRNA
12404	25177		1.77	1.0E-35	11418110	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
12747	25398		1.67	1.0E-35	BET92332.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
4011	17050	29596	2.95	9.0E-38	AW82707.1	EST_HUMAN	RCS-510315-180200-013-112 S1015 Homo sapiens cDNA
6123	16201	32426	0.75	8.0E-38	X76478.1	NT	B beta BBSc mRNA for scolden
6536	22647	38540	0.51	8.0E-38	AA548483.1	EST_HUMAN	EST 54838 Hippocampus II Homo sapiens cDNA 5' and similar to endogenous retrovirus 9, 5' LTR
6536	22648		0.45	8.0E-38	7702559	NT	Homo sapiens Cdc42 protein (LOC51650), mRNA
9243	18100	28923	1.68	7.0E-38	AW 85759.1	EST_HUMAN	ONT-C10315-301280-053-307 C10315 Homo sapiens cDNA
3135	18100		0.93	7.0E-38	4551468	NT	Homo sapiens C-terminal binding protein 2 (CTBP2), mRNA
7916	20859	34247	6.33	7.0E-38	U08972.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2), mRNA
7916	20859	34248	6.31	7.0E-38	U08972.1	NT	Human cationomyosin antigen gene family member 12 (COM12) gene, exon 1 and LIN
12558	23278	31778	2.01	7.0E-38	AF823651.1	NT	Homo sapiens cationomyosin antigen gene family member 12 (COM12) gene, exon 1 and LIN
2021	19042	28553	4.16	8.0E-38	7708922	NT	Homo sapiens insulin 2 (INS2), mRNA
2427	16434		8.3	9.0E-38	AB333346.1	NT	Homo sapiens TGA1 gene, exon 12
3653	16609	22811	1.89	9.0E-38	BF16101.1	EST_HUMAN	U1-BV11 svnc-12-21J at NCL CGAP Sub2 Homo sapiens cDNA clone IMAGE:3034542 3'
5404	18507	31384	5.66	8.0E-38	AA35163.1	EST_HUMAN	h433064.X1 Sorens NSF FR 9W OT PA P S1 Homo sapiens cDNA clone IMAGE:323616 3' similar to h261102.X1 NCL CGAP C014 Homo sapiens cDNA clone IMAGE:303627 3' similar to SW1MA2_HUMAN
7316	20287	33629	3.46	9.0E-38	AW760143.1	EST_HUMAN	h261102.X1 NCL CGAP C014 Homo sapiens cDNA clone IMAGE:303627 3' similar to SW1MA2_HUMAN
8069	21945	35350	2.51	9.0E-38	AF205161.1	NT	P92302 IMPORTIN ALPHA-2 SUBUNIT
10945	23507		0.6	9.0E-35	C19827.1	EST_HUMAN	Homo sapiens synovial precursor, mRNA, complete cds
11874	24756	38339	3.51	9.0E-38	A360469.1	EST_HUMAN	C19827 Clonhep human acute polya+ mRNA (R6372) Homo sapiens cDNA clone GEN-585011 5'
12563	28004	31526	1.9	9.0E-38	BE73154.1	EST_HUMAN	h261102.X1 NCL CGAP C014 Homo sapiens cDNA clone IMAGE:303627 3' similar to SW1MA2_HUMAN
138	13243	26179	12.86	5.0E-38	A3771735.1	NT	h261102.X1 NCL CGAP C014 Homo sapiens cDNA clone IMAGE:303627 3' similar to SW1MA2_HUMAN
2781	15763	26773	12.8	5.0E-38	BE398438.1	EST_HUMAN	h261102.X1 NCL CGAP C014 Homo sapiens cDNA clone IMAGE:303627 3' similar to SW1MA2_HUMAN
3626	16669	26681	1.32	5.0E-38	AL163263.2	NT	h261102.X1 NCL CGAP C014 Homo sapiens cDNA clone IMAGE:303627 3' similar to SW1MA2_HUMAN

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6907	22728	38166	0.57	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 1-3) (USP13) mRNA
888	19341	26165	2.74	1.0E-36	BE009310.1	EST	HUMAN
2155	16171	26780	1.06	1.0E-36	BE148523.1	EST	HUMAN
2155	16171	26780	1.06	1.0E-36	BE148523.1	EST	HUMAN
2212	16227	26248	1.35	1.0E-36	BF673761.1	EST	HUMAN
3355	16408	32562	1.34	1.0E-36	AF166602.1	NT	Homo sapiens human endogenous retrovirus W provirus-19 protease (pro) gene, partial cds
5516	16598	32562	0.82	1.0E-36	AL044448.1	EST	HUMAN
6033	16686	32261	1.13	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (zinc finger protein 147) (ZNF147) mRNA
6037	16376		3.88	1.0E-36	AB87714.1	EST	HUMAN
6526	19502	32862	1.34	1.0E-36	226512.1	EST	HUMAN
6526	19502	32863	1.34	1.0E-36	226512.1	EST	HUMAN
6539	19902	33187	2.77	1.0E-36	AF09173.1	EST	HUMAN
8293	21262	34071	2.77	1.0E-36	AF12042.1	EST	HUMAN
8293	21262	34071	2.77	1.0E-36	AF12042.1	EST	HUMAN
8389	21367	34764	1.15	1.0E-36	AA120467.1	EST	HUMAN
8389	21367	34765	1.15	1.0E-36	AA120467.1	EST	HUMAN
8520	21469	34002	0.46	1.0E-36	AF141668.1	EST	HUMAN
8520	21469	34003	0.46	1.0E-36	AF141668.1	EST	HUMAN
9384	22349	35781	2.72	1.0E-36	AF103958.1	EST	HUMAN
10473	23395	36602	3.95	1.0E-36	BF364169.1	EST	HUMAN
10691	23613	37107	0.65	1.0E-36	AF555968.1	EST	HUMAN
10691	23613	37108	0.65	1.0E-36	AF555968.1	EST	HUMAN
11264	24244	37771	2.64	1.0E-36	AF097938.1	EST	HUMAN
11709	24074	38251	2.68	1.0E-36	AF1904143.1	EST	HUMAN
12338	25136		5.61	1.0E-36	11416177	NT	Homo sapiens chromosome 21 segment H82T013
12777	25414		4.97	1.0E-36	AL163213.1	NT	Homo sapiens chromosome 21 segment H82T013
13034	23570	33929	4.02	1.0E-36	AF202723.1	NT	Homo sapiens Sac1-unc-54 domain protein 2 (SUN2) mRNA, partial cds
7607	20560	33929	2.3	9.0E-37	AF009377.1	EST	HUMAN
7607	20568	33930	2.3	9.0E-37	AF009377.1	EST	HUMAN
3388	16416	26542	1.17	6.0E-37	4757979	NT	Homo sapiens chimera (chimerin) 2 (CH2) mRNA
5320	16426		1.6	6.0E-37	BE588077.1	EST	HUMAN

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5927	10913	32206	3.73	8.0E-37	BC556927.1	EST_HUMAN	NR0301.x1 NCI_GCAP_1c13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
5927	10913	32206	3.73	8.0E-37	BC556927.1	EST_HUMAN	NR0301.x1 NCI_GCAP_1c13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
5977	10902	32363	6.65	8.0E-37	AW94946.1	EST_HUMAN	MEF29.33 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
8216	21185	34566	6.58	8.0E-37	AB7344.1	NT	H sapiens DMA, DM8, HLA-21, P22, LMP2, TAP2, DOB, DQ52 and RN38, 8, 13 and 14
1289	14324		2.33	7.0E-37	AL042800.1	EST_HUMAN	DKF263456E22.1 434 (synonym: bias) Homo sapiens cDNA clone IMAGE:263456E22.5
1759	14788	27773	0.82	7.0E-37	AF11167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cdc gene, complete cds; and unknown gene
1759	14788	27774	0.92	7.0E-37	AF11167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cdc gene, complete cds; and unknown gene
9161	18170	31049	1.59	7.0E-37	AW95826.1	EST_HUMAN	EST380566 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR3.12
11109	24069	37591	8.45	7.0E-37	AB17700.1	EST_HUMAN	EST380566 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR3.12
11241	24194	37712	1.83	7.0E-37	AB9702.1	EST_HUMAN	EST380566 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR3.12
8762	21749	35171	0.99	8.0E-37	AF16989.1	NT	repetitive element
12603	25487		3.88	6.0E-37	AF202723.1	NT	repetitive element
6212	10286	32518	4.33	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sclt1 unc-84 domain protein 2 (SUN2) mRNA, complete cds
6212	10286	32518	4.33	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sclt1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
9109	22078	35501	0.88	5.0E-37	AV760211.1	EST_HUMAN	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
11295	24217		3.87	5.0E-37	7857117	NT	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
12333	25183		6.43	5.0E-37	AF149733.1	NT	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
2431	15438	28465	2.41	4.0E-37	AA02794.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4914	17831	30729	1.08	4.0E-37	AF16976.1	NT	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
5268	18275		0.93	4.0E-37	NC0251.1	EST_HUMAN	Human endogenous intron DNA (4-1), complete intron segment
9419	19496	32735	0.99	4.0E-37	AV74602.1	EST_HUMAN	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
9711	22834	31721	0.97	4.0E-37	AF33036.1	EST_HUMAN	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
2033	19532	28068	1.07	3.0E-37	AF4658.1	EST_HUMAN	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
253	19532	28068	1.07	3.0E-37	AF4658.1	EST_HUMAN	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
2578	19532		3.71	3.0E-37	AV69118.1	EST_HUMAN	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33
5694	19040	32260	0.73	3.0E-37	AL188274.1	EST_HUMAN	EST178635 Cdc42 oncogene (C42) cDNA clone IMAGE:3146256 3' similar to contains MFR29.33

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Acceesion No.	Top Hit Database Source	Top Hit Descriptor
5670	18765	31533	1.48	8.0E-38	11420114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5670	18765	31538	1.48	8.0E-38	11420114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7650	20513	33571	0.51	8.0E-38	8523130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7613	20573	33588	0.74	8.0E-38	AJ010690.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
7613	20573	33587	0.74	8.0E-38	AJ010690.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
12189	20355	33587	0.74	8.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12877	23477	31780	1.80	8.0E-38	AB020859.1	NT	Homo sapiens DNA for human P2X1, complete cds
13002	27333	31916	1.88	8.0E-38	11418184	NT	Homo sapiens adenylsuccinate lyase (ADSL), mRNA
728	13780	20724	1.28	8.0E-38	AW971819.1	EST_HUMAN	Homo sapiens RBIR gene (partial), exon 8
2450	15464	29487	1.24	5.0E-38	AJ237740.1	EST_HUMAN	061450148F1 NHLMC 86 Homo sapiens cDNA clone IMAGE3854074 5'
7228	20250	33594	1.8	5.0E-38	BE671910.1	EST_HUMAN	9.1aurine mitochondrial aspartate aminotransferase mRNA, complete CDS
119	13228	28154	3.85	4.0E-38	Z25466.1	NT	9.1aurine mitochondrial aspartate aminotransferase mRNA, complete CDS
119	13228	28155	3.85	4.0E-38	Z25466.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2110	19127	31721	3.98	3.0E-38	AF003530.1	NT	Homo sapiens HRA interacting protein 4 (Hraip4) (HRAIP4), mRNA
3710	18743	31721	1.24	3.0E-38	7548807	NT	SSU72 PROTEIN
3888	19008	29817	1.88	3.0E-38	P65538	SWISSPROT	SSU72 PROTEIN
3888	19008	29818	1.88	3.0E-38	P65538	SWISSPROT	SSU72 PROTEIN
8917	25871	33284	7.83	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7455	20421	33776	0.8	3.0E-38	AW302491.1	EST_HUMAN	EST148189 SWISSPROT Q6AP_Br-63 Homo sapiens cDNA clone IMAGE2827008 3'
7832	20760	34167	0.97	3.0E-38	AW302491.1	EST_HUMAN	EST148189 SWISSPROT Q6AP_Br-63 Homo sapiens cDNA 5' end
7844	20761	34167	0.97	3.0E-38	AW302491.1	EST_HUMAN	EST148189 SWISSPROT Q6AP_Br-63 Homo sapiens cDNA 5' end
8957	21963	33588	1.97	3.0E-38	AF373864.1	EST_HUMAN	CD3-F10181.140703-247-097 F10181 Homo sapiens cDNA
8957	21963	33588	1.97	3.0E-38	AF373864.1	EST_HUMAN	CD3-F10181.140703-247-097 F10181 Homo sapiens cDNA
10331	22255	31771	1.46	3.0E-38	AL163448.2	NT	Y48504.11 Soma melanocyte 2N4M Homo sapiens cDNA clone IMAGE246715 5'
12958	19333	31771	1.46	3.0E-38	AL163448.2	NT	Y48504.11 Soma melanocyte 2N4M Homo sapiens cDNA clone IMAGE246715 5'
1380	14474	27384	2.28	2.0E-38	6503207	NT	Homo sapiens chromosome 21 segment HS21C048
1380	14474	27384	2.28	2.0E-38	6503207	NT	Homo sapiens chromosome 21 segment HS21C048
14635	27555	27555	2.07	2.0E-38	AA437533.1	EST_HUMAN	Homo sapiens SNT3 (suppressor of mit w/o 3, yeast) homolog 2 (SNT3-2), mRNA
14635	27555	27555	2.07	2.0E-38	AA437533.1	EST_HUMAN	SW_M12.1 RABIT PA45701 MANNOSE-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
14635	27555	27555	2.07	2.0E-38	AA437533.1	EST_HUMAN	SW_M12.1 RABIT PA45701 MANNOSE-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
2418	15425	29448	1.11	2.0E-38	W78571.1	EST_HUMAN	SW_M12.1 RABIT PA45701 MANNOSE-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
2418	15425	29448	1.11	2.0E-38	W78571.1	EST_HUMAN	SW_M12.1 RABIT PA45701 MANNOSE-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
5271	18190	31040	0.79	2.0E-38	AA437181.1	EST_HUMAN	Z67460.1 Soma, testis, NHT Homo sapiens cDNA clone IMAGE788728 5' similar to FR-0817957
5271	18190	31040	0.79	2.0E-38	AA437181.1	EST_HUMAN	Z67460.1 Soma, testis, NHT Homo sapiens cDNA clone IMAGE788728 5' similar to FR-0817957

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5807	18397	32079	0.61	2.0E-38	Z39534.2	NT	Homo sapiens mRNA for myosin B (440 IDa)
5907	18397	32080	0.61	2.0E-38	Z39534.2	NT	Homo sapiens mRNA for myosin B (440 IDa)
7888	20927	34322	1.27	2.0E-38	AF721103.1	EST_HUMAN	AV72103 HTB Homo sapiens cDNA clone HYBARH11 8'
8828	21765		5.59	2.0E-38	BE16980.1	EST_HUMAN	MR3-HT0487-159200-113-p01 HT0487 Homo sapiens cDNA
9246	22212	33542	0.55	2.0E-38	F08450.1	EST_HUMAN	HSC-BF031 normalized Infant brain cDNA Homo sapiens cDNA clone c-1803
9518	22281	35711	1.21	2.0E-38	AF069785.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9978	22338		1.04	2.0E-38	BE22255.1	EST_HUMAN	hUG902.x1 NCI-GCAP_Lu24 Homo sapiens cDNA clone IMAGE3188130 3' similar to TR-002710 002710
10815	23746	37239	1.74	2.0E-38	D83479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11819	24702	38284	4.62	2.0E-38	BE17290.1	EST_HUMAN	QY24T0988-080800-385-408 HT088 Homo sapiens cDNA
11955	24834	39429	3.06	2.0E-38	AF195051.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 8 (LCR8) mRNA, partial cds
11955	24834	39430	3.66	2.0E-38	AF195051.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 8 (LCR8) mRNA, partial cds
12240	25071		3.38	2.0E-38	AF72388.1	EST_HUMAN	AY72888 HTG Homo sapiens cDNA clone HTGASH07 5'
12242	25072		2.13	2.0E-38	AB012723.1	NT	Homo sapiens gamma 13 fibrinogen chain, complete cds
12538	25082		2.51	2.0E-38	NC05500.1	NT	Homo sapiens gamma 13 fibrinogen chain, complete cds
12548	25071	31810	0.8	2.0E-38	AF55471.1	EST_HUMAN	CH-920380 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
13055	25595		3	2.0E-38	11418248	NT	Homo sapiens sulfatrasferrin-related protein (SULT3) mRNA
1095	14139		2.38	1.0E-38	AA401570.1	EST_HUMAN	pat2002.x1 Scava. tests, NHT Homo sapiens cDNA clone IMAGE745359 3' similar to contains element
2015	15768	39007	1.92	1.0E-38	4985298	NT	MER19 repeat element
2015	15768	39007	1.92	1.0E-38	4985298	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1) mRNA
2015	15954	28071	1.17	1.0E-38	7851959	NT	Homo sapiens KIAA0173 gene product (KIAA0173) mRNA
2020	15955	28532	2.01	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4182	17213	30101	0.60	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4352	17379	30259	10.48	1.0E-38	AL19203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4352	17379	30260	10.48	1.0E-38	AL19203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4427	17448	30536	0.83	1.0E-38	8022843	NT	Homo sapiens hypothetical protein FLJ110600 (FLJ110600) mRNA
5413	18152	31032	0.77	1.0E-38	AA07558.1	EST_HUMAN	7B344H06 Chromosome 7 fetal Brain cDNA Library Homo sapiens cDNA clone 7B344H06
6143	19218	32447	6.56	1.0E-38	7305500	NT	Mus musculus actopodin (Olog) mRNA
6143	19218	32448	6.56	1.0E-38	7305500	NT	Mus musculus actopodin (Olog) mRNA
7834	20594	33957	3.03	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0512 protein, partial cds
9506	22471	33915	0.55	1.0E-38	11402250	NT	Homo sapiens hypothetical protein FLJ110600 (FLJ110600) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9705	27709	39182	6.34	1.0E-39	BE350127.1	EST_HUMAN	h03g01.x1 NC1_OGAP Xid13 Homo sapiens cDNA clone IMAGE3148256 3' similar to contains MER28.i3 MER29 repetitive element;
12401	25712		2.08	1.0E-39	AL163384.2	NT	Homo sapiens chromosome 21 segment HS21C084
98	13178	20067	5.73	8.0E-39	4502312	NT	Homo sapiens ATPase, H+ translocating, vacuolar (vacuolar proton pump) 16C (ATP6C) mRNA
1395	14429	27368	0.84	8.0E-39	4756229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1948	14872		1.54	8.0E-39	AB23404.1	EST_HUMAN	wh3510.x1 NC1_OGAP Xid11 Homo sapiens cDNA clone IMAGE3284491 3' similar to TR-397990 P97800 POL PROTEIN;
1948	15122	28142	5.19	7.0E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
11100	24118	37945	1.8	8.0E-39	BF331826.1	EST_HUMAN	G171-B17051-040900357-502 B17051 Homo sapiens cDNA 7844503.x1 NC1_OGAP L1044 Homo sapiens cDNA clone IMAGE3284356 3' similar to VPR5161.6 C280628;
12981	25545		3.12	6.0E-39	BE77094.1	EST_HUMAN	Homo sapiens X-linked endothelial endothelial dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1029	14038	27010	1.45	5.0E-39	AF03326.1	NT	
			8.19	5.0E-39	AJ750154.1	EST_HUMAN	af6504.x1 Bacterial clone HPIBB7 Homo sapiens cDNA clone IMAGE3274093 3' similar to TR-Q15408 C15408 NEUTRAL PROTEASE LARGE SUBUNIT contains L1771 L177 repetitive element;
12909	25326	28976	2.33	5.0E-39	11420269	NT	Homo sapiens hypothetical protein FL10803 (FL10803). mRNA
652	18521	26542	20.77	4.0E-39	AB015910.1	NT	Chlorococcus anthracis mRNA for ribosomal protein S4X, complete cds
3987	18932	26550	0.92	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6928	19014	32207	0.85	4.0E-39	11422119	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100). mRNA
6928	19014	32208	0.85	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100). mRNA
			1.14	4.0E-39	AA092946.1	EST_HUMAN	aa0294.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE31020438 3' similar to contains O-PR141 ORF repetitive element;
8411	21390	34766	1.14	4.0E-39	AA092946.1	EST_HUMAN	Homo sapiens DNA for prothylactin synthetase, exon 2
9684	22637	35052	0.91	4.0E-39	D34116.1	NT	Homo sapiens DNA for prothylactin synthetase, exon 2
9684	22637	35053	0.91	4.0E-39	D34116.1	NT	Homo sapiens DNA for prothylactin synthetase, exon 2
12704	25393		3.29	4.0E-39	11419177	NT	Homo sapiens RNA for prothylactin synthetase, exon 2
12818	25441		3.15	4.0E-39	BE339452.1	EST_HUMAN	Q107-FN0083-200600-278-006 FN0083 Homo sapiens cDNA Q107-FN0083-200600-278-006 FN0083 Homo sapiens cDNA
49	13109	20075	14.8	3.0E-39	AA031946.1	EST_HUMAN	fmic16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	13109	20076	14.8	3.0E-39	AA031946.1	EST_HUMAN	fmic16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	13109	20077	14.8	3.0E-39	AA031946.1	EST_HUMAN	fmic16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
			8.14	3.0E-39	A084457.1	EST_HUMAN	ccs040.11 Score: 119.999999 3' similar to SW:GTR5_PAT p43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
12233	25095	38183	8.14	3.0E-39	A084457.1	EST_HUMAN	ccs040.11 Score: 119.999999 3' similar to SW:GTR5_PAT p43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;
12233	25095	38184	6.14	3.0E-39	A084457.1	EST_HUMAN	p43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
597	13027	28546	1.8	9.0E-40	5903270	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1239	14275	27234	14.94	9.0E-40	4755148	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1239	14275	27235	14.94	9.0E-40	4755143	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1443	14478	27453	0.59	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Scrb3) (undue dystrophy, pseudoinflammatory) (TIMP3), mRNA
3799	16539	28748	0.88	9.0E-40	4507594	NT	Homo sapiens fragile X mental retardation 1 (FMR1), mRNA
3997	18315	29843	4.05	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4527	17401	30281	0.78	9.0E-40	4507849	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 13) (USP13), mRNA
3054	18111	29026	0.81	9.0E-40	AA079185.1	EST	H115A04 Chromosome T HLA cDNA Library Homo sapiens cDNA clone H115A04
3945	16985		2.35	8.0E-40	BC098441.1	EST	HUMAN
7985	20924	34317	2.22	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7986	20924	34318	2.22	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11243	24198	37715	1.78	7.0E-40	AL103248.2	NT	Homo sapiens chromosome 21 segment 15210348
2737	15731	28746	7.5	9.0E-40	AA361275.1	EST	HUMAN
2737	15731	28747	7.5	9.0E-40	AA361275.1	EST	HUMAN
6049	19130	295	2.05	8.0E-40	BE004765.1	EST	HUMAN
6270	18343	29369	3.35	8.0E-40	1487029	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7121	20355	33929	3.35	8.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10336	23260	36735	9.47	8.0E-40	AV650281	EST	HUMAN
10336	23260	36739	9.47	8.0E-40	AV650281	EST	HUMAN
2812	16611	26835	1.12	5.0E-40	AL183285.2	NT	Homo sapiens chromosome 21 segment 15210385
1854	14919	27915	3.21	4.0E-40	AB980051	EST	HUMAN
2117	15734		2.22	4.0E-40	AF003525.1	NT	Homo sapiens X-linked aniridia, ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4416	17442	30333	8.67	4.0E-40	7862117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8218	21187	34597	0.44	4.0E-40	AI12783.1	EST	HUMAN
8324	21593	34797	4.81	4.0E-40	AA743005.1	EST	HUMAN
9410	23375	33912	5.53	4.0E-40	BE008416.1	EST	HUMAN

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9410	22715	35813	6.53	4.0E-40	BE009416.1	EST_HUMAN	PIC-BN0167-070650-002-112 BN0167 Homo sapiens cDNA
11071	24023	37587	1.66	4.0E-40	AW941585.1	EST_HUMAN	RC1-CN0017-120200-012-04T CN0017 Homo sapiens cDNA
4155	17188	30077	1.02	3.0E-40	A929346.1	EST_HUMAN	WT1267.21 NCI CGAP_KJUT1 Homo sapiens cDNA clone IMAGE:3380549.3
6807	16965	32240	0.66	3.0E-40	4508738	NT	Homo sapiens ribosomal protein S6 (Rplp6), polypeptide 1 (RP39CB1) mRNA
0766	16950	33155	7.69	3.0E-40	11417342	NT	Homo sapiens sems domain, seven thrombopodin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 9A (SEM9A), mRNA
8724	21992	35116	3.94	3.0E-40	6454167	NT	Homo sapiens HBV associated factor (XBP4) mRNA
0320	22285	35716	1.25	3.0E-40	AF078776.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
0666	22258	35977	1.34	3.0E-40	AF078776.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11597	24535	38002	6.33	3.0E-40	6005613	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
325	13418		4.69	2.0E-40	A022038.1	EST_HUMAN	ig22708.21 Soares, Jests, WIT1 Homo sapiens cDNA clone IMAGE:163847.3
795	13554		29.26	2.0E-40	AV933888.1	EST_HUMAN	ig22708.21 Soares, Jests, WIT1 Homo sapiens cDNA clone IMAGE:163847.3
1842	14958		1.71	2.0E-40	AF731807.1	EST_HUMAN	ig22708.21 Soares, Jests, WIT1 Homo sapiens cDNA clone IMAGE:163847.3
1061	14974	27973	1.94	2.0E-40	4506168	NT	HY751607.1TFE Homo sapiens cDNA clone HTF4Z508.6
1951	14974	27974	1.94	2.0E-40	4506168	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2085	15102	28110	1.01	2.0E-40	A806592.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2170	15194	28315	1.84	2.0E-40	6453592	NT	W6041.1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2514716.3 similar to TR-091029 Q91029
2700	16506		1.79	2.0E-40	BE279502.1	EST_HUMAN	ZINC FINGER PROTEIN, 1
3143	16200	29711	4.44	2.0E-40	6453592	NT	Homo sapiens adenyl/yl cyclase-associated protein 2 (CAP2) mRNA
4637	17953	30845	1.77	2.0E-40	AL163280.2	NT	601121567FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784.5
4637	17953	30846	1.77	2.0E-40	AL163280.2	NT	Homo sapiens adenyl/yl cyclase-associated protein 2 (CAP2) mRNA
5237	18245	31117	1.12	2.0E-40	4505960	NT	Homo sapiens chromosome 21 segment HS21C080
884	13899		1.03	1.0E-40	AA225589.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2020	15628	28663	1.47	1.0E-40	BF00681.1	EST_HUMAN	Homo sapiens plasmalogin (PLG) mRNA
2698	16922		1.54	1.0E-40	BE018348.1	EST_HUMAN	nc050609.1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:1007603
2747	15740	28766	1.38	1.0E-40	BF541030.1	EST_HUMAN	b074603.0y NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3946576.5 similar to TR-082169 Q82169
2747	15740	28767	1.38	1.0E-40	BF541030.1	EST_HUMAN	SYNTAXIN 17, 1
3309	16962		1.56	1.0E-40	4507142	NT	052006950AF NIH_MGC_38 Homo sapiens cDNA clone IMAGE:4087738.5
4840	17901	30049	4.18	1.0E-40	4508712	NT	052006950AF NIH_MGC_38 Homo sapiens cDNA clone IMAGE:4087738.5
							Homo sapiens sorting nexin 3 (SNX3) mRNA
							Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products

Single Exon Probes Expressed in Bone Marrow

Probe ID	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1641	14973	27646	8.9	4.0E-41	AA020406.1	EST_HUMAN	intra24.4 of NCI-GCAP_Bind2 Homo sapiens cDNA clone IMAGE:216568.3 similar to contains OPR.1
3669	16534	28970	3.95	4.0E-41	AI22944.1	NT	OFR (positive element);
3669	16534	28970	3.95	4.0E-41	AI22944.1	NT	Homo sapiens 589 to centromere between AML1 and CBRT1 on chromosome 21q22, segment 1/3
3669	16534	28971	3.96	4.0E-41	AI22944.1	NT	Homo sapiens 589 to centromere between AML1 and CBRT1 on chromosome 21q22, segment 1/3
4198	17199	30055	2.26	4.0E-41	Q02688.1	NT	H. sapiens DNA31 hypermethylated site (HSS-3) enhancer element
6658	19715		3.1	4.0E-41	AF176268.1	EST_HUMAN	AV175628 BM Homo sapiens cDNA clone BMFB1C09.5
6658	19715		3.1	4.0E-41	AF176268.1	EST_HUMAN	001689090NF1_H1_JGC, V7 Homo sapiens cDNA clone IMAGE:4127219.5
10032	22097	39448	8.41	4.0E-41	BF504883.1	EST_HUMAN	AV174040 XMT Homo sapiens cDNA clone XACAC097.5
11881	24658		11.59	4.0E-41	AF171048.1	EST_HUMAN	Homo sapiens PAD-H19 mRNA for cysteine/arginine diaminase type II, complete cds
947	14900	29552	2.51	3.0E-41	AB030176.1	NT	Homo sapiens DNA, D1ECT to ORCTL4 gene region, section 1/2 (D1ECT, ORCTL4, ORCTL4 genes, complete cds)
4392	17389	30271	2.6	3.0E-41	AB026898.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5148	18197		1.15	3.0E-41	AB030748.1	NT	H. sapiens mRNA for putative p94 GLOP protein
5509	18695	31625	6.18	3.0E-41	X97866.1	NT	H. sapiens mRNA for KIAA1387 protein, partial cds
6713	20631	33739	1.91	3.0E-41	AB037926.1	EST_HUMAN	Homo sapiens mRNA for KIAA1387 protein, partial cds
7478	20949	33979	0.92	3.0E-41	AA356118.1	EST_HUMAN	YF764983 Juked1 T-cells V1 Homo sapiens cDNA 1
8072	21069	34407	0.92	3.0E-41	RA07976.1	EST_HUMAN	YF764983 Juked1 T-cells V1 Homo sapiens cDNA 1
8212	24688	35937	3.48	3.0E-41	AF199464.1	EST_HUMAN	OV-BR004947.10300-165-108 BM040 Homo sapiens cDNA
8212	24688	35938	3.48	3.0E-41	AF199464.1	EST_HUMAN	OV-BR004947.10300-165-108 BM040 Homo sapiens cDNA
12118	25940	38568	1.49	3.0E-41	AA060768.1	EST_HUMAN	AF171011 S. aureus_36033_VNT Homo sapiens cDNA clone IMAGE:1031947.3
12195	28940		1.49	3.0E-41	U43071.1	NT	Human neuronal protein L2a mRNA, complete cds
18441	18441	27570	15.21	2.0E-41	U43071.1	NT	EST F338188 Entero3, 3' end 1 Homo sapiens cDNA 5' end
1975	14998	27698	2.16	2.0E-41	AA031940.1	EST_HUMAN	Human DNA for KIAA0257 gene, complete cds
2228	15242	26267	1.37	2.0E-41	D08952.1	NT	Human DNA for KIAA0257 gene, complete cds
2278	15289	26314	4.34	2.0E-41	D08952.1	NT	Human DNA for KIAA0257 gene, complete cds
2639	14998	27700	0.89	2.0E-41	U43071.1	NT	Human neuronal protein L2a mRNA, complete cds
3851	19691	29759	0.9	2.0E-41		NT	Human neuronal protein L2a mRNA, complete cds
4652	17783	30550	1.13	2.0E-41	AF163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4652	17783	30551	1.13	2.0E-41	AF163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
5517	18173	31871	0.51	2.0E-41	AA458457.1	EST_HUMAN	PEPTIDYL-PROLYL-CIS-TRANS ISOMERASE A (HUMAN);
6762	19337	33321	0.85	2.0E-41	4564778	NT	Homo sapiens Insign, beta 6 (ITGB6) mRNA
7035	20877	34267	6.38	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nucleos (Ntheds) mRNA, complete cds
8148	21055	34484	0.6	2.0E-41		NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog-like) (ORCBL), mRNA
8403	21372	34760	1.83	2.0E-41	N09844.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8403	21372	34761	1.83	2.0E-41	N09844.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6039	18052		1.49	6.0E-42	AJ284770.1	EST_HUMAN	qu24f03.x1 NC1_COAP_B12 Homo sapiens cDNA clone IMAGE:1065761 similar to contains Alu repetitive element
6543	18940	31590	1.6	6.0E-42	AB028690.1	NT	Homo sapiens mRNA for KIAA1097 protein, partial cds
5805	18940	31592	1.37	6.0E-42	AB028690.1	NT	Homo sapiens mRNA for KIAA1097 protein, partial cds
138	13241		5.99	6.0E-42	AJ271935.1	NT	Homo sapiens Xq pseudobisomeric region, segment 1/2
438	13512	28443	1.7	6.0E-42	BE217813.1	EST_HUMAN	h3716f1.x1 NC1_COAP_Luz2 Homo sapiens cDNA clone IMAGE:375952.3
497	13560		4.65	6.0E-42	5790038	NT	Homo sapiens SET domain and merlin transposase fusion gene (SETMAR) mRNA
488	13591		1.37	6.0E-42	5790038	NT	Homo sapiens SET domain and merlin transposase fusion gene (SETMAR) mRNA
6944	19897	33191	1.07	6.0E-42	11433083	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6944	19897	33192	1.07	6.0E-42	11433083	NT	Homo sapiens myoblastin related protein 3 (MYR3), mRNA
6971	20194	33522	2.61	6.0E-42	11471957	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta isoform mRNA, complete cds
7409	20376	33737	4.6	6.0E-42	AJ071569.1	NT	Homo sapiens melan (RELN) mRNA
8133	21047	34447	0.51	6.0E-42	AB037715	EST_HUMAN	Homo sapiens mRNA for KIAA1284 protein, partial cds
9133	22097	35524	2.88	6.0E-42	AB037715	NT	Homo sapiens 5-hydroxytryptophan 5,4-dioxygenase (HMOX1) mRNA
10970	23860	37403	0.48	6.0E-42	11431168	NT	Homo sapiens 3-hydroxytryptophan 5,4-dioxygenase (HMOX1) mRNA
10970	23860	37404	0.48	6.0E-42	11431168	NT	Homo sapiens 3-hydroxytryptophan 5,4-dioxygenase (HMOX1) mRNA
12097	24659	38555	3.26	6.0E-42	X98411.1	NT	H. sapiens mRNA for myo-h-E
12097	24659	38556	3.28	6.0E-42	X98411.1	NT	H. sapiens mRNA for myo-h-E
754	13815	20758	23.04	4.0E-42	AJ055098.1	NT	Homo sapiens MHC class I region
754	13815	20759	23.04	4.0E-42	AJ055098.1	NT	Homo sapiens MHC class I region
1057	14112	27092	2.03	4.0E-42	AJ189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4223	17262	30139	1.24	4.0E-42	X9417.1	NT	H. sapiens PROS-27 mRNA
4255	17284	30186	1.12	4.0E-42	AJ24219.1	NT	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
4277	17306	30185	4.28	4.0E-42	4506496	NT	Homo sapiens regulatory factor X.4 (influenza H1A class II expression) (RFX4) mRNA
4613	17334	30555	10.96	4.0E-42	4506028	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5290	18395	31155	1	4.0E-42	AL183203.2	NT	Homo sapiens chromosome 21 segment HS210033
5290	18395	31156	1	4.0E-42	AL183203.2	NT	Homo sapiens chromosome 21 segment HS210033
10850	23770	37269	0.54	4.0E-42	AJ371201.1	EST_HUMAN	CMD-B10282-171289-127-503 B10282 Homo sapiens cDNA
11010	23876	37499	1.88	4.0E-42	AJ371201.1	EST_HUMAN	RC1-S10278-040400-016-111 S10278 Homo sapiens cDNA
11010	23876	37500	1.88	4.0E-42	AJ371201.1	EST_HUMAN	RC1-S10278-040400-016-111 S10278 Homo sapiens cDNA
11741	24528	38305	2.89	4.0E-42	BF08327.1	EST_HUMAN	BF1458531F11F1_NG3_38 Homo sapiens cDNA clone IMAGE:3662366.6

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10448	23308	36550	4.15	9.0E-43	4737698	NT	Homo sapiens chromodomain protein, Y chromosome-linked (CDYL) mRNA
853	13719	26541	14	8.0E-43	AV738824.1	EST_HUMAN	AV738824 CB Homo sapiens cDNA clone CBLAK108 5'
653	13719	26542	14	8.0E-43	AV738824.1	EST_HUMAN	AV738824 CB Homo sapiens cDNA clone CBLAK108 5'
701	13763	26595	4.8	9.0E-43	8623276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297) mRNA
701	13763	26595	4.8	9.0E-43	8623276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297) mRNA
9783	18875	32057	0.78	8.0E-43	8623276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297) mRNA
3655	19898	26013	7.28	7.0E-43	AV13852.1	EST_HUMAN	y98a11.1 Spermis placenta NUS2P-Homo sapiens cDNA clone IMAGE148172 5'
9121	22037		3.41	7.0E-43	AA93748.1	EST_HUMAN	2022281 Spymis NHT_MGC_7 Homo sapiens cDNA clone IMAGE2822281 5'
1347	14882		14.15	8.0E-43	AA481800.1	EST_HUMAN	O15475 UNMANED HERV-H PROTEIN, contains LTR 5' LTR negative element ;
2598	15559		2.91	9.0E-43	AV782001.1	EST_HUMAN	RI82008.51 NCI_CGAP_Bmt5 Homo sapiens cDNA clone ADQACC10 5'
6444	19509	32789	2.16	8.0E-43	6945973	NT	AV782001 ADC Homo sapiens cDNA clone IMAGE509803 similar to pL05085 60S
7059	20027	33331	1.91	8.0E-43	AV68897.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family C (GTPTRMP), member 3 (ABCC3), transcript variant 1
10210	21135	36022	2.31	8.0E-43	AA195154.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
11437	24380		2.08	8.0E-43	AA195154.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
144	13247		1.8	8.0E-43	AA195154.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
603	13576	28495	3.96	8.0E-43	AA326780.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
2859	15919	28840	1.83	8.0E-43	AV72578.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
8439	20021	33323	1.15	8.0E-43	AA195154.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
7087	20021	33323	0.85	8.0E-43	AA195154.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
8528	21495	34910	0.7	8.0E-43	AA442271.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
9231	22197		0.89	8.0E-43	AA442271.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
9719	22747	36188	4.22	8.0E-43	AA465388.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
10763	23884	37180	2.36	8.0E-43	AV733244.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
10802	27273	37226	1.45	8.0E-43	AA465388.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
11115	24073	37598	4.88	8.0E-43	AV783007.1	EST_HUMAN	ABCC3.1 Homo sapiens cDNA clone IMAGE261991 3' similar to contains
11783	23541	37483	3.46	8.0E-43	AA195154.1	NT	Human mRNA for alpha-actinin

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
974	18018	28679	3.95	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5331	18437	31189	1.18	4.0E-43	AUG5338.1	EST_HUMAN	cythod.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:16897/3 3'
6505	19559	32821	0.78	4.0E-43	6999009	NT	Homo sapiens glycyRNA synthetase (GARS), mRNA
7337	20308		1.94	4.0E-43	11419793	NT	Homo sapiens procaspase beta 6 (PCDH6), mRNA
8518	21486	34900	5.73	4.0E-43	A124341.1	EST_HUMAN	q76602.x1 NCI CGAP K03 Homo sapiens cDNA clone IMAGE:165354/3 similar to contains MER10.13
8518	21486	34901	5.73	4.0E-43	A124341.1	EST_HUMAN	q76602.x1 NCI CGAP K03 Homo sapiens cDNA clone IMAGE:165354/3 similar to contains MER10.13
10578	23600	37095	1.39	4.0E-43	605997	NT	Homo sapiens zinc finger protein 181 (ZNF181), mRNA
12306	25115		8.39	4.0E-43	P05800.1	EST_HUMAN	q95803.r1 Soares fibrin chain TMB Homo sapiens cDNA clone IMAGE:31938/3 similar to contains MER10 repetitive element
1218	14295		3.85	3.0E-43	A72233.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1704	14734	27718	1.03	3.0E-43	X07839.1	NT	H sapiens gene encoding La antigen
3586	16531	28540	1.32	3.0E-43	S96002.1	NT	hA4.1-EV14-MAM1.1-EV14 fusion protein (nearreag transcription) [human, leukemic cell line SKH1, mRNA mutant, 9538 nt]
4318	17248	30232	1.02	3.0E-43	A45491.1	EST_HUMAN	hA5506.x1 NCI CGAP P77 Homo sapiens cDNA clone IMAGE:1017419
5331	17349	30232	0.98	3.0E-43	A1303786.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
5423	18027	31405	0.51	3.0E-43	M62259.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
5423	18027	31405	0.51	3.0E-43	M62259.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
5423	18027	32277	0.9	3.0E-43	D34613.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
5959	19350	32877	1.86	3.0E-43	Z93350	NT	Mus musculus oagalin (Oag), mRNA
6492	19557	32806	1.86	3.0E-43	Z93350	NT	Mus musculus oagalin (Oag), mRNA
6492	19557	32806	1.86	3.0E-43	Z93350	NT	Human ribosome RNA upstream binding transcription factor (UBTF) gene, partial cds
6890	19942	35238	4.38	3.0E-43	U65497.1	NT	Human ribosome RNA upstream binding transcription factor (UBTF) gene, partial cds
8003	21471		8.69	3.0E-43	A446824.1	EST_HUMAN	hA8971.1 rat Stragene fetal retina 697202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR 12 THR repetitive element
9172	22138	35554	1.92	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011919), mRNA
10223	23198	36837	0.6	3.0E-43	11430217	NT	Homo sapiens similar to ornithine carbonyltransferase (H. sapiens) (LOC88548), mRNA
185	13285		9.29	2.0E-43	A1190764.1	EST_HUMAN	q81608.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:173398/3 similar to contains PTRY.13
6620	16678	32845	0.95	2.0E-43	BE222778.1	EST_HUMAN	PTRY PTRY repetitive element
							hA53008.x1 NCI CGAP Brn41 Homo sapiens cDNA clone IMAGE:317375/3 similar to contains element MER40 repetitive element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E-Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
16820	16878	32658	1.06	2.0E-43	BE22278.1	EST - HUMAN	hUGS08.1.X1, GCG, Bmt4 Homo sapiens cDNA clone IMAGE:3137590.3 similar to coxlinb element
7461	20450	33814	0.97	2.0E-43	AI0207300.1	EST - HUMAN	MER40, repetitive element; UH-B11, rat-595-G.U1, NGI, GCG, S343 Homo sapiens cDNA clone IMAGE:2717172.3'
6951	21619	33814	2.84	2.0E-43	AG47091.1	NT	Human ribosomal protein L26a mRNA, complete cds
11832	2473	34273	2.36	2.0E-43	U030701.1	EST - HUMAN	FBIG3 Fetal brain, Stragziano Homo sapiens cDNA clone F8103 and similar to LINE-1
1087	14889	27654	4.13	1.0E-43	AF146836.1	NT	Human sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1 and 2
1087	14889	27655	4.13	1.0E-43	AF146836.1	NT	Human sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1 and 2
1774	14727	27733	2.93	1.0E-43	AF143284.2	NT	Human sapiens chromatinin 21 segment HS21.0284
2734	15728	28742	2.18	1.0E-43	BP42626.1	EST - HUMAN	80322313F1, NC1, GCG, Bmt5 Homo sapiens cDNA clone IMAGE:157866.8'
54924	18584	31496	0.77	1.0E-43	4895544	NT	Human sapiens pyruvate dehydrogenase kinase, isozyme gamma (PDK3) mRNA
6784	18818	33098	6.3	1.0E-43	4407158.1	EST - HUMAN	Human sapiens Sp1 transcription factor (SP1) mRNA
6784	18818	33098	6.3	1.0E-43	4407168.1	EST - HUMAN	Human sapiens Sp1 transcription factor (SP1) mRNA
7169	19019	31235	1.87	1.0E-43	AF10781.1	EST - HUMAN	940601.1 Soares infant TNB Homo sapiens cDNA clone IMAGE:34732.5' similar to
8426	21253	34414	0.97	1.0E-43	AF170265.1	NT	GP-BD38, MOUSE Sp2866 BRAIN PROTEIN DN38
8426	21253	34414	0.97	1.0E-43	AF170265.1	NT	Human sapiens vacular sorting protein 35 (VPS35) mRNA, complete cds
9189	23145	35584	3.15	1.0E-43	AF184940.1	NT	Human sapiens 86221.1 region and MGH (GBFA37) gene, partial cds
10884	23576	37075	0.62	1.0E-43	AF185076.1	EST - HUMAN	EST137679 IMAGE, sequences, IMAGE Homo sapiens cDNA
11131	24421	37375	3.19	1.0E-43	AF185222.1	EST - HUMAN	EST137679 IMAGE, sequences, IMAGE Homo sapiens cDNA
11603	24688	38226	6.35	1.0E-43	AF185444.1	EST - HUMAN	W67N1.1, NC1, GCG, Bmt1 Homo sapiens cDNA clone IMAGE:3484793.3'
12244	25074	38226	2.28	1.0E-43	AF184764.1	EST - HUMAN	94752751D10.1 F178 (cysynzyr: ham2) Homo sapiens alpha 1b tubulin (CA03481) mRNA
12244	25074	38226	2.28	1.0E-43	AF184764.1	EST - HUMAN	94752751D10.1 F178 (cysynzyr: ham2) Homo sapiens alpha 1b tubulin (CA03481) mRNA
25255	31960	31757	2.88	8.0E-44	U1148322.1	EST - HUMAN	94752751D10.1 F178 (cysynzyr: ham2) Homo sapiens alpha 1b tubulin (CA03481) mRNA
12745	23394	31757	2.88	8.0E-44	U1148322.1	EST - HUMAN	94752751D10.1 F178 (cysynzyr: ham2) Homo sapiens alpha 1b tubulin (CA03481) mRNA
891	31949	26905	7.09	8.0E-44	U122983.1	EST - HUMAN	94752751D10.1 F178 (cysynzyr: ham2) Homo sapiens alpha 1b tubulin (CA03481) mRNA
891	31949	26905	7.09	8.0E-44	U122983.1	EST - HUMAN	94752751D10.1 F178 (cysynzyr: ham2) Homo sapiens alpha 1b tubulin (CA03481) mRNA
10702	27932	37120	0.47	8.0E-44	U104362.1	EST - HUMAN	94752751D10.1 F178 (cysynzyr: ham2) Homo sapiens alpha 1b tubulin (CA03481) mRNA
10702	27932	37120	0.47	8.0E-44	U104362.1	EST - HUMAN	94752751D10.1 F178 (cysynzyr: ham2) Homo sapiens alpha 1b tubulin (CA03481) mRNA
11459	24442	37923	3.33	8.0E-44	U104362.1	EST - HUMAN	94752751D10.1 F178 (cysynzyr: ham2) Homo sapiens alpha 1b tubulin (CA03481) mRNA
11695	24872	39469	2.24	8.0E-44	U29138.1	NT	Human sapiens small polypeptide protein 2C (SPR22C) mRNA
12495	25237	31891	2.85	8.0E-44	U11527839.1	EST - HUMAN	Human sapiens small polypeptide protein 2C (SPR22C) mRNA
12495	25237	31891	2.85	8.0E-44	U11527839.1	EST - HUMAN	Human sapiens small polypeptide protein 2C (SPR22C) mRNA
12930	25575	31510	2.68	8.0E-44	U1148038.1	EST - HUMAN	Human sapiens myosin mRNA, partial cds
12930	25575	31510	2.68	8.0E-44	U1148038.1	EST - HUMAN	Human sapiens myosin mRNA, partial cds
13079	25795	31968	1.87	8.0E-44	U1148038.1	EST - HUMAN	Human sapiens myosin mRNA, partial cds
13079	25795	31968	1.87	8.0E-44	U1148038.1	EST - HUMAN	Human sapiens myosin mRNA, partial cds
13079	25795	31968	1.87	8.0E-44	U1148038.1	EST - HUMAN	Human sapiens myosin mRNA, partial cds
13079	25795	31968	1.87	8.0E-44	U1148038.1	EST - HUMAN	Human sapiens myos

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Table 4

Single Exon Probes Expressed in Bone Marrow

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1370	14404	27374	1.05	2.0E-44	BE483235.1	EST_HUMAN	hw14003.x1 NGL CGAP_Lux24 Homo sapiens cDNA clone IMAGE:3162588 3' similar to SW-637B_HUMAN
2167	15177	28188	2.57	2.0E-44	AF070851.1	NT	P22059 OXYSTEROL-BINDING PROTEIN.1
2616	16816		2.01	2.0E-44	65016033	NT	Homo sapiens testis-type bone marrow zinc finger protein 4 mRNA, complete cds
3484	16930	28455	1.16	2.0E-44	D67767.1	NT	Homo sapiens adipocyte-related protein complex 4, sigma 1 subunit (GLAP3), mRNA
4900	17921	30514	1.8	2.0E-44	AW64378.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6214	18286	32321	1.59	2.0E-44	11149901	NT	PMK-SN016c:12650-003-004 SN0018 Homo sapiens cDNA
7037	18396	31266	1.73	2.0E-44	AF33808.1	NT	Homo sapiens chemokine (C-C motif) receptor 6 (CCR6), mRNA
7943	20955	33970	3.8	2.0E-44	11416228	NT	Homo sapiens general transcription factor 24 (GTF24) mRNA, alternatively spliced product, complete cds
7943	20955	33971	3.8	2.0E-44	11416228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8771	21738	33188	0.72	2.0E-44	770870	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8771	21738	33189	0.72	2.0E-44	770870	NT	Homo sapiens vesicle transport-related protein (VAMP3), mRNA
8900	21923	35337	1.83	2.0E-44	BE339036.1	EST_HUMAN	Homo sapiens vesicle transport-related protein (VAMP3), mRNA
12152	25010		1.44	2.0E-44	BE244024.1	EST_HUMAN	8912851 THF1 NPL_NG2_24 Homo sapiens cDNA clone IMAGE:3613685 5'
12655	25688		1.32	2.0E-44	40299833	NT	homo sapiens HLA-DQA1 gene, pre-B cell acute lymphoblastic leukemia T-cell line TCR-TCR-TCR-TCR
13047	25887		1.56	2.0E-44	11532333	NT	Homo sapiens neuronal cell adhesion molecule (NCAM), mRNA
54	13174	26044	7.76	1.0E-44	7657334	NT	Homo sapiens cell surface sialoglycoprotein, candidate 1 (CECR1), mRNA
64	13174	26045	7.76	1.0E-44	7657334	NT	Homo sapiens Mashkin/NK-related kinase (MNK), mRNA
892	13960	28564	1.65	1.0E-44	AW658132.1	EST_HUMAN	RC1-C10248-030302-026-112 G10248 Homo sapiens cDNA
1302	14241		1.85	1.0E-44	AW654803.1	EST_HUMAN	RC1-BN0336-110300-012407 BN0336 Homo sapiens cDNA
1577	14810		7.03	1.0E-44	153303.2	NT	Homo sapiens chromosome 21 segment 1521C103
2223	15247	28270	4.49	1.0E-44	AA34554.1	EST_HUMAN	zwd33402.1 Soares. beta, beta, N247F8_3w Homo sapiens cDNA clone IMAGE:773763 5' similar to
2223	15247	28271	4.49	1.0E-44	AA34554.1	EST_HUMAN	zwd33402.1 Soares. beta, beta, N247F8_3w Homo sapiens cDNA clone IMAGE:773763 5' similar to
2290	15969	28327	0.95	1.0E-44	AA338099.1	EST_HUMAN	2885711.1 Soares. beta, beta, N247F8_3w Homo sapiens cDNA clone IMAGE:726478 5'
2770	15762	29783	2.3	1.0E-44	AF18778.1	NT	Homo sapiens transcription factor 10H1 enhancer 3, JM11 protein, JM1 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel alpha 1D subunit (L-type calcium channel alpha 1D)
3128	18760		3.01	1.0E-44	AA458989.1	EST_HUMAN	hmo7008.1 Soares. N1940F1, ST Homo sapiens cDNA clone IMAGE:811944 3'
3153	18765	31043	0.84	1.0E-44	AA370783.1	NT	Homo sapiens alpha satellite DNA, MT monomer type
3753	19769	31044	0.84	1.0E-44	AA370783.1	NT	Homo sapiens alpha satellite DNA, MT monomer type

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Table 4
Cytokines Expressed in Bone Marrow[illegible]

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
12003	24180	38478	2.3	5.0E-45	85023098	NT	Homo sapiens gadin-like protein (GLP), mRNA
1146	14188	27139	10.78	4.0E-45	X98308.1	NT	H.sapiens ART14 gene
2266	15311	28331	1.91	4.0E-45	BE26952.1	EST_HUMAN	801191440.F1 NH_100277 Homo sapiens cDNA clone IMAGE338425 5'
4555	17558	30446	0.72	4.0E-45	4759249	NT	Homo sapiens TRAF family member-associated NFkB activator (TANK) mRNA
9306	22273		0.89	4.0E-45	AA228220.1	EST_HUMAN	nc83607 at NCI, COMP_P11 Homo sapiens cDNA clone IMAGE106284 similar to contains element L1 repetitive element;
12197	25664	31418	1.4	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
4115	18353		0.99	3.0E-45	U71480.1	EST_HUMAN	p53B01.r1 Sarcos fetal liver spleen NH_8 Homo sapiens cDNA clone IMAGE110245 5'
5384	19433	32678	1.13	3.0E-45	8753951	NT	Mus musculus dyx1c1, exon, heavy chain 11 (Dnaicr1), mRNA
9344	19433	32677	1.13	3.0E-45	8753951	NT	Mus musculus dyx1c1, exon, heavy chain 11 (Dnaicr1), mRNA
9143	21761		1.63	3.0E-45	AV728976.1	EST_HUMAN	AY728976 HTB Homo sapiens cDNA clone HTBAAG01 5'
9143	21768		3.82	3.0E-45	AV728976.1	EST_HUMAN	Homo sapiens gong subunit, gong subfamily a, 2 (GONG2) mRNA
10570	23308	37587	0.88	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS210327
10570	23308	37587	0.88	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS210327
12664	29888		1.93	3.0E-45	AL163227.1	NT	H.sapiens DNA for endonuclease III sensitive element
2511	18814		1.96	2.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS210327
3046	18102	28018	1.6	2.0E-45	AL163227.1	NT	Homo sapiens partial 5'UTR14 receptor gene, exons 2 to 5
8671	19728	33004	5.17	2.0E-45	U01695.1	NT	Human osteonin/osteocalcin/calcin crystal (CLO) protein (lysochalcin/bone) gene, promoter and exon 1
7680	20812	31189	1.25	2.0E-45	BE782184.1	EST_HUMAN	801467765.F1 NH_100277 Homo sapiens cDNA clone IMAGE307068 5'
8788	21725	35148	1.08	2.0E-45	AW183483.1	EST_HUMAN	RQ31.10091.1182005.032.d11 L10921 Homo sapiens cDNA
11154	25704	37639	25.98	2.0E-45	BE834350.1	EST_HUMAN	NR0-H10923-182005.201.d03 HT0923 Homo sapiens cDNA
11511	24492	38002	3.5	2.0E-45	AA468776.1	EST_HUMAN	sa89712.1 Shalagene fetal retina 887202 Homo sapiens cDNA clone IMAGE538319 5' similar to
11832	24715	38296	1.67	2.0E-45	AW170280.1	EST_HUMAN	xp72005.xt NCI_OGAP_O40 Homo sapiens cDNA clone IMAGE274898 3'
11832	24715	38300	1.67	2.0E-45	AW170280.1	EST_HUMAN	xp72005.xt NCI_OGAP_O40 Homo sapiens cDNA clone IMAGE274898 3'
12099	25595		3.48	2.0E-45	11418159	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA1), mRNA
134	13482		1.84	1.0E-45	BE388955.1	EST_HUMAN	801284350.F1 NH_100277 Homo sapiens cDNA clone IMAGE306183 5'
409	13482		2.09	1.0E-45	BE388955.1	EST_HUMAN	801284350.F1 NH_100277 Homo sapiens cDNA clone IMAGE306183 5'
473	13946	26474	1.69	1.0E-45	4604412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1178	14219	27175	1.84	1.0E-45	7857290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGRIN), mRNA
3120	19177	28088	7.12	1.0E-45	U32186.1	NT	Human pro-alpha2 chain of collagen type XI (COL11A2) gene, complete cds
3533	16590	28477	0.84	1.0E-45	8695659	NT	Homo sapiens chromosome 21 open reading frame 1 (C21ORF1), mRNA
4933	17828	30413	4.06	1.0E-45	BE396633.1	EST_HUMAN	8012891.F1 NH_100277 Homo sapiens cDNA clone IMAGE311803 5'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
3539	16585	20500	1.01	5.0E-46	BE677164.1	EST_HUMAN	748 gp130.L1.Lupakl_Gerard_Kodl_GOGAP_Kodl1 Homo sapiens cDNA clone IMAGE:3275408.3 nas9801.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3268767.3 similar to TR-O7502
8899	19551	33548	1.54	5.0E-46	BF590442.1	EST_HUMAN	075022.HOMOLOG OF RAT KIDNEY SPECIFIC: 502021.T64F1 NCL_CGAP_Bim97 Homo sapiens cDNA clone IMAGE:4156670.5
7128	20104	33415	3.97	5.0E-46	BF347220.1	EST_HUMAN	QV45.T0212.120100.076-09.910212 Homo sapiens cDNA
2023	33609	33609	0.67	5.0E-46	AW682353.1	EST_HUMAN	7538009.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230487.3
7614	20574	33698	0.95	5.0E-46	BE449744.1	EST_HUMAN	ns54609.a1 NCL_CGAP_S51 Homo sapiens cDNA clone IMAGE:1194520.3 similar to gb:XB3741.1_mn1 FIBLIN-1, ISOFORM A PRECURSOR (HUMAN);
642	13708		2.88	4.0E-46	AA801143.1	EST_HUMAN	h86403.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008886.5 similar to gb:U14008.1_mn1 LYSOZYM C PRECURSOR (HUMAN); contains element MER37 repetitive element:
1715	14745	27729	7.91	4.0E-46	AW770544.1	EST_HUMAN	h86403.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008886.5 similar to gb:U14008.1_mn1 LYSOZYM C PRECURSOR (HUMAN); contains element MER37 repetitive element:
1715	14745	27730	7.91	4.0E-46	AW770544.1	EST_HUMAN	h86403.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008886.5 similar to gb:U14008.1_mn1 LYSOZYM C PRECURSOR (HUMAN); contains element MER37 repetitive element:
2749	17342	26799	3.28	4.0E-46	MT8048.1	NT	Human endogenous retrovirus RTV-LR2
4447	17473	30381	0.95	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIA00622 protein, partial cds
1715	14745	30386	0.98	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIA00622 protein, partial cds
5194	18203	31077	0.78	4.0E-46	BE044503.1	EST_HUMAN	h84260.x1 Sraae_NFL_T1_OBC_S1 Homo sapiens cDNA clone IMAGE:3040020.3
5194	18203	31077	0.78	4.0E-46	BE044503.1	EST_HUMAN	h84260.x1 Sraae_NFL_T1_OBC_S1 Homo sapiens cDNA clone IMAGE:3040020.3
5811	18811	31543	2.11	4.0E-46	BE348562.1	NT	Human g gamma gene 3 heavy-chain gene Y region, partial cds
5811	18811	31543	2.11	4.0E-46	BE348562.1	NT	Human g gamma gene 3 heavy-chain gene Y region, partial cds
12792	25422	31707	2.51	4.0E-46	AB020269.1	NT	Homo sapiens cDNA for Human P2X ₂ , complete cds
4421	17448	30339	1.21	4.0E-46	4596376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP3K3) mRNA
4809	17826	30722	2.84	3.0E-46	Z73950.1	NT	H.sapiens h1 lambda light chain variable region gene (7c.11.2) germline; (h4-light-Lambda; VLambda
4809	17826	30723	2.84	3.0E-46	Z73950.1	NT	H.sapiens h1 lambda light chain variable region gene (7c.11.2) germline; (h4-light-Lambda; VLambda
9102	22068	35694	10	3.0E-46	AB831482.1	EST_HUMAN	W4924.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406750.3 similar to contains THR12 THR repetitive element:
9358	22323	35750	0.59	3.0E-46	U8850.1	NT	Human AD amyloid mRNA, complete cds
9358	22323	35751	0.59	3.0E-46	U8850.1	NT	Human AD amyloid mRNA, complete cds
11898	24778	38395	2.01	3.0E-46	U31785.1	NT	Human mRNA for KIA0061 gene, partial cds
838	13885	26550	10.84	2.0E-46	AA468046.1	EST_HUMAN	nc0806.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:880408.3 similar to contains THR32 THR repetitive element:

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Exon/Intron Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1584	14597		2.13	2.0E-46	AA578246.1	EST_HUMAN	327x11a1 Source: fetal liver, spleen, INFLS 5' Homo sapiens cDNA clone IMAGE:421988 3'
1647	14679	27652	4.43	2.0E-46	U78027.1	NT	Homo sapiens Brucella's tyrosine kinase (BTK), alpha-D-glucosylase 4 (GLA), L44-like ribosomal protein (L44), and FTF3 (FTF3) genes, complete cds
5610	18024	30910	1.08	2.0E-46	AA392286.1	EST_HUMAN	28940211 Source: testis, NHT Homo sapiens cDNA clone IMAGE:726860 5' similar to SW:RSB1_MOUSE
7728	20582	34048	7.69	2.0E-46	9910899	NT	Q01730 HSP-1 PROTEIN.1
8404	21737		1.18	2.0E-46	BE686181.1	EST_HUMAN	Male muscular sperm cell associated protein (Slap) mRNA
11979	24514		1.82	2.0E-46	7867233	NT	501448197171 NH: JMC-351 Homo sapiens cDNA clone IMAGE:3949287 5'
12657	25741	31619	3.22	2.0E-46	AW277214.1	EST_HUMAN	Homo sapiens small ribosomal protein L16 (MRPL16) mRNA
1267	14273	27253	0.68	1.0E-46	4902894	NT	327803321 NCI: CGAP_L103 Homo sapiens cDNA clone IMAGE:2766768 3'
2289	15302	28328	3.28	1.0E-46	AV1676518.1	EST_HUMAN	Homo sapiens alpha-2-macroglobulin (A2M) mRNA
2409	15416	28440	2.9	1.0E-46	H07330.1	EST_HUMAN	EST:380358 IMAGE:380358 MAGP Homo sapiens cDNA
3262	16316	25296	1.32	1.0E-46	AA531912.1	EST_HUMAN	EST:380358 IMAGE:380358 MAGP Homo sapiens cDNA clone 484065
4608	17926		2.83	1.0E-46	AA531912.1	EST_HUMAN	EST:380358 IMAGE:380358 MAGP Homo sapiens cDNA clone 484065
5784	18776	32058	7.03	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0900 protein, partial cds
6969	25933	32352	0.87	1.0E-46	BF194707.1	EST_HUMAN	7623901 x1 NCI: CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6985	25933	32383	5.87	1.0E-46	8823782	NT	Homo sapiens containin-alpha 2 protein (HSA272195) mRNA
6766	19220	31102	0.65	1.0E-46	BF198247.1	EST_HUMAN	Homo sapiens containin-alpha 2 protein (HSA272195) mRNA
11211	16976	33002	3.81	1.0E-46	BF194707.1	EST_HUMAN	7623901 x1 NCI: CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
12223	25124	31845	1.82	1.0E-46	BF198247.1	EST_HUMAN	8020722841 NCI: CGAP_Bm37 Homo sapiens cDNA clone IMAGE:4213388 5'
12423	25124	31846	1.82	1.0E-46	BF198247.1	EST_HUMAN	8020722841 NCI: CGAP_Bm37 Homo sapiens cDNA clone IMAGE:4213388 5'
15925	26960		4.54	1.0E-46	AV176371.1	EST_HUMAN	AV176371 VGB Homo sapiens cDNA clone DCBA103 5'
787	13326		3.24	0.0E-47	AJ271755.1	NT	Homo sapiens Aq pseudotubercular region, segment 1/2
4996	17983	30073	3.91	0.0E-47	AW170926.1	EST_HUMAN	HYPOTHETICAL 12.4 KD PROTEIN.1
6613	18977	33832	1.96	0.0E-47	11425439	NT	Homo sapiens zinc finger protein ZNF268 (ZNF268) mRNA
12816	25843	31432	2.29	0.0E-47	11417956	NT	Homo sapiens zinc finger protein ZNF268 (ZNF268) mRNA
1825	14852	27648	47.72	0.0E-47	Y176839.1	NT	Homo sapiens HLAC gene, exon 5, individual 19023
1825	14852	27647	47.72	0.0E-47	Y176839.1	NT	Homo sapiens HLAC gene, exon 5, individual 19023
2728	16722	28739	1.77	0.0E-47	5453956	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R4E) mRNA
3036	16094	28012	2.12	0.0E-47	AJ122043.1	NT	Homo sapiens 959 to contig between AML1 and CBR1 on chromosome 2 q22, segment 3/3

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Table 4
Single Exon Probes Expressed in Bone Marrow

[illegible]

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1970	14030			1.06	2.0E-47	AB082878.1	EST_HUMAN
1870	14029	27604	2.2	2.0E-47	7682109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1837	14718	27688	3.87	2.0E-47	AA524514.1	EST_HUMAN	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
4374	17402	30282	1.82	2.0E-47	4904860	NT	Homo sapiens ring finger protein (RNF8), mRNA
4411	17430	30327	1.48	2.0E-47	AA569592.1	EST_HUMAN	h23p07.s1 NCI_OGAP_P11 Homo sapiens cDNA clone IMAGE:387007 3'
4411	17430	30328	1.48	2.0E-47	AA569592.1	EST_HUMAN	h23p07.s1 NCI_OGAP_P11 Homo sapiens cDNA clone IMAGE:387007 3'
4834	17587	30445	1.68	2.0E-47	5174648	NT	Homo sapiens RAB17A protein-binding protein (RAB17A), mRNA
4850	17587	30760	1.22	2.0E-47	AW085166.1	EST_HUMAN	EST1377239 IMAGE:2955560 3' similar to gp-M22665
5187	18190		0.7	2.0E-47	AB041126.1	EST_HUMAN	ov6f103.s1 Soares, Isola, NHT Homo sapiens cDNA clone IMAGE:1541545 3'
5880	18699	32160	1.22	2.0E-47	AB041126.1	NT	Homo sapiens regulator of G-protein signaling 3 variant form (RGS3), complete cds
6088	19108	32380	1.26	2.0E-47	BE778475.1	EST_HUMAN	h07463532P1 NIH_MGC_571 Homo sapiens cDNA clone IMAGE:3861467 5'
6088	19108	32381	1.26	2.0E-47	BE778475.1	EST_HUMAN	h07463532P1 NIH_MGC_571 Homo sapiens cDNA clone IMAGE:3861467 5'
7864	25652		1.43	2.0E-47	U09731.1	NT	Homo sapiens 5'-phosphatase 1D receptor pseudogene with an A/U repeat insertion
8297	21266	34677	1.76	2.0E-47	U09731.1	NT	Homo sapiens 5'-phosphatase 1D receptor pseudogene with an A/U repeat insertion
8297	21266	34678	1.76	2.0E-47	U09731.1	NT	Homo sapiens 5'-phosphatase 1D receptor pseudogene with an A/U repeat insertion
9068	22034	35457	1.78	2.0E-47	A0701771.1	NT	Homo sapiens DNA to amyloid precursor protein, complete cds
9443	22781	38235	0.78	2.0E-47	11326136	NT	Homo sapiens SPH-1, a novel protein, complete cds
11900	23955	37478	2.31	2.0E-47	M76125.1	NT	Homo sapiens 5'-phosphatase 1D receptor pseudogene with an A/U repeat insertion
12358	25886	31415	2.12	2.0E-47	R42423.1	EST_HUMAN	Homo sapiens 5'-phosphatase 1D receptor pseudogene with an A/U repeat insertion
1454	14437	27403	6.16	1.0E-47	A034229.1	EST_HUMAN	h0590303.s21 Soares, Isola, NHT, NIH, 19W Homo sapiens cDNA clone IMAGE:1931482 3'
1838	17419	27679	1.18	1.0E-47	BE280477.1	EST_HUMAN	h01156332P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:313893 5'
3833	18915	29715	1.18	1.0E-47	BE280477.1	EST_HUMAN	h01156332P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:313893 5'
5172	19123	30897	2.55	1.0E-47	AV041306.1	EST_HUMAN	RC3-ST0197-130400-017-A02 ST0197 Homo sapiens cDNA
7244	19076	33276	6.6	1.0E-47	A080986.1	EST_HUMAN	h19063.s1 Barak, Isola, NHT, NIH, 19W Homo sapiens cDNA clone IMAGE:2955560 3' similar to gp-M22665
9220	22186		0.77	1.0E-47	AW084648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10721	22843	37136	2.41	1.0E-47	30115.1	NT	h84e11.s1 Soares, Isola, NHT, NIH, 19W Homo sapiens cDNA clone IMAGE:2078972 3' similar to gp-M23528
10721	22843	37136	2.41	1.0E-47	30115.1	NT	h84e11.s1 Soares, Isola, NHT, NIH, 19W Homo sapiens cDNA clone IMAGE:2078972 3' similar to gp-M23528
1616	14648	27823	3.85	9.0E-48	AF223391.1	EST_HUMAN	keratin, type I cytoskeletal, 18 (HUMAN);
3569	16914	26536	0.87	9.0E-48	BF309947.1	EST_HUMAN	keratin, type I cytoskeletal, 18 (HUMAN);
5763	18655	32335	0.84	9.0E-48	BE068196.1	EST_HUMAN	keratin, type I cytoskeletal, 18 (HUMAN);
5763	18655	32336	0.84	9.0E-48	BE068196.1	EST_HUMAN	keratin, type I cytoskeletal, 18 (HUMAN);

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Table 4
Antibodies Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9220	10294	32528	0.73	9.0E-48	AF123831.168.1	EST_HUMAN	atf5l09.47 Baristaad codon HPLR87 Homo sapiens cDNA clone IMAGE:277869.3 similar to TR060844
9351	19420	32661	0.6	9.0E-48	AI123234.1	EST_HUMAN	OB6844-HOMOLOG OF RAT ZWIMGEN GRANULE MEMBRANE PROTEIN. ;
11482	14395	37940	2.49	9.0E-48	BE389381.1	EST_HUMAN	AT123240-NO72M17 Homo sapiens cDNA clone NT2891000978.5
12355	14281		1.5	8.0E-48	4501900.NT	EST_HUMAN	601310749F1 NH_1JGC_44 Homo sapiens cDNA clone IMAGE:383203.5 ³
1236	14281		1.54	8.0E-48	4501900.NT	EST_HUMAN	Homo sapiens aminocycloleas 1 (ACY1), mRNA
3152	10239	29123	3.31	8.0E-48	AY1768477.1	EST_HUMAN	Hf16103.X1 NCI_GCAP_Lym12 Homo sapiens cDNA clone IMAGE:3301133.3 similar to gb:364707
3182	16209	29124	3.31	8.0E-48	AY1768477.1	EST_HUMAN	BREAST BASIC MEMBRANE PROTEIN 1 (HUMAN);
4921	13504		1.54	9.0E-48	AB030335.1	NT	BREAST BASIC MEMBRANE PROTEIN 2 (HUMAN);
4982	14529		22.81	7.0E-48	AB030335.1	NT	Homo sapiens MNRV for KIAA1209 protein, partial cds
1468	14529	27501	1.04	7.0E-48	8792719	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
17483	14075	27948	4.5	7.0E-48	5790038	NT	Homo sapiens toubic-like kinase 1 (TLK1), mRNA
6707	19783	33042	24.74	7.0E-48	11419831	NT	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR) mRNA
3812	16057	25875	1.2	6.0E-48	AT167111.1	EST_HUMAN	w69R033.X1 NCI_GCAP_K1472 Homo sapiens cDNA clone IMAGE:2388613.3 ³
6178	19251	32484	1.12	6.0E-48	AB008958.1	NT	w69R033.X1 NCI_GCAP_K1472 Homo sapiens cDNA clone IMAGE:2388613.3 ³
6853	20177	33502	0.89	6.0E-48	11420995	NT	Homo sapiens BAX non-receptor tyrosine kinase (BAX), mRNA
7102	25897	34022	0.95	6.0E-48	AB048841.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
7732	23607	34023	0.95	6.0E-48	AB048841.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8479	23607	34023	1.94	6.0E-48	AB048841.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8998	23632	35511	1.78	6.0E-48	11421428	NT	Homo sapiens hypothetical protein T1037 (T1037) mRNA
10047	22974	36441	3.3	6.0E-48	AA168080.1	EST_HUMAN	281848.41 Stailinger's protein T1037 (687283) Homo sapiens cDNA clone IMAGE:632927.3 similar to
3320	18193	29092	1.58	5.0E-48	46286821	NT	281848.41 Stailinger's protein T1037 (687283) Homo sapiens cDNA clone IMAGE:632927.3 similar to
3621	16187	38314	1.11	5.0E-48	BE064410.1	EST_HUMAN	RC4187031.1441189201.1008 BT03111 Homo sapiens cDNA
11355	14459	37762	2.93	3.0E-48	AB020323.1	EST_HUMAN	1474623.31 NCI_GCAP_P728 Homo sapiens cDNA clone IMAGE:2254154.3 ³
1335	14419	27368	1.83	3.0E-48	AB069041.1	EST_HUMAN	AB069043.4 GKG Homo sapiens cDNA clone GCGR0612.5
1693	19041	26201	16.21	3.0E-48	46881070	NT	Homo sapiens chromosome X open reading frame 5 (CXORF6) mRNA
1993	18014	28021	18.21	3.0E-48	46881070	NT	Homo sapiens chromosome X open reading frame 5 (CXORF6) mRNA
3429	16477	29395	0.93	3.0E-48	AF174483.1	NT	Homo sapiens speed factor receptor mRNA, complete cds
3647	16690	29608	0.75	3.0E-48	AB646531.1	EST_HUMAN	3114012.X1 NCI_GCAP_GU1 Homo sapiens cDNA clone IMAGE:297255.3 similar to SW102CB1 HUMAN
3825	17304		0.6	3.0E-48	AA009584.1	EST_HUMAN	P56568 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
4279	14759		25.03	3.0E-48	AA009584.1	EST_HUMAN	261403.17 Scaevola field liner isolat. INFLS. S1 Homo sapiens cDNA clone IMAGE:238844.5 ⁴

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Table 4
Single Exon Probe Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5697	19061	32278	2.41	3.0E-48	BE304571.1	EST_HUMAN	HK4-BT0957-000-400-201-wt10 BT0957 Homo sapiens cDNA
7216	20237	33571	1.00	3.0E-49	AJ208793.1	NT	nc3005 at NC1 CGAP_P22 Homo sapiens cDNA clone IMAGE:1210137 3' similar to contains PTR6.1 PTR6 repetitive element;
8734	21702		4.11	3.0E-48	AA656930.1	EST_HUMAN	UH-HW1-etha-10-00-001 at NC1 CGAP_S407 Homo sapiens cDNA clone IMAGE:3082267 3'
11221	24174	37700	6.89	3.0E-48	BF51470.1	EST_HUMAN	256003.11 Sources over tumor NHOT Homo sapiens cDNA clone IMAGE:810032 3'
6	13126	26025	2.4	2.0E-48	AA485007.1	EST_HUMAN	fm67 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone ORF-256
47	13167	26072	1.23	2.0E-48	AA631940.1	EST_HUMAN	ym568.01 Source Infant brain TM8 Homo sapiens cDNA clone IMAGE:52182 9' similar to SP-M88 MOUSE J95803 MEMO-PANE GLYCOPTO1EIN
1223	14281		0.65	2.0E-48	H54278.1	EST_HUMAN	TCGAP-103842 Pediatric med8 cell acute lymphoblastic leukemia Baylor-HGSC project-TC8A Homo sapiens cDNA clone TCGAP-3542
4592	17885	30477	0.52	2.0E-48	BE246005.1	EST_HUMAN	nc16907.1 NC1 CGAP_P101 Homo sapiens cDNA clone IMAGE:1101072 3'
5912	18888	32188	0.63	2.0E-48	AA613171.1	EST_HUMAN	nc16907.1 NC1 CGAP_P101 Homo sapiens cDNA clone IMAGE:1101072 3'
5912	18888	32188	0.63	2.0E-48	AA613171.1	EST_HUMAN	nc16907.1 NC1 CGAP_P101 Homo sapiens cDNA clone IMAGE:1101072 3'
7762	20715	34086	3.9	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for GDA1551 protein, partial cds
7762	20715	34087	3.9	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for GDA1551 protein, partial cds
7777	20730	34103	3.52	2.0E-48	1166238	NT	Homo sapiens y-crystallin cDNA clone (nuclear factor of kappa light chain polypeptide gene enhancer in B-cells 3 (NFkB)) (RELA) mRNA
8595	21866	35089	1.37	2.0E-48	AJ704611.1	EST_HUMAN	AY745457.03 Homo sapiens cDNA clone CROCGG10 3'
12518	13126	26025	2.8	2.0E-48	AA485007.1	EST_HUMAN	256003.11 Sources over tumor NHOT Homo sapiens cDNA clone IMAGE:810032 3'
98	13177	26089	3.37	1.0E-48	7706524	NT	Homo sapiens disipalin resistance-associated overexpressed protein (LOC55747) mRNA
874	13930	28888	1.61	1.0E-48	492166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neuro-in, Alzheimer disease) (APP) mRNA
1077	14122	27073	1.8	1.0E-48	7657330	NT	Homo sapiens EBNA-2 co-activator (1000) (p100) mRNA
1077	14122	27074	1.8	1.0E-48	7657330	NT	Homo sapiens EBNA-2 co-activator (1000) (p100) mRNA
1289	14135	27298	5.06	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1353	14937	27854	14.5	1.0E-48	AL183302.2	NT	Homo sapiens chromosome 21 segment H321C102
3505	16847	28473	0.83	1.0E-48	AL183246.2	NT	Homo sapiens chromosome 21 segment H321C102
6420	19487	32736	1.17	1.0E-48	AJ895077.1	EST_HUMAN	BT7001 at NC1 CGAP_C016 Homo sapiens cDNA clone IMAGE:2079504 3' similar to TR014888 O14888 SIMILARITY TO U73841
6420	19487	32737	1.17	1.0E-48	AJ895077.1	EST_HUMAN	BT7001 at NC1 CGAP_C016 Homo sapiens cDNA clone IMAGE:2079504 3' similar to TR014888 O14888 SIMILARITY TO U73841
6548	19708		1.03	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
6748	18602	33092	0.7	1.0E-48	AJ802894.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6748	18602	33093	0.7	1.0E-48	AJ802894.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7471	20437	33784	3.15	1.0E-48	4756137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
9183	22149	33876	0.40	1.0E-48	4768093	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
9183	22149	33877	0.49	1.0E-48	4768095	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
0586	22530	35860	1.19	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9623	22567	39017	7.13	1.0E-48	AB03307.1	NT	Homo sapiens mRNA for KIAA1246 protein, partial cds
0624	22608	36920	0.80	1.0E-48	BC109410.1	EST_HUMAN	QV3-H10513-090400-147-301 H10513 Homo sapiens cDNA
0641	22668	36930	4.48	1.0E-48	BF324983.1	EST_HUMAN	00188095F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE4122118 8'
10736	23058	37151	3.85	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10736	23058	37152	3.85	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
12280	23630	37182	1.93	1.0E-48	11429808	NT	T536 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8171	10246	32478	3	8.0E-49	10048417	NT	Mac musculus T-box 20 (Tbx20), mRNA
8171	10246	32479	3	8.0E-49	10048417	NT	Mac musculus T-box 20 (Tbx20), mRNA
7017	20143	33460	0.87	8.0E-49	AA424035.1	EST_HUMAN	nt181037T NC_020407_G05T Homo sapiens cDNA clone IMAGE1184021 8'
8638	21009	35020	3.32	8.0E-49	U2950.1	NT	Homo sapiens gene for action receptor type 1B, complete cds
10348	23272	39748	2.1	8.0E-49	AB00881.1	NT	Homo sapiens gene for action receptor type 1B, complete cds
11204	24139	37068	2.32	8.0E-49	AI82722.1	EST_HUMAN	183847LX1 NC_020407_G05T Homo sapiens cDNA clone IMAGE220871 3' similar to contains AU repetitive element/contains element TTS reads
140	13408	25395	2.24	7.0E-49	5728900	NT	Homo sapiens profilin (profilin, parvophilin) 26S subunit, ATPase, 4 (PSM24) mRNA
140	13408	25396	2.24	7.0E-49	5728900	NT	Homo sapiens profilin (profilin, parvophilin) 26S subunit, ATPase, 4 (PSM24) mRNA
393	13408	25397	1.33	7.0E-49	5728900	NT	Homo sapiens profilin (profilin, parvophilin) 26S subunit, ATPase, 4 (PSM24) mRNA
393	13408	25398	1.33	7.0E-49	5728900	NT	Homo sapiens profilin (profilin, parvophilin) 26S subunit, ATPase, 4 (PSM24) mRNA
394	13408	25399	2.06	7.0E-49	5728900	NT	Homo sapiens profilin (profilin, parvophilin) 26S subunit, ATPase, 4 (PSM24) mRNA
394	13408	25399	2.06	7.0E-49	5728900	NT	Homo sapiens profilin (profilin, parvophilin) 26S subunit, ATPase, 4 (PSM24) mRNA
1223	14263	27220	2.85	7.0E-49	AI43284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5535	16632	31571	1.97	7.0E-49	AI807191.1	EST_HUMAN	Y2594X.1 Sawie_VF_T_GGC_S1 Homo sapiens cDNA clone IMAGE235969 3' similar to TR.O4023
5545	16642	31582	1.35	7.0E-49	AI120393.1	EST_HUMAN	044029 RSE015: DKF276760C03.1 762 (synonym: hml2) Homo sapiens cDNA clone DKF276760C03 3'
5903	16632	31571	0.84	7.0E-49	AI807191.1	EST_HUMAN	Y2594X.1 Sawie_VF_T_GGC_S1 Homo sapiens cDNA clone IMAGE235969 3' similar to TR.O4023
108	13209	20227	85.86	6.0E-49	AW731740.1	EST_HUMAN	hs4505X.1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE200504 3' similar to pbX17008 40S
4142	17173	30062	1.14	6.0E-49	AI182091.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN); p3A120632 Mouse L1Rep3 protein mRNA from a repetitive element, complete (MOLISE).
6932	19842	32068	0.95	6.0E-49	AI140745.1	EST_HUMAN	DKF276761A138.1 761 (synonym: hmy2) Homo sapiens cDNA clone DKF276761A138 3'
							AU140742 PLACE2 Homo sapiens cDNA clone PLACE200148 5'

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe	Exon	Expr	Most Similar	Top Hit	Top Hit
SEQ ID	SEQ ID	SEQ ID	(BLAST) Hit	Accession	Hit
NO.	NO.	NO.	Value	No.	Source
11609	24547	38107	2	6.0E-40	AI452218.1
11610	24548	38108	2	6.0E-40	AI452218.1
11611	24549	38109	8.0E-40	AA306569.1	EST_HUMAN
11612	24550	38110	4.0E-40	AA306569.1	EST_HUMAN
11613	24850	38447	4.0E-40	AA306569.1	EST_HUMAN
12845	26723	38145	7.0E-40	AF047167.1	EST_HUMAN
12846	26724	38146	8.21	6.0E-40	AI183210.2
13171	33716	26708	8.21	6.0E-40	AI183210.2
13172	33717	26709	8.21	6.0E-40	AI183210.2
13173	33718	26710	8.21	6.0E-40	AI183210.2
13174	33719	26711	8.21	6.0E-40	AI183210.2
13175	33720	26712	8.21	6.0E-40	AI183210.2
13176	33721	26713	8.21	6.0E-40	AI183210.2
13177	33722	26714	8.21	6.0E-40	AI183210.2
13178	33723	26715	8.21	6.0E-40	AI183210.2
13179	33724	26716	8.21	6.0E-40	AI183210.2
13180	33725	26717	8.21	6.0E-40	AI183210.2
13181	33726	26718	8.21	6.0E-40	AI183210.2
13182	33727	26719	8.21	6.0E-40	AI183210.2
13183	33728	26720	8.21	6.0E-40	AI183210.2
13184	33729	26721	8.21	6.0E-40	AI183210.2
13185	33730	26722	8.21	6.0E-40	AI183210.2
13186	33731	26723	8.21	6.0E-40	AI183210.2
13187	33732	26724	8.21	6.0E-40	AI183210.2
13188	33733	26725	8.21	6.0E-40	AI183210.2
13189	33734	26726	8.21	6.0E-40	AI183210.2
13190	33735	26727	8.21	6.0E-40	AI183210.2
13191	33736	26728	8.21	6.0E-40	AI183210.2
13192	33737	26729	8.21	6.0E-40	AI183210.2
13193	33738	26730	8.21	6.0E-40	AI183210.2
13194	33739	26731	8.21	6.0E-40	AI183210.2
13195	33740	26732	8.21	6.0E-40	AI183210.2
13196	33741	26733	8.21	6.0E-40	AI183210.2
13197	33742	26734	8.21	6.0E-40	AI183210.2
13198	33743	26735	8.21	6.0E-40	AI183210.2
13199	33744	26736	8.21	6.0E-40	AI183210.2
13200	33745	26737	8.21	6.0E-40	AI183210.2
13201	33746	26738	8.21	6.0E-40	AI183210.2
13202	33747	26739	8.21	6.0E-40	AI183210.2
13203	33748	26740	8.21	6.0E-40	AI183210.2
13204	33749	26741	8.21	6.0E-40	AI183210.2
13205	33750	26742	8.21	6.0E-40	AI183210.2
13206	33751	26743	8.21	6.0E-40	AI183210.2
13207	33752	26744	8.21	6.0E-40	AI183210.2
13208	33753	26745	8.21	6.0E-40	AI183210.2
13209	33754	26746	8.21	6.0E-40	AI183210.2
13210	33755	26747	8.21	6.0E-40	AI183210.2
13211	33756	26748	8.21	6.0E-40	AI183210.2
13212	33757	26749	8.21	6.0E-40	AI183210.2
13213	33758	26750	8.21	6.0E-40	AI183210.2
13214	33759	26751	8.21	6.0E-40	AI183210.2
13215	33760	26752	8.21	6.0E-40	AI183210.2
13216	33761	26753	8.21	6.0E-40	AI183210.2
13217	33762	26754	8.21	6.0E-40	AI183210.2
13218	33763	26755	8.21	6.0E-40	AI183210.2
13219	33764	26756	8.21	6.0E-	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3593	16028	26547	0.78	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
6000	15932	33249	1.14	2.0E-49	AV171935.1	EST_HUMAN	AV171938 DOB Homo sapiens cDNA clone DOBA.B01 5'
8436	21405		1.52	2.0E-49	AF040033.1	EST_HUMAN	EST102558 Fetal brain, Striatum (cnp35295) Homo sapiens cDNA clone HFBC160
12903	29521		2.57	2.0E-49	AF15384.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9000	13045		8.35	1.0E-49	BF033327.1	EST_HUMAN	001498331 F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE3362086 5'
1557	14589	27600	1.27	1.0E-49	4657867	NT	Homo sapiens keratin 18 (KRT18) mRNA
1818	14845	27837	3.33	1.0E-49	BE25216.1	EST_HUMAN	001117699 F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE3359273 5'
5433	18335	31444	5.72	1.0E-49	BF131007.1	EST_HUMAN	001820059 F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE4152052 5'
6196	19270	32605	0.87	1.0E-49	H16251.1	EST_HUMAN	YH4904.17 Sarcos adult brain N25RH557 Homo sapiens cDNA clone IMAGE:171703 5' similar to SP-68G1
6202	19278	32610	1	1.0E-49	AF094640.1	EST_HUMAN	EST137673 IMAGE:171703 Homo sapiens cDNA clone IMAGE:171703 5' similar to SP-68G1
7427	20394	33744	0.88	1.0E-49	AV170300.1	EST_HUMAN	AV170300 ADB Homo sapiens cDNA clone ADBCOV11 5'
7427	20394	33745	0.88	1.0E-49	AV170300.1	EST_HUMAN	AV170300 ADB Homo sapiens cDNA clone ADBCOV11 5'
7433	20400	33753	3.3	1.0E-49	BE398110.1	EST_HUMAN	001260339 F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3525863 5'
7433	20400	33754	3.3	1.0E-49	BE398110.1	EST_HUMAN	001260339 F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3525863 5'
7520	20485	33846	2.2	1.0E-49	N25884.1	EST_HUMAN	YH4904.17 Sarcos, placenta, Biowetlab_ZNP496407 Homo sapiens cDNA clone IMAGE:356408 3' similar to g058673 KINESIN Heavy CHAIN (HUMAN);
7520	20485	33847	2.2	1.0E-49	N25884.1	EST_HUMAN	YH4904.17 Sarcos, placenta, Biowetlab_ZNP496407 Homo sapiens cDNA clone IMAGE:356408 3' similar to g058673 KINESIN Heavy CHAIN (HUMAN);
8414	21363	34780	0.89	1.0E-49	11321490	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8414	21363	34781	0.89	1.0E-49	11321490	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8041	22069	35794	1.14	1.0E-49	8904184	EST_HUMAN	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
9344	22409	35794	1.14	1.0E-49	BE409493.1	EST_HUMAN	DKF264340Z23.1T.434 (onym: hsa3) Homo sapiens cDNA clone IMAGE:3635388 5'
10485	23407	36903	1.22	1.0E-49	AL043128.2	EST_HUMAN	DKF264340Z23.1T.434 (onym: hsa3) Homo sapiens cDNA clone DKF14540Z243 5'
11359	24344	37877	1.99	1.0E-49	AB020335.1	NT	Homo sapiens Ponceau-specific (SA305) mRNA, complete cds
11940	24577	38143	3.12	1.0E-49	11427369	NT	Homo sapiens Ponceau-specific (SA305) mRNA, complete cds
12107	25097		1.7	1.0E-49	BE16943.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:284406 3'
12602	25241		2.08	1.0E-49	11418322	NT	Homo sapiens cDNA clone IMAGE:284406 3'
6544	25697		1.75	1.0E-49	BE256758.1	EST_HUMAN	Homo sapiens calnexin EGF LAG seven-pass C-type receptor 1 (CEL5R1), mRNA
1701	13273	26188	3.5	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS210002
720	13742	26716	2.14	8.0E-50	X59507.2	NT	Homo sapiens mRNA for VIP receptor 2
720	13742	26717	2.14	8.0E-50	X59507.2	NT	Homo sapiens mRNA for VIP receptor 2
1778	14807	27763	4	8.0E-50	4501800	NT	Homo sapiens mRNA for VIP receptor 2
2710	15704	28720	2.18	8.0E-50	4829608	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2710	15704	28720	2.18	8.0E-50	4829608	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
621	13496	28604	0.88	7.0E-50	BE089591.1	EST_HUMAN	QV05-BT0703-286400-211-402 BT0703 Homo sapiens cDNA
652	20776	33500	1.21	7.0E-50	BF091622.1	EST_HUMAN	RC05-TN0075-105900-011-412 TN0073 Homo sapiens cDNA
682	20776	33501	1.21	7.0E-50	BF091622.1	EST_HUMAN	RC05-TN0075-105900-011-412 TN0073 Homo sapiens cDNA
7226	20490	33852	0.62	7.0E-50	AA027822.1	EST_HUMAN	nc90412.1 NCL CGAP_C09 Homo sapiens cDNA clone IMAGE:114203 3' similar to gb:365391.60S
11108	20498	37590	28.05	7.0E-50	AA027137.1	EST_HUMAN	REBOSOMAL PROTEIN L2 (HUMAN); wmb5111.1 X1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:3059511 3' similar to contains MER26.43
8559	21224		6.69	6.0E-50	BE044076.1	EST_HUMAN	h036104.1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:3059511 3' similar to contains MER26.43
11106	24124	37652	7.98	6.0E-50	AA0312079.1	EST_HUMAN	MER26.43 repetitive element.
11106	24124	37653	7.98	6.0E-50	AA0312079.1	EST_HUMAN	EST162773 Juntai Cells (V) Homo sapiens cDNA 5' end
1308	14530	27626	1.18	3.0E-50	BF332638.1	EST_HUMAN	EST162773 Juntai Cells (V) Homo sapiens cDNA 5' end
1308	14530	27627	1.18	3.0E-50	BF332638.1	EST_HUMAN	QV05-BT0703-306500-588-003 BT0703 Homo sapiens cDNA
9448	22412		5.65	5.0E-50	AA457063.1	EST_HUMAN	QV05-BT0703-306500-588-003 BT0703 Homo sapiens cDNA repetitive element: nc54609.1 NCL CGAP_S51 Homo sapiens cDNA clone IMAGE:104420 3' similar to gb:353741.1 not FIBLIN-1, ISCFORM A, PRECURSOR (HUMAN); Homo sapiens cystathionine synthetase (CATS) mRNA
6497	19361	33813	0.54	4.0E-50	AA001143.1	EST_HUMAN	QV1-BT0881-280300-127412 BT0881 Homo sapiens cDNA
7445	20411	33763	0.93	4.0E-50	BE097258.1	EST_HUMAN	Human endogenous reovirus RTV1-H2
2525	14528	26549	1.11	3.0E-50	BE259198.1	EST_HUMAN	601109717F1 NCL MGCC_18 Homo sapiens cDNA clone IMAGE:335009 5'
3510	16363	26253	0.88	3.0E-50	AA474812.1	EST_HUMAN	382098.1 NCL CGAP_K43 Homo sapiens cDNA clone IMAGE:332927 3'
6834	19487	33190	0.8	3.0E-50	11418317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
6834	19487	33191	0.6	3.0E-50	11418317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
6834	19487	33191	0.6	3.0E-50	11418317	NT	Homo sapiens similar to serum domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC83232), mRNA
6929	20153	33472	1.56	3.0E-50	11421514	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7005	20949	34224	4.3	3.0E-50	AF293438.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7905	20949	34225	4.3	3.0E-50	AF293438.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8029	21955	35213	0.61	3.0E-50	6901589	NT	Homo sapiens mRNA for transmembrane domains 1 (ANKT1), mRNA
10177	23102	35652	1.1	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1189 protein, partial cds
9186	23111	35655	0.96	3.0E-50	11418514	NT	Homo sapiens complex 10 (a murine top homolog) (TCF10), mRNA
10385	23905	37309	0.74	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0399 gene, partial cds
11438	24381	37920	1.99	3.0E-50	11439855	NT	Homo sapiens GNB-associated binder 2 (KIAA0571), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11702	23947	37469	8.4	3.0E-50	AJ245821.1	NT	Homo sapiens CTL2 gene
778	19357		6.8	2.0E-50	AF055065.1	NT	Homo sapiens MHC class I region
1081	14135	27079	6.73	2.0E-50	AF557782	NT	Homo sapiens midline 1 (Olig2/BBB syndrome) (MID1) mRNA
1437	14470	27448	0.95	2.0E-50	AF138033.1	NT	Homo sapiens diatom D mRNA, complete cds, alternatively spliced
3300	16353	28272	0.83	2.0E-50	AF111668.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
4289	17318	30167	0.75	2.0E-50	D66424.1	NT	Mus musculus keratin protein, subunit 10, complete cds
7051	20073	33360	0.71	2.0E-50	AJ24065.1	EST	HUMAN
8659	21627	33947	1.09	2.0E-50	AB039162.1	NT	Homo sapiens TFF gene cluster for trid factor, complete cds
8659	21627	33948	1.09	2.0E-50	AB039162.1	NT	Homo sapiens TFF gene cluster for trid factor, complete cds
8792	21792	35189	6.78	2.0E-50	X09556.1	NT	Homo sapiens TFF gene cluster for trid factor, complete cds
10244	21798	35190	6.78	2.0E-50	X09556.1	NT	Homo sapiens TFF gene cluster for trid factor, complete cds
10244	23189	36657	1.43	2.0E-50	X09556.1	NT	Homo sapiens TFF gene cluster for trid factor, complete cds
10244	23189	36658	1.43	2.0E-50	X09556.1	NT	Homo sapiens TFF gene cluster for trid factor, complete cds
11711	24849		1.52	2.0E-50	AF228671.1	NT	Homo sapiens TFF gene cluster for trid factor, complete cds
482	13535	26481	2.26	1.0E-50	AF165209.2	NT	Mus musculus keratin complex 2, gene 5g (K25g), mRNA
2373	15381		9.27	1.0E-50	AJ271735.1	NT	Mus musculus keratin complex 2, gene 5g (K25g), mRNA
7970	20969		0.85	1.0E-50	AJ271735.1	NT	Mus musculus keratin complex 2, gene 5g (K25g), mRNA
10533	23475	36970	0.87	1.0E-50	D11078.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
6095	19174	32360	1.01	9.0E-51	AF151225.1	EST	HUMAN
8390	19419	32950	0.71	9.0E-51	AF144857.1	EST	HUMAN
8020	21686	35407	0.95	9.0E-51	AJ701154.1	EST	HUMAN
8079	23532	36068	1.2	9.0E-51	AA343788.1	EST	HUMAN
8858	22734	36245	0.92	9.0E-51	AJ701154.1	EST	HUMAN
9858	22734	36246	0.92	9.0E-51	AJ701154.1	EST	HUMAN
11804	23559	37483	1.5	9.0E-51	AB07078.1	EST	HUMAN
11804	23559	37484	1.6	9.0E-51	AB07078.1	EST	HUMAN
4599	17620	30513	8.51	8.0E-51	AA810842.1	EST	HUMAN
7914	20637	34245	2.04	8.0E-51	AF143957	NT	Heterogeneous nuclear ribonucleoprotein A1 (HNRNPA1)
8919	22698		0.99	8.0E-51	AJ138550.1	EST	HUMAN

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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NC:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3395	16348	29208	1.66	7.0E-51	AW88218.1	EST_HUMAN	QY4-NT0026-200400-180-458 NT0026 Homo sapiens cDNA
3374	18424	29349	0.72	7.0E-51	AW274720.1	EST_HUMAN	QY34603.3 of NCI COAP_K011 Homo sapiens cDNA clone IMAGE:266554 3' similar to TR-052340
4196	17227	30116	1.4	7.0E-51	AL079628.1	EST_HUMAN	Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
4196	17227	30117	1.4	7.0E-51	AL079628.1	EST_HUMAN	DKF254B482229.71.434 (synonym: hns3) Homo sapiens cDNA clone DKF254B482228.9
4196	17227	30286	1.54	7.0E-51	AW295603.1	EST_HUMAN	DKF254B482229.71.434 (synonym: hns3) Homo sapiens cDNA clone DKF254B482228.9
11963	24870	38456	2.13	7.0E-51	AF181449.1	NT	UIH-BWD-46-1209-0-UI.1 NCI COAP_S048 Homo sapiens cDNA clone IMAGE:2728817 3'
1530	14583	27534	0.91	6.0E-51	6078703	NT	Homo sapiens HSP-C381 mRNA, partial cds
							Homo sapiens putative DNA binding protein (M69), mRNA
1696	16017	28024	5.54	6.0E-51	7687286	NT	Homo sapiens KIA00629 protein Mac2 interacting nuclear target (MNT) homolog (KIA00629), mRNA
3487	16533	29498	17.23	6.0E-51	7687286	NT	Homo sapiens KIA00629 protein Mac2 interacting nuclear target (MNT) homolog (KIA00629), mRNA
4338	17565	30247	0.69	6.0E-51	8970553	NT	Homo sapiens acute cancer family 2 (accelerated glucose transporter), member 3 (SLC22A9), mRNA
4338	17565	30248	0.69	6.0E-51	8970553	NT	Homo sapiens acute cancer family 2 (accelerated glucose transporter), member 3 (SLC22A9), mRNA
6105	19184	32403	2.28	6.0E-51	X01788.1	NT	Human Nucleoside diphosphate kinase 3
6116	19184	32417	8.29	6.0E-51	AF070083.1	NT	Homo sapiens Nucleoside diphosphate kinase 3
6625	20746	32418	8.29	6.0E-51	AF070083.1	NT	Homo sapiens Nucleoside diphosphate kinase 3
6625	20746	32418	1.13	6.0E-51	408378	NT	Homo sapiens Nucleoside diphosphate kinase 3
7076	20788	32408	1.03	6.0E-51	1110789	NT	Homo sapiens Nucleoside diphosphate kinase 3
7157	19388	32253	0.23	6.0E-51	1110789	NT	Homo sapiens Nucleoside diphosphate kinase 3
9422	22458	35893	0.23	6.0E-51	1110789	NT	Homo sapiens Nucleoside diphosphate kinase 3
9422	22458	35893	0.23	6.0E-51	1110789	NT	Homo sapiens Nucleoside diphosphate kinase 3
10742	22460	38456	2.04	6.0E-51	1110789	NT	Homo sapiens Nucleoside diphosphate kinase 3
10742	22460	38456	2.04	6.0E-51	1110789	NT	Homo sapiens Nucleoside diphosphate kinase 3
11185	24323	39078	1.56	6.0E-51	U60083.1	NT	Homo sapiens Nucleoside diphosphate kinase 3
792	13851	28798	8.67	6.0E-51	AL103203.2	NT	Homo sapiens Nucleoside diphosphate kinase 3
804	13862	28812	1.9	6.0E-51	4907500	NT	Homo sapiens Nucleoside diphosphate kinase 3
968	15866	28988	1.23	6.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1612	14844	27620	1.02	6.0E-51	5031890	NT	Homo sapiens 35S proteasome-associated pod1 homolog (POH1) mRNA
2569	16000	29819	7.72	6.0E-51	AJ075581.1	NT	Homo sapiens mRNA for nucleoside diphosphate kinase 3
3945	17005	29819	1.86	6.0E-51	MA00938.1	NT	Human Ku (p70p80) subunit mRNA, complete cds
3965	17005	29820	1.86	6.0E-51	MA00938.1	NT	Human Ku (p70p80) subunit mRNA, complete cds
11910	24448	38708	4.07	6.0E-51	5603138	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1351	13240	26171	1.93	3.0E-51	AI873448.1	EST_HUMAN	181083.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:224720 3' similar to gbM1423_0546 KERATIN, TYPE I CYTOSKELETAL, 18 (HUMAN)
1180	14221	27177	3.31	3.0E-51	AI873448.1	EST_HUMAN	181083.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:224720 3' similar to gbM1423_0546 KERATIN, TYPE I CYTOSKELETAL, 18 (HUMAN)
1940	14654	27851	1.09	3.0E-51	AA211296.1	EST_HUMAN	339760.x1 Striatum INT neuron (1807233) Homo sapiens cDNA clone IMAGE:944800 5' similar Novel human gene mapping to chromosome 22
4354	17381	30263	2.23	3.0E-51	AL159142.1	NT	
7831	20779	34157	1.2	3.0E-51	R15914.1	EST_HUMAN	y44708.r1 Scania infant brain -NB Homo sapiens cDNA clone IMAGE:53235 5' similar to gbM14123_0546 RETROVIRUS-RELATED POLYOMAVIRUS (HUMAN) contains LTR repetitive element.
9191	22157		4.32	3.0E-51	M29035.1	NT	Human TRAP C2 protein mRNA
9423	26008		0.48	3.0E-51	AW95777.1	EST_HUMAN	304063.77 Human Pancreatic Islets Homo sapiens cDNA 5'
12810	25495		1.36	3.0E-51	AF003528.1	NT	Homo sapiens X-linked endothelial dysplasia protein gene (EDA), exon 2 and flanking repeat regions
368	13402	28380	1.19	2.0E-51	4507798	NT	Homo sapiens 1 (beta) tubulin, ligase E3A (human) papilloma virus E3-associated protein, Angedman protein (UBES3A) mRNA
689	13752	28078	0.88	2.0E-51	BE301083.1	EST_HUMAN	30728502.x1 NIH_JGCG_44 Homo sapiens cDNA clone IMAGE:3607463 5'
868	13762	28079	0.88	2.0E-51	BE301083.1	EST_HUMAN	30728502.x1 NIH_JGCG_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1697	14272	27710	4.99	2.0E-51	AA233352.1	EST_HUMAN	326005.r1 Synaptonemal complex RT-PCR precursor 33720 Homo sapiens cDNA clone IMAGE:944800 5' similar to TR-0338226 2283226 RTV-LH PROTEIN, somatostatin LTR 18 LTR repetitive element;
3745	16737	26690	2.48	2.0E-51	AA62415.1	EST_HUMAN	127653.x1 NCI_CGAP_K6411 Homo sapiens cDNA clone IMAGE:2131732 3'
4521	17546	30433	0.86	2.0E-51	AW137626.1	EST_HUMAN	U4H-B11-af1-42-92-01.1 NCI_CGAP_S343 Homo sapiens cDNA clone IMAGE:2710851 3'
5513	18613	31545	0.57	2.0E-51	AI732851.1	EST_HUMAN	364409.x1 NCI_CGAP_K45 Homo sapiens cDNA clone IMAGE:132609 3' similar to SW-ANM1_MOUSE P8439 GLUTAMATE NMDA RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
5513	18613	31546	0.57	2.0E-51	AI732851.1	EST_HUMAN	364409.x1 NCI_CGAP_K45 Homo sapiens cDNA clone IMAGE:132609 3' similar to SW-ANM1_MOUSE P8439 GLUTAMATE NMDA RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
9131	16208	32433	4.17	2.0E-51	BE762015.1	EST_HUMAN	364409.x1 NCI_CGAP_K45 Homo sapiens cDNA clone IMAGE:132609 3' similar to SW-ANM1_MOUSE P8439 GLUTAMATE NMDA RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
7531	20494		0.88	2.0E-51	AF119227.1	NT	Homo sapiens diacylglycerol kinase beta (DGK) gene, exon 23
7690	20549	34012	0.91	2.0E-51	7662349	NT	Homo sapiens cell recognition molecule Csepr2 (KIAA0668), mRNA
9046	22012	34934	1.54	2.0E-51	BE901944.1	EST_HUMAN	8016767971 NIH_JGCG_21 Homo sapiens cDNA clone IMAGE:3956013 5'
9046	22012	34934	1.54	2.0E-51	BE901944.1	EST_HUMAN	8016767971 NIH_JGCG_21 Homo sapiens cDNA clone IMAGE:3956013 5'
8389	22354	33785	0.97	2.0E-51	11037094	NT	Homo sapiens discoidin domain containing 1 (DISC1), mRNA
9870	22623	36276	1.35	2.0E-51	AI917076.1	EST_HUMAN	3174607.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:223680 3' similar to SW-TRKC_HUMAN Q1028 NT-S GROWTH FACTOR RECEPTOR PRECURSOR;
8692	22859	35350	6.78	2.0E-51	BE165960.1	EST_HUMAN	MR3-170487-16020-113-9071 HTP047 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9677	22804	34368	0.53	2.0E-51	AB007626.1	NT	Homo sapiens mRNA for KIAA0457 protein, partial cds
10766	23720	37223	1.54	2.0E-51	AF662474.1	EST_HUMAN	AV193574 GDB Homo sapiens cDNA clone GKBG05 5'
10838	23759	37258	1.14	2.0E-51	AA378559.1	EST_HUMAN	EST191288 Synovial sarcoma Homo sapiens cDNA 5' end
11655	18613	31545	7.03	2.0E-51	AF173285.1	EST_HUMAN	db3406.33 NC1 CGAP_K56 Homo sapiens cDNA clone IMAGE:1325909 3' similar to SWNM1_MOUSE
11655	18613	31546	7.03	2.0E-51	AF173285.1	EST_HUMAN	P34-95 GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
12122	24981	38552	2.3	2.0E-51	AA911688.1	EST_HUMAN	db3406.33 NC1 CGAP_K56 Homo sapiens cDNA clone IMAGE:1325909 3' similar to SWNM1_MOUSE
12122	24981	38552	2.3	2.0E-51	AA911688.1	EST_HUMAN	P34-95 GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
12803	25430	37140	2	2.0E-51	11418159	NT	20367.11 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:426872 5'
114	13225	25146	8.48	1.0E-51	403328	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(10p13)) homology; translocated to, 4 (MLL1), mRNA
1491	14624	33332	3.71	1.0E-51	AF722483.1	EST_HUMAN	Homo sapiens leukocyte translation initiation factor 4b, isoform 1 (EIF4A1) mRNA
4371	17463	33332	0.86	1.0E-51	4736071	NT	AV17422483 OS Homo sapiens cDNA clone G816072 5'
5457	19355	34133	3.84	1.0E-51	4736071	NT	Homo sapiens small inducible cytokine subfamily 1A (Cys-Cys), member 15 (SCYA15) mRNA
5457	19355	34133	3.84	1.0E-51	4736071	NT	Homo sapiens small inducible cytokine subfamily 1A (Cys-Cys), member 15 (SCYA15) mRNA
7911	20364	34242	0.58	1.0E-51	AF197552.1	EST_HUMAN	BT2046 Fetal 1 Homo sapiens cDNA clone 132035
8235	21924	34609	0.79	1.0E-51	BF434339.1	EST_HUMAN	435902.x1 Soares_NH40P1_S1 Homo sapiens cDNA clone IMAGE:048106 3'
12073	26124		1.67	1.0E-51	AF769590.1	EST_HUMAN	759402.x1 NC1 CGAP_Ov18 Homo sapiens cDNA clone IMAGE:364491 3' similar to TRP7882 Pt882
12899	25203						PROTEASE ;
103	13296	26184	9.3	8.0E-52	AA720574.1	EST_HUMAN	db3407.11 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to
1456	14328	27500	1.77	8.0E-52	X84900.1	NT	contains THR18 THR repetitive element ;
							THR repetitive element ;
							H.sapiens mRNA for laminin-3, alpha3 chain
1622	14594	27659	2.98	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myo downstream regulated 3 (FLJ13556), mRNA
1622	14594	27670	2.98	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myo downstream regulated 3 (FLJ13556), mRNA
4019	14884	27659	6.44	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myo downstream regulated 3 (FLJ13556), mRNA
4019	14884	27670	6.44	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myo downstream regulated 3 (FLJ13556), mRNA
7760	20713	34062	0.89	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 88KD (TGFB1), mRNA
7760	20713	34063	0.89	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 88KD (TGFB1), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Database Value	Top Hit Accession No.	Top Hit Source	Top Hit Description
7128	20105	33416	0.73	2.0E-52	AF02146.1	EST_HUMAN	0245012.6 NC1 CGAP_352 Homo sapiens cDNA clone IMAGE:160811 8'
8121	21056	34465	0.62	2.0E-52	6032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8121	21056	34466	0.62	2.0E-52	6032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
9000	21060		11.69	2.0E-52	AF147860.1	NT	Muscula multilata beta-tubulin mRNA, complete cds
9268	22254	39684	0.87	2.0E-52	AA778765.1	EST_HUMAN	2745905.41 Scores: fetal_liver_glioma_NFLS_S1 Homo sapiens cDNA clone IMAGE:435272 3'
9834	22893		1.06	2.0E-52	4758769	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (160D) (NADH-coenzyme Q reductase) (NDUFS8) mRNA
10474	23390	36803	6.19	2.0E-52	5730038	NT	Homo sapiens SET domain and mermer transposase fusion gene (SETMAR) mRNA
10474	23390	36804	6.19	2.0E-52	5730038	NT	Homo sapiens SET domain and mermer transposase fusion gene (SETMAR) mRNA
11538	24479	38020	3.09	2.0E-52	AB51462.1	EST_HUMAN	w44804.x1 NC1 CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR b2 THR repetitive element;
11538	24479	38020	3.09	2.0E-52	AB51462.1	EST_HUMAN	w44804.x1 NC1 CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR b2 THR repetitive element;
11531	24492	38046	2.73	2.0E-52	AY175371.1	EST_HUMAN	2349512.1 Scores: fetal_liver_NFLS_H18W Homo sapiens cDNA clone IMAGE:444038 5'
11560	24946		12.33	2.0E-52	W70260.1	EST_HUMAN	Homo sapiens LIM domain protein 2 (LIM2) mRNA
11536	24910		2.73	2.0E-52	11417890	NT	3072407.x1 NC1 CGAP_Ou1 Homo sapiens cDNA clone IMAGE:2700038 3' similar to contains ALU repetitive element; contains element LTR2 repetitive element;
12201	25982	31300	18.6	2.0E-52	AW236397.1	EST_HUMAN	w87265.x1 Scores: NFL_T1 GRG_S1 Homo sapiens cDNA clone IMAGE:2306049 3' similar to TR-C16659 Q10850 CARBOXYLESTERASE;
12833	25319		7.6	2.0E-52	AB080985.1	EST_HUMAN	z175612.1 Scores: testis_NHT Homo sapiens cDNA clone IMAGE:74379 3'
834	13963	26824	1.48	1.0E-52	AA554445.1	EST_HUMAN	Homo sapiens glutamate ammonia lyase (glutamine synthase) (GLUL) mRNA
1373	14407	27377	9.6	1.0E-52	4594026	NT	Homo sapiens erythrokinase D (ARSD), transcript variant 1, mRNA
2543	15544		2.17	1.0E-52	4592238	NT	pot-reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element] RT(L)Pp1, Genomic, 680 nt
3072	16129	29041	1.98	1.0E-52	S61070.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
5405	18509	31366	4.22	1.0E-52	U02626.1	NT	Human PMS2 related (HPMSR2) gene, complete cds
5405	18509	32850	2.4	1.0E-52	33694.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
7864	20623	33697	2.35	1.0E-52	X07282.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8150	21087	34486	0.55	1.0E-52	U00117.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p-44) gene, partial cds, neuronal apoptosis inhibitory protein (aip) and survival motor neuron protein (smn) genes, complete cds
8800	21776		1.13	1.0E-52	AL16327.2	NT	Homo sapiens chromosome 21, segment HS21C027
9543	22504	35645	0.7	1.0E-52	AF078778.1	NT	Rattus norvegicus putative four repeat for channel mRNA, complete cds
10941	23867		1.21	1.0E-52	AF02070.1	EST_HUMAN	df6505.y1 Morton Fetal Cochrane Homo sapiens cDNA clone IMAGE:2483146 5'
10951	23871		1.14	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21, segment HS21C0302

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BASE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2795	15730	28744	1.17	2.05-53	4757615	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2796	15730	28745	1.17	2.05-53	4757615	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3232	16387	29209	1.46	2.05-53	7705687	NT	Homo sapiens luciferase aminopeptidase (LOC57056), mRNA
3265	16313	29234	0.6	2.05-53	AF063822.1	NT	Homo sapiens tyrosine receptor alpha 2 subunit (CA2N207) gene, exon 8
4098	17123	30016	2.76	2.05-53	M1873.1	NT	Human (Huespa)-related DNA-binding protein (TF34) gene, partial cds
4520	17458	30432	1.23	2.05-53	4595962	NT	Homo sapiens SQUF95 homologue (SQUF-HOM) mRNA
5193	18202	31074	0.96	2.05-53	AL18281.2	NT	Homo sapiens chromosome 21 segment HS21O381
5193	18202	31075	0.96	2.05-53	AL18281.2	NT	Homo sapiens chromosome 21 segment HS21O381
5500	18600	31512	3.33	2.05-53	BF334740.1	EST_HUMAN	PW1-1210358-178600-201-g03 C10386 Homo sapiens cDNA
5500	18600	31513	3.33	2.05-53	BF334740.1	EST_HUMAN	PW1-1210358-178600-201-g03 C10386 Homo sapiens cDNA
8203	21731	34583	1.13	2.05-53	AW975584.1	EST_HUMAN	EST1387177 IMAGE repository, 12/08/98 Homo sapiens cDNA
8203	21731	34583	0.81	2.05-53	AW975584.1	EST_HUMAN	EST1387177 IMAGE repository, 12/08/98 Homo sapiens cDNA
9753	22704		13.48	2.05-53	AI725676.1	EST_HUMAN	3823265 Splice site 1, NM_174747.4, Lambda ZAP cDNA Homo sapiens cDNA 5'
1440	14713	27450	2	1.05-53	A271758.1	NT	Human (Huespa)-related DNA-binding protein, segment 22
3421	16460	29386	1.26	1.05-53	AB029898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
5707	19015	30920	1.32	1.05-53	BE520386.1	EST_HUMAN	60116725F1 NH, MGC_17 Homo sapiens cDNA clone IMAGE3361919 5'
6560	19203	31156	1.41	1.05-53	BE542291.1	EST_HUMAN	CM4-NN1036-250500-545-402 HN1036 Homo sapiens cDNA
7459	20335	31781	0.84	1.05-53	BE101207.1	EST_HUMAN	RC6-BN1036-270400-037-D01 BN1036 Homo sapiens cDNA
8297	21365	34627	0.55	1.05-53	A246072.1	EST_HUMAN	19571 seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9444	22098	35445	13.12	1.05-53	X79538.1	NT	H sapiens mRNA for hnRNPCalpha protein A1
12103	24076	38574	3.08	1.05-53	X68411.1	NT	H sapiens mRNA for myosin-IIe
12103	24076	38575	3.08	1.05-53	X68411.1	NT	H sapiens mRNA for myosin-IIe
5373	25559	31353	5.13	6.05-54	4809786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
208	13509	28236	1.73	6.05-54	BE386785.1	EST_HUMAN	60127893F1 NH, MGC_20 Homo sapiens cDNA clone IMAGE3574031 5'
1852	14978	27874	2.4	6.05-54	4894610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6545	19127	32333	23.25	6.05-54	6005700	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
11952	24841	39434	1.67	6.05-54	AI919259.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8) mRNA
11952	24841	39435	1.67	6.05-54	AI919259.1	EST_HUMAN	Hf44605.k1 Source, NE_1, ABC1, S1 Homo sapiens cDNA clone IMAGE2534752 3'
11952	24841	39435	1.67	6.05-54	AI919259.1	EST_HUMAN	Hf44605.k1 Source, NE_1, ABC1, S1 Homo sapiens cDNA clone IMAGE2534752 3'
384	13497	28429	1.85	7.05-54	AA812537.1	EST_HUMAN	al78c12.k1 Source, Icthis, NHT Homo sapiens cDNA clone 1377049 3' similar to contains MER30.15 MER30 repetitive element;
1847	14673	27858	1.51	7.05-54	V18645.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Subs E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2215	16220	26262	4.54	7.0E-54	N27177.1	EST_HUMAN	yw8812.1 Srcras, <i>Biobricks_2</i> , NIGH1P69W Homo sapiens cDNA clone IMAGE:287399 3' similar to contains LTR1, L2, LTR1 repetitive element;
10487	23409	38606	1.81	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (N1, sapiens) (LOC83182), mRNA contains ORF1.1 ORF repetitive element;
11623	24061		3.26	7.0E-54	A1180186.1	EST_HUMAN	Homo sapiens DNA for MCB, exon 4, 5 and partial cds
25	13145	25045	2.05	6.0E-54	AB003616.1	NT	Homo sapiens hypodermal protein DKF2p434M033 (DKF2p434M033), mRNA
385	13488	25430	0.67	6.0E-54	8922148	NT	Homo sapiens hypodermal protein DKF2p434M033 (DKF2p434M033), mRNA
385	13488	25431	0.67	6.0E-54	8922148	NT	Homo sapiens hypodermal protein DKF2p434M033 (DKF2p434M033), mRNA
3298	16349	25269	0.99	6.0E-54	8922148	NT	Homo sapiens hypodermal protein DKF2p434M033 (DKF2p434M033), mRNA
3348	16982	25517	0.96	6.0E-54	AL163247.2	NT	Homo sapiens chromosome 21 segment RS1047
4030	17088	25669	1.48	6.0E-54	4802872	NT	Homo sapiens chlamydia channel 6 (CLCN6) mRNA
4489	17514	35402	0.78	6.0E-54	AV754746.1	EST_HUMAN	AT724746 TP Homo sapiens cDNA clone TP03AC0.6
4819	17836	30734	0.94	6.0E-54	AV72685.1	EST_HUMAN	AT72685 HTB Homo sapiens cDNA clone HTBACE2.6
4890	17897	30796	1.98	6.0E-54	4390606	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA), mRNA
4900	17928		1.23	6.0E-54	109846.1	NT	H-sapiens pte preadipocyte, pte term
5353	17928		1.21	6.0E-54	109846.1	NT	H-sapiens pte preadipocyte, pte term
11711	23928	31446	1.8	6.0E-54	11433623	NT	Homo sapiens KIAA0071 protein (KIAA0071), mRNA
11711	23928	31447	1.8	6.0E-54	11433623	NT	Homo sapiens KIAA0071 protein (KIAA0071), mRNA
2180	17176	28197	3.75	3.0E-54	PH4529	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
194	13294		310.9	4.0E-54	AF110103.1	NT	Tuella balgongi beta-actin mRNA, partial cds
987	14010	26963	29.86	4.0E-54	AA309764.1	EST_HUMAN	EST177698, L-actin 1-cells V1 Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1822	14849	27842	2.91	4.0E-54	D38531.1	EST_HUMAN	Human mRNA for KIAA0071 gene, partial cds
1822	14849	27843	2.91	4.0E-54	D38531.1	NT	Human mRNA for KIAA0071 gene, partial cds
3217	18272		1.03	4.0E-54	AI830968.1	EST_HUMAN	w82841.1 Srcras, N1, GBC, S1 Homo sapiens cDNA clone IMAGE:236269 3' similar to TRO22711
7524	20498		0.86	4.0E-54	BE344888.1	EST_HUMAN	002711 PRO-POUT-UPASE POLYPROTEIN;
- 63	13209	28133	13.66	3.0E-54	AA313487.1	EST_HUMAN	60107803AF1 NIH JGCG, 12 Homo sapiens cDNA clone IMAGE:3461017 5'
2632	19531		1.1	3.0E-54	AI003757.1	EST_HUMAN	EST1183371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8007	19200	32260	1.32	3.0E-54	4502454	NT	Human sapiens BLNK non-receptor tyrosine kinase (BLNK) mRNA
7619	20579	33942	1.49	3.0E-54	AA944051.1	EST_HUMAN	052028.1 Srcras, parathyroid, tumor, NHPHA Homo sapiens cDNA clone IMAGE:198270 3'
7619	20579	33943	1.49	3.0E-54	AA944051.1	EST_HUMAN	052028.1 Srcras, parathyroid, tumor, NHPHA Homo sapiens cDNA clone IMAGE:198270 3'
6091	21018	34418	0.51	3.0E-54	AI742522.1	EST_HUMAN	w54401.1 Srcras, NSF, 9W, OT, PA, P, S1 Homo sapiens cDNA clone IMAGE:2367633 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11583	24312		4.82	3.0E-54	11434806	NT	Homo sapiens gldg1 subunit, protein subfamily a, s (GOLGA8), mRNA
11423	24367	37602	3.55	3.0E-54	BF34500.1	EST_HUMAN	60201640P1 NCI CGAP Bmi1 Homo sapiens cDNA clone IMAGE:418121 5'
11866	24661	38239	2.11	3.0E-54	AA383302.1	EST_HUMAN	AT0712.7 Source: testis, NT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G161315
12334	25734	31850	4.08	3.0E-54	AW094589.1	EST_HUMAN	G161315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
12380	25942		1.67	3.0E-54	AW176865.1	EST_HUMAN	EST336628 IMAGE resources, MAGC Homo sapiens cDNA
643	13769	26629	6.22	2.0E-54	5031900	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1387	14401	27371	1.48	2.0E-54	4897184	NT	Homo sapiens nuclear antigen SP100 (SP100) mRNA
1650	14883	27654	1.32	2.0E-54	AA055008.1	EST_HUMAN	ntF668.1 NCI CGAP P33 Homo sapiens cDNA clone IMAGE:126460 similar to contains element L1 repetitive element.
2546	15547	28570	1.04	2.0E-54	AW163175.1	EST_HUMAN	at2403.7 J. Shikama, Fed. Inst. 00924 Homo sapiens cDNA clone IMAGE:2783794 5' similar to
2593	15607	28631	1.45	2.0E-54	AL16270.2	NT	SP100 L1, J. Shikama, Fed. Inst. 00924 Homo sapiens cDNA clone IMAGE:2783794 5' similar to
2605	15664	28607	1.4	2.0E-54	AW037524.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2352827 3' similar to
3550	16905		5.43	2.0E-54	AA433205.1	EST_HUMAN	TRQ02034 060804 PHOSPHOLIPASE C-NEIGHBORING ;
4270	17681		1.18	2.0E-54	AF208161.1	NT	ntF509.1 NCI CGAP P36 Homo sapiens cDNA clone IMAGE:986488 similar to gp-X53777 60S
4914	17931	30622	0.96	2.0E-54	7709446	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
5278	18364	31147	1.07	2.0E-54	4606982	NT	Homo sapiens enoyl-CoA hydratase, L-complex subunit 5 (CCT5) mRNA
5551	18548	31681	1.8	2.0E-54	4790069	NT	Homo sapiens enoyl-CoA hydratase, L-complex subunit 5 (CCT5) mRNA
5584	18479	31632	1.25	2.0E-54	BE047864.1	EST_HUMAN	Homo sapiens SKAP55 homologous (SKAP-HOM) mRNA
5586	18468	32131	3.9	2.0E-54	11426657	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5661	19046	32245	10.03	2.0E-54	AB040811.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
5691	19046	32245	10.03	2.0E-54	AB040811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
5914	19868	33157	0.77	2.0E-54	AF008015.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
6983	20200	33535	0.73	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
6983	20200	33535	0.73	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
7330	20301	33645	7.68	2.0E-54	11426544	NT	Homo sapiens neurofilament 1 (neurofilament, von Recklinghausen disease, Watson disease) (NF1), mRNA
6987	22914	36379	4.03	2.0E-54	AB001026.1	NT	Homo sapiens mRNA for brain y-aminobutyrate receptor, complete cds
10366	23292	36768	1.61	2.0E-54	11429127	NT	Homo sapiens Janus Kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10480	23402	36860	0.86	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe NO.	Seq ID	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10450	24202	30900		0.88	2.0E-54	11476732	NT	Human sapiens serologically defined colon cancer antigen 10 (SDCAG10), mRNA
12034	24910			4.31	2.0E-54	7697454	NT	Human sapiens serologically defined colon cancer antigen 1, containing BRC1 domain (PES1), mRNA
4462	17517			1.6	1.0E-54	9F31416.1	EST_HUMAN	001869220F.NIH_MGC_19 Homo sapiens cDNA clone IMAGE:1728353.5'
9081	22047	33470		0.51	1.0E-54	11417222	NT	Human sapiens similar to nuclear factor related B binding protein (H_sapiens) (LOC38182), mRNA
10815	29337	37035		0.51	1.0E-54	AA412409.1	EST_HUMAN	zu1060971 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:791464.5'
10015	29337	37039		0.51	1.0E-54	AA412403.1	EST_HUMAN	zu1060971 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:791464.5'
12998	26554			4.2	1.0E-54	AL077841.1	EST_HUMAN	GU47341 Sugano cDNA library/Homo sapiens cDNA clone Zr4C980 similar to 5' end region of Human gamma-glutamyl transpeptidase mRNA, 5' end
12047	28948	37139		0.95	9.0E-55	BE381469.1	EST_HUMAN	QV2-970635-162409-143-112 B70835 Homo sapiens cDNA
1318	14393			0.96	8.0E-55	VT0789.2	EST_HUMAN	Human sapiens RFB30 gene for RING finger protein
1321	14396			2.83	8.0E-55	VT0789.2	NT	Human sapiens RFB30 gene for RING finger protein
11528	24456			1.73	8.0E-55	AV440974.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
12390	25167			1.3	8.0E-55	BE327189.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
1083	14127	27091		1.52	7.0E-55	R09246.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
9186	22122			1.54	7.0E-55	AV10389.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
9356	22449	35947		1.25	7.0E-55	AV10389.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
1970	24456	36025		2.19	7.0E-55	AV10389.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
1972	24456	36025		2.19	7.0E-55	AV10389.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
11544	24456	36028		1.8	7.0E-55	H49714.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
12355	24456			1.8	7.0E-55	H49714.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
12998	26570			1.78	7.0E-55	H23346.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
11843	24768	39813		1.95	6.0E-55	AA404082.1	NT	Human sapiens similar to N11B Homo sapiens cDNA clone IMAGE:26444.5'
1795	14814	27768		1.3	5.0E-55	AA704971.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
1795	14814	27768		1.3	5.0E-55	AA704971.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
6850	19747	33023		1.65	5.0E-55	4602240	NT	Human sapiens arylsulfatase E (cholesterol sulfatase protease 1) (ARSE), mRNA
6850	19747	33024		1.65	5.0E-55	4602240	NT	Human sapiens arylsulfatase E (cholesterol sulfatase protease 1) (ARSE), mRNA
9690	19747	33562		1.65	5.0E-55	7382477	NT	Human sapiens Rho GTPase activating protein 6 (RHARGAP6), transcript variant 6, mRNA
7513	29178	33830		0.68	5.0E-55	11434422	NT	Human sapiens smooth-muscle POU protein (SPOF), mRNA
9339	32264	34711		2.57	5.0E-55	11526491	NT	Human sapiens BCL-2 associated thymopressin (BAG1), mRNA
9339	32264	35766		2.57	5.0E-55	4605302	NT	Human sapiens BCL-2 associated thymopressin (BAG1), mRNA
9339	32264	35766		2.57	5.0E-55	4605302	NT	Human sapiens BCL-2 associated thymopressin (BAG1), mRNA
11843	24768	39813		1.95	6.0E-55	AA404082.1	NT	Human sapiens similar to N11B Homo sapiens cDNA clone IMAGE:26444.5'
1795	14814	27768		1.3	5.0E-55	AA704971.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
1795	14814	27768		1.3	5.0E-55	AA704971.1	EST_HUMAN	h02420.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2662007.5'
6850	19747	33023		1.65	5.0E-55	4602240	NT	Human sapiens arylsulfatase E (cholesterol sulfatase protease 1) (ARSE), mRNA
6850	19747	33024		1.65	5.0E-55	4602240	NT	Human sapiens arylsulfatase E (cholesterol sulfatase protease 1) (ARSE), mRNA
9690	19747	33562		1.65	5.0E-55	7382477	NT	Human sapiens Rho GTPase activating protein 6 (

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Probe SEQ ID NO:	Exon SEQ ID NO:	OPF SEQ ID NO:	Expression Signal	Max Similarity (BLAST E Value)	Top HA Accession No.	Top Hit Database Source	Top Hit Descriptor
9874	23627		1.9	0.0E-55	BE049388.1	EST_HUMAN	RC4-BT0310-110300-016-10 BT0310 Homo sapiens cDNA
10397	23519	39601	1.31	0.0E-55	AB014811.1	NT	Homo sapiens mRNA for KIA0811 protein, partial cds
10397	23519	39602	1.31	0.0E-55	AB014811.1	NT	Homo sapiens mRNA for KIA0811 protein, partial cds
10562	23504	39667	1.2	0.0E-55	5453766	NT	Homo sapiens na (globin)-like 2 (NELL2), mRNA
12419	25189		3.4	0.0E-55	11417972	NT	Homo sapiens pascadrol (pascadrol) homolog 1, containing BRCT domain (PES1), mRNA
57	15631	20088	1.49	0.0E-55	AW97994.1	EST_HUMAN	EST370004 IMAGE-responses, IMAGE Homo sapiens cDNA
673	13737	26604	3.41	0.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, 1, chromosome, family 1, member A1 (RBMY1A1) mRNA
1517	14549		1.97	0.0E-55	BF06141.1	EST_HUMAN	7025-10.1.1 Scans, NSF_P3_BH_OT_PJA_P_31 Homo sapiens cDNA clone 3360A03.3 similar to contains 1.10.1.1 repetitive element.
2040	15559	28078	1.04	0.0E-55	4506180	NT	Homo sapiens Proteasome (prosome, multicatalytic) subunit, alpha type, 2 (PSMA2), mRNA
2040	15559	28079	1.04	0.0E-55	4506180	NT	Homo sapiens Proteasome (prosome, multicatalytic) subunit, alpha type, 2 (PSMA2), mRNA
2097	15114	28134	8.73	0.0E-55	4633174	NT	Homo sapiens Proteasome (prosome, multicatalytic) subunit, alpha type, 2 (PSMA2), mRNA
2097	15114	28135	8.73	0.0E-55	4633174	NT	Homo sapiens Proteasome (prosome, multicatalytic) subunit, alpha type, 2 (PSMA2), mRNA
2319	15260	28554	2.11	0.0E-55	4637794	NT	Homo sapiens Ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
2319	15260	28555	2.11	0.0E-55	AL183218.2	NT	Homo sapiens chromosome 21, segment HS210510
11569	21003		2.89	0.0E-55	V028169.1	EST_HUMAN	43-51 Human retina cDNA, randomly primed, auxiliary Homo sapiens cDNA
13235	21015		3.64	0.0E-55	VS03945.1	EST_HUMAN	601865762 NH MG. 17 Homo sapiens cDNA clone IMAGE-4120333.5
8751	19905	33066	0.78	3.0E-55	AA007158.1	EST_HUMAN	7B90A09 Chromosome 7 fetal Brain cDNA Library Homo sapiens cDNA clone 7B90A09
42211	25093		1.91	3.0E-55	BE178519.1	EST_HUMAN	PMH-HT0802-080300-001-008 HT0803 Homo sapiens cDNA
13007	25560		1.9	3.0E-55	AL183284.2	NT	Homo sapiens chromosome 21, segment HS210684
537	13481	28351	2.24	2.0E-55	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
553	13023		1.56	2.0E-55	M10976.1	NT	Human endogenous retrovirus DNA (4-1), complete retroviral segment
650	13716	28638	3.28	2.0E-55	4507296	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
2970	18028	28951	1.02	2.0E-55		EST_HUMAN	CM1-HT0810-108030-357-g03 HT0810 Homo sapiens cDNA
4808	17025	30721	2.19	2.0E-55	BE719688.1	EST_HUMAN	UIHF-BT08-ws4-000-CJ111 NH MG. 50 Homo sapiens cDNA clone IMAGE-3078278.5'
7747	25569	34007	0.69	2.0E-55	AW001988.1	EST_HUMAN	UIHF-BT08-ws4-000-CJ111 NH MG. 50 Homo sapiens cDNA clone IMAGE-3134463.3'
9420	22385	33523	0.51	2.0E-55	BF224432.1	EST_HUMAN	ht7808.x1 NC1 CGAP_Kjrl1 Homo sapiens cDNA clone IMAGE-3134463.3'
9420	22385	33524	0.51	2.0E-55	BF224432.1	EST_HUMAN	ht7808.x1 NC1 CGAP_Kjrl1 Homo sapiens cDNA clone IMAGE-3134463.3'
9615	22478		8.16	2.0E-55	A002838.1	EST_HUMAN	am805L1 Stragene scilabo brain S11 Homo sapiens cDNA clone IMAGE-1984185.3 similar to contains THR L2 THR repetitive element.
9989	22536		0.78	2.0E-55	BE007969.1	EST_HUMAN	QVC-BN0147-280-000-213-g08 BN0147 Homo sapiens cDNA
10007	23520	37024	0.43	2.0E-55	AI435401.1	EST_HUMAN	103008.x1 NC1 CGAP_Ges4 Homo sapiens cDNA clone IMAGE-2140479.3'
11286	24240	31773	1.84	2.0E-55	AL119344.1	EST_HUMAN	AUT189244 HEMBA1 Homo sapiens cDNA clone HEMBA1005683.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	OSE SEQ ID NO:	Expression Signal	Most Similar Uniprot Entry Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12113	24683	36634	1.51	2.0E-45	BC09056.1	EST_HUMAN	00150771-0F1-NH_MGC_71 Homo sapiens cDNA clone IMAGE3906076 5'
961	13212	26193	2.4	1.0E-45	4630900	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
191	13262	26216	93.01	1.0E-45	U09823.1	NT	Oryzologus carinatus New Zealand white elongation factor 1 alpha (Rae1efc2) mRNA, complete cds
576	13945	26550	0.76	1.0E-45	A030718.1	EST_HUMAN	0085905.XT Soare, testis, N1T Homo sapiens cDNA clone IMAGE104100 3'
1152	14194	27146	4.22	1.0E-45	A0302710.1	NT	Homo sapiens mRNA for KIA04005 protein, partial cds
1997	14998	27660	1.65	1.0E-45	BE277661.1	EST_HUMAN	00112011-0F1-NH_MGC_30 Homo sapiens cDNA clone IMAGE2667027 5'
1997	14998	27661	1.65	1.0E-45	BE277661.1	EST_HUMAN	00112011-0F1-NH_MGC_30 Homo sapiens cDNA clone IMAGE2667027 5'
2333	15344	27997	3.95	1.0E-45	6803174	NT	Homo sapiens SMAD3 (SMAD3), mRNA
2345	15924	28370	1.31	1.0E-45	AF000960.1	NT	Homo sapiens testis-specific protein Transcriber Y1 (TTY1) mRNA, partial cds
2024	15927	28540	52.04	1.0E-45	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2581	15902	29580	4.82	1.0E-45	A0007894.2	NT	Homo sapiens mRNA for KIA04100 protein, partial cds
2581	15902	29581	4.82	1.0E-45	A0007894.2	NT	Homo sapiens mRNA for KIA04100 protein, partial cds
2019	15917	29541	4.76	1.0E-45	L04057.1	NT	Homo sapiens CUP mRNA, partial cds
2601	15793	29811	0.90	1.0E-45	A0333045.1	NT	Homo sapiens mRNA for KIA01276 protein, partial cds
3420	16488	29855	0.90	1.0E-45	W21061.1	EST_HUMAN	3437 Human retina cDNA library partial cDNA sequence
4015	17034	29955	4.23	1.0E-45	AL133507.2	NT	Homo sapiens chromosome 21, segment H537C097
4323	17352	30236	1.08	1.0E-45	AL133507.2	NT	Homo sapiens chromosome 21, segment H537C097
4792	17782	30769	1.21	1.0E-45	AF172910.1	EST_HUMAN	3442-03.1T Source fetal liver, spleen, 1HE S Homo sapiens cDNA clone IMAGE245620 5'
4693	17862	30769	1.21	1.0E-45	AF172910.1	EST_HUMAN	Homo sapiens DISCR15 mRNA, complete cds
5177	19106	31070	1.70	1.0E-45	A0307183.1	NT	Homo sapiens DISCR15 mRNA, complete cds
5177	19106	31070	1.70	1.0E-45	A0307183.1	NT	Homo sapiens DISCR15 mRNA, complete cds
5575	19971	31854	0.96	1.0E-45	6022126	NT	Homo sapiens hypodermal protein FL20730 (FL20730), mRNA
6403	19470	32716	7	1.0E-45	AF118955.1	NT	Homo sapiens heat domain and RLD 2 (HERC2), mRNA
6403	19470	32716	7	1.0E-45	AF118955.1	NT	Homo sapiens heat domain and RLD 2 (HERC2), mRNA
7323	20016	32716	0.99	1.0E-45	AF118955.1	NT	Homo sapiens heat domain and RLD 2 (HERC2), mRNA
8321	21230	34704	1.35	1.0E-45	AF194201.1	NT	Homo sapiens F-box protein FBL4 (FBL-4) mRNA, complete cds
8321	21230	34705	1.35	1.0E-45	AF194201.1	NT	Homo sapiens F-box protein FBL4 (FBL-4) mRNA, complete cds
8410	21378	34765	0.46	1.0E-45	11433694	NT	Homo sapiens disc, large (Oncofocal) homolog 2 (chrys-10) (DLG2), mRNA
8410	21378	34766	0.46	1.0E-45	11433694	NT	Homo sapiens disc, large (Oncofocal) homolog 2 (chrys-10) (DLG2), mRNA
8416	21397	34766	1.27	1.0E-45	AF224492.1	NT	Homo sapiens SKAP-65 homolog (SKAP-HOM), mRNA
8416	21397	34767	1.27	1.0E-45	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
11776	23931	37462	1.05	1.0E-45	U09069.1	NT	Human infant brain unknown product mRNA, complete cds
11776	23930	37471	1.95	1.0E-45	T10046.1	EST_HUMAN	seq1575 bAHB3361A Code-HAP-Fi Homo sapiens cDNA clone bAHB3361A-Fi similar to similar to Chinese Hamster OHEP-compliment protein mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Source	Top Hit Descriptor
11602	24763	33871	1.74	1.0E-56	U95782.1	EST	Homo sapiens DNA-binding protein (LOC59424), mRNA
7560	20351	33812	1.80	9.0E-56	BC379074.1	EST	901237707F NIH MGCC 44 Homo sapiens cDNA clone IMAGE:306952 5'
2743	15737	26783	6.5	7.0E-50	H19634.1	EST	Y10293.1 Source adult brain N2656B057 Homo sapiens cDNA clone IMAGE:173044 5' similar to contains YHR repetitive element
7902	20046	34228	2.13	7.0E-56	AW361213.1	EST	HUMAN
7902	20046	34220	2.13	7.0E-50	AW361213.1	EST	HUMAN
1701	14131	27713	1.96	9.0E-50	AW69712.1	EST	HUMAN
9516	22476	35923	0.61	9.0E-50	AW075507.1	EST	HUMAN
10754	22476	35923	1.7	9.0E-50	W28180.1	EST	HUMAN
12607	25930	31309	5.41	9.0E-50	H56096.1	EST	HUMAN
30	13150	25049	12.5	4.0E-50	AF147346.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
30	13150	25049	12.5	4.0E-50	AF147346.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2719	15713	26730	4.9	4.0E-56	4507726.1	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2719	15713	26731	4.9	4.0E-56	4507726.1	NT	Homo sapiens X-linked aniridia 2 ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
2823	13186	26516	3.60	4.0E-56	AF003528.1	NT	Homo sapiens
2843	15620	28644	1.16	4.0E-56	A632448.1	EST	HUMAN
2843	15620	28645	1.16	4.0E-50	A632448.1	EST	HUMAN
6397	19455	32750	5.65	4.0E-50	A721759.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6397	19455	32751	5.65	4.0E-50	A721759.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10872	23762	37263	3.94	4.0E-50	AF49346.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
11568	24201	37743	7.82	4.0E-56	A488006.1	EST	HUMAN
11568	24201	37744	7.82	4.0E-56	A488006.1	EST	HUMAN
1346	14380	27349	1.74	3.0E-50	8624026.1	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1719	14808	27744	0.96	3.0E-50	6912749.1	NT	Homo sapiens 5'-3' exon-intron 2 (XRN2), mRNA
3142	16196	29108	1.83	3.0E-50	AA329803.1	EST	HUMAN
3142	16196	29110	1.83	3.0E-50	AA329803.1	EST	HUMAN
3947	16878	29603	1.73	3.0E-50	AF05069.1	NT	Homo sapiens 5'-3' exon-intron 2 (XRN2), mRNA
3947	16878	29603	1.73	3.0E-50	AF05069.1	NT	Homo sapiens 5'-3' exon-intron 2 (XRN2), mRNA
4454	17490	30369	4.84	3.0E-50	BE330512.1	EST	HUMAN
4803	17924	30517	2.34	3.0E-50	AL103268.2	NT	Homo sapiens superfamily viral-like activity 2 (S. cerevisiae homolog-like (SKV2L)), mRNA
4841	17598		1.81	3.0E-56	BE863572.1	EST	HUMAN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Annotation	Top HT Database Source	Top HT Descriptor
5797	185659	320293	1.84	3.0E-26	4759163	NT	Homo sapiens sparcisomectin, ovov and kazai-like domain a proteoglycan (testis) (SPOCK) mRNA
5797	185659	320293	1.84	3.0E-26	4759163	NT	Homo sapiens sparcisomectin, ovov and kazai-like domain a proteoglycan (testis) (SPOCK) mRNA
7059	20960	33389	5.05	3.0E-26	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
9189	22134	35500	5	3.0E-26	11419704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10172	22134	35507	1.12	3.0E-26	03547672	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10848	23789	37295	1.83	3.0E-26	11249698	NT	Homo sapiens KIAA0373 gene product (KIAA0373), mRNA
11943	24360	39147	4.57	3.0E-26	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11943	24360	39148	4.57	3.0E-26	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11943	24360	39145	4.57	3.0E-26	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11983	24590	38455	7.15	3.0E-26	U46900.1	NT	Homo sapiens NACP/duple-synuclein gene, exon 5
11983	24590	38468	7.15	3.0E-26	U46900.1	NT	Homo sapiens NACP/duple-synuclein gene, exon 5
12278	26150	37812	2.98	3.0E-26	11434576	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12378	26150	37813	2.98	3.0E-26	11434576	NT	Homo sapiens caveolin 3 (CAV3), mRNA
925	13359		1.92	3.0E-26	AA198918.1	EST: HUMAN	2226968 at Stragelene neoplasmatum (H83723) Homo sapiens cDNA clone IMAGE345508.3
734	13549	28732	2.02	2.0E-26	BE049361.1	EST: HUMAN	RC491031C1-10390-015-10 B10310 Homo sapiens cDNA
734	13549	28733	2.02	2.0E-26	BE049361.1	EST: HUMAN	RC491031C1-10390-015-10 B10310 Homo sapiens cDNA
2382	15400	28425	1.22	2.0E-26	U23951.1	NT	Human cDNA phosphodiesterase alpha subunit (GPRNA), complete cds
2382	15400	28426	1.22	2.0E-26	U23951.1	NT	Human cDNA phosphodiesterase alpha subunit (GPRNA), complete cds
3501	16309	28978	1.32	2.0E-26	U303153.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3271	16375	28615	1.71	2.0E-26	AD303881.1	EST: HUMAN	Homo sapiens gene for actin receptor type IIB, complete cds
3271	16375	28616	1.71	2.0E-26	AD303881.1	EST: HUMAN	707015P1 ADB10000-015-10 Homo sapiens cDNA gene ADB07470.3
7297	20960	33594	1.19	3.0E-26	AY1731747003	EST: HUMAN	Homo sapiens gene for actin receptor type IIB, complete cds
981	14032		1.58	3.0E-26	AA195098.1	EST: HUMAN	Homo sapiens gene for actin receptor type IIB, complete cds
3558	18731	29642	2.05	1.0E-26	AW184987.1	EST: HUMAN	Homo sapiens gene for actin receptor type IIB, complete cds
3558	18731	29643	2.05	1.0E-26	AW184987.1	EST: HUMAN	Homo sapiens gene for actin receptor type IIB, complete cds
3888	18731	29643	2.05	1.0E-26	AW184987.1	EST: HUMAN	Homo sapiens gene for actin receptor type IIB, complete cds
9071	18981	30952	1.22	1.0E-26	U095192.1	EST: HUMAN	726211.11 NC_024562 C33 Homo sapiens cDNA, clone IMAGE:29464592.3
9071	18981	30953	1.22	1.0E-26	U095192.1	EST: HUMAN	726211.11 NC_024562 C33 Homo sapiens cDNA, clone IMAGE:29464592.3
6995	20121	33435	0.95	1.0E-26	AW184987.1	EST: HUMAN	726211.11 NC_024562 C33 Homo sapiens cDNA, clone IMAGE:29464592.3
10315	22368		0.81	1.0E-26	AA183303.1	EST: HUMAN	WR3.510703.1-80100-238-103 S10203 Homo sapiens cDNA
10468	23330	38615	1.82	1.0E-26	AW184987.1	EST: HUMAN	Homo sapiens chromosome 21 segment H8270063
626	13891	38926	2.17	9.0E-27	AW180685.1	EST: HUMAN	RC2410185-20399-001-E02 C10183 Homo sapiens cDNA
12584	24464	38926	1.51	9.0E-27	AF22947.1	NT	Q16-070033-07030-182-103 OT09033 Homo sapiens cDNA
11554	24464	38926	1.51	9.0E-27	AF22947.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11554	24464	38926	1.51	9.0E-27	AF22947.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11950	24733	39320	2.28	9.0E-27	AB023881.1	NT	Homo sapiens mRNA for cdtB B2, complete cds

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
14	13134	28532	3.14	8.0E-57	8823349	NT	Homo sapiens hypothetical protein FL20371 (FL20371), mRNA
297	13391	28519	3.11	8.0E-57	AW816405.1	EST_HUMAN	QV4-510234-118199-037-040 510234 Homo sapiens cDNA
985	13940	28688	8.74	8.0E-57	AV294596.1	EST_HUMAN	AF5610.1 NC1 CGAT_Bm53 Homo sapiens cDNA clone IMAGE279251 3' similar to gb-U05875
1533	14860	27698	2.19	8.0E-57	AA489190.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
4945	17592	30852	1.11	8.0E-57	4351930	NT	275152.121 5 bases, 36151 1NT Homo sapiens cDNA clone IMAGE757161 5'
5073	18383	30695	1.32	8.0E-57	BE286916.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIN4) mRNA
5312	23948	31435	1.68	8.0E-57	11418168	NT	508444401-1NH1J0C-17 Homo sapiens cDNA clone IMAGE285084 5'
5852	19591	32693	0.84	8.0E-57	AB020703.1	NT	Homo sapiens scintilla 2, microtubule (ACO2), mRNA
9808	19560	32641	12.85	8.0E-57	AB020717.1	NT	Homo sapiens mRNA for KIL1858 protein, partial cds
9808	19560	32641	12.85	8.0E-57	AB020717.1	NT	Homo sapiens mRNA for KIL1858 protein, partial cds
7823	20540	34352	1.29	8.0E-57	AB020717.1	NT	Homo sapiens mRNA for KIL1858 protein, partial cds
8024	20541	34357	2.69	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIL1857 protein, partial cds
8024	20541	34358	2.69	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIL1857 protein, partial cds
10348	23768	37297	0.44	8.0E-57	1148710	NT	Homo sapiens protein box gene 5 (B-cell lineage specific activator protein) (FAS3), mRNA
11807	13134	28532	0.44	8.0E-57	8823349	NT	Homo sapiens hypothetical protein FL20371 (FL20371), mRNA
13088	24960	38457	1.67	8.0E-57	11431260	NT	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
12733	25368	31751	3.29	8.0E-57	11457323	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12748	25368	31751	1.38	8.0E-57	11457323	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
3263	16317	28227	1.09	7.0E-57	7242158	NT	Homo sapiens NMIF (NMIF), mRNA
3263	16317	28228	1.09	7.0E-57	7242158	NT	Homo sapiens NMIF (NMIF), mRNA
3284	16338	28268	0.05	7.0E-57	6005679	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3891	16331	28640	2.63	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik4230) mRNA, complete cds
3891	16331	28641	2.63	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik4230) mRNA, complete cds
4816	17533	30731	1.03	7.0E-57	U11058.2	NT	Homo sapiens large conductance calcium- and voltage-dependent potassium channel alpha subunit (MaxK) mRNA, complete cds
13075	23884		3.96	6.0E-57	AJ271735.1	NT	Homo sapiens Xla pseudotubercular region, segment 1/2
3766	16808	28718	2.12	4.0E-57	AB023888.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L4 genes, complete cds)
805	13863	28813	0.53	3.0E-57	4607708	NT	Homo sapiens Uguinin protein, ligase E3A (human papilloma virus E6-associated protein, Angiogenin syndrome) (UBSEA) mRNA
1334	14388		88.46	3.0E-57	AA20279.1	EST_HUMAN	nc1307.1 NC1 CGAT_p1 Homo sapiens cDNA clone IMAGE108037 similar to SWR310_HUMAN
2400	15407	28451	0.95	3.0E-57	AA348335.1	EST_HUMAN	PA6783.405 RIBOSOMAL PROTEIN S10... EST154770 Hippocampus II Homo sapiens cDNA 5' end

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Table 4
Antibodies Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2714	15708	28724	1.19	3.0E-57	BEE67622.1	EST_HUMAN	753510.41 NCL_COAP_GLI1 Homo sapiens cDNA IMAGE:328643.3 similar to WP:V47H6C.2
2714	15708	28726	1.19	3.0E-57	BEE67622.1	EST_HUMAN	CE202683 : 753510.41 NCL_COAP_GLI1 Homo sapiens cDNA IMAGE:328643.3 similar to WP:V47H6C.2
3711	16754		28.47	3.0E-57	AU185994.1	EST_HUMAN	RCS_C070354-1103003-027-410 CT02534 Homo sapiens cDNA CE202683 :
6145	19319	32540	1.37	3.0E-57	BT123608.1	EST_HUMAN	Homo sapiens angiotensin converting enzyme (peptidyl-diesterase A) 2 (ACE2), mRNA
8426	18292	32549	1.49	3.0E-57	BT67453.1	EST_HUMAN	BD158986Bf.H11_IGKC_7 Homo sapiens cDNA clone IMAGE:394343.02 5'
8484	21452	34870	2.81	3.0E-57	W21830.1	EST_HUMAN	4285 Homo sapiens cDNA randomly primed testicular Homo sapiens cDNA
8501	21478	34897	1.8	3.0E-57	111456708	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
8514	21478	34892	1.1	3.0E-57	111456708	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
8520	21562	35011	0.83	3.0E-57	11427757	NT	Homo sapiens KIAA0646 gene product (KIAA0646), mRNA
8772	21739	35160	0.86	3.0E-57	J05262.1	EST_HUMAN	Human fetal ratyri phosphatase synthetase mRNA, complete cds
8772	21739	35160	0.86	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMAT Homo sapiens cDNA clone HEIM40101910 5'
9605	22609	39001	0.7	3.0E-57	111456708	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
9605	22609	39001	0.7	3.0E-57	111456708	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
12384	22607	37729	2.86	3.0E-57	AW248374.1	EST_HUMAN	28240173 Soares fad11_MGC_7 Homo sapiens cDNA clone IMAGE:3820473.5
15000	14333	31514	7.83	3.0E-57	W23871.1	EST_HUMAN	254561711 Sporne fad11_MGC_7 Homo sapiens cDNA clone IMAGE:306546.5
15000	14333	27604	1.05	2.0E-57	AF242918.1	NT	Homo sapiens SNARE protein kinase SNRK, complete cds
15000	14333	27604	1.05	2.0E-57	AF242918.1	NT	Homo sapiens SNARE protein kinase SNRK, complete cds
3432	19458		2.19	2.0E-57	AL183204.2	EST_HUMAN	yee890711 Soares fad11 trypsin TNLS Homo sapiens cDNA clone IMAGE:73500.5
3432	19458	25829	0.85	2.0E-57	R0702.1	EST_HUMAN	yee890711 Soares fad11 trypsin TNLS Homo sapiens cDNA clone IMAGE:73500.5
3502	18008	28330	0.85	2.0E-57	R0702.1	EST_HUMAN	yee890711 Soares fad11 trypsin TNLS Homo sapiens cDNA clone IMAGE:73500.5
3502	18008	28330	0.85	2.0E-57	BT73584.1	EST_HUMAN	NABD1710351-040000-103-501 BT10591 Homo sapiens cDNA
4538	17531	30446	0.69	2.0E-57	AL183203.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS210083
4538	18146	31267	1.74	2.0E-57	AL183204.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS210083
5751	18846		1.87	2.0E-57	AAG016311	EST_HUMAN	285160611 Soares refseq NZS-HR Homo sapiens cDNA clone IMAGE:360394.5 similar to contigins 1.12 L1
6193	19226		32.23	2.0E-57	BF115956.1	EST_HUMAN	TNPO3431 NCI COAP_Ov18 Homo sapiens cDNA clone IMAGE:357068.3 similar to contigins TARI.1T
6930	19315	32561	0.7	2.0E-57	111437281	EST_HUMAN	MER22 testis cDNA
8078	21044	35968	1.62	2.0E-57	AF045452.1	NT	Homo sapiens small inducible cytokine subfamily A (Opn-9), member 22 (CY422), mRNA
8679	20130	36617	1.03	2.0E-57	AF057223.1	NT	Homo sapiens cell line EG1 Transcriptional regulatory protein p18A, mRNA, complete cds
10001	24539	38097	1.88	2.0E-57	111424934	NT	Homo sapiens 1-beta hydroxysteroid dehydrogenase IV (HSD17B5) gene, exon 3 and 4
11601	24539	38097	1.88	2.0E-57	111424934	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11601	24539	38098	1.88	2.0E-57	111424934	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11842	24579	38145	1.74	2.0E-57	AI245903.1	NT	Homo sapiens partial mRNA for PEX3 related protein
11842	24579	38146	1.74	2.0E-57	AI245903.1	NT	Homo sapiens partial mRNA for PEX3 related protein
11842	24579	38146	1.74	2.0E-57	AI245903.1	NT	UHF-BN-ang-10-Q-UT1 NIH_JGCG 30 Homo sapiens cDNA clone IMAGE:3076846 5'
2240	15254	28278	1.46	1.0E-57	AW503208.1	EST_HUMAN	hcd32d3.x1 NC1 CGAP L242 Homo sapiens cDNA clone IMAGE:3030602 3' similar to TR00246 000246
9041	22007		4.47	1.0E-57	BE943031.1	EST_HUMAN	HYPOPHOSPHATASE 3 KIAA01612 HOMO SAPIENS cDNA clone IMAGE:3076409 3' similar to contains THR33
12537	25291		3.95	1.0E-57	AW470794.1	EST_HUMAN	THR negative element
5760	18883	32033	1.01	9.0E-58	AA287847.1	EST_HUMAN	EST11346888 Homo sapiens cDNA clone IMAGE:3651000 5'
12795	25424	37738	2.37	9.0E-58	BE369861.1	EST_HUMAN	80134670471 NIH_JGCG 30 Homo sapiens cDNA clone IMAGE:3860100 5'
591	13088		2.43	8.0E-58	BE588715.1	EST_HUMAN	80134670471 NIH_JGCG 30 Homo sapiens cDNA clone IMAGE:3860100 5'
655	13721	28644	2.84	8.0E-58	AI768376.1	EST_HUMAN	80134670471 NIH_JGCG 30 Homo sapiens cDNA clone IMAGE:3860100 5'
855	13721	28645	2.84	8.0E-58	AI768376.1	EST_HUMAN	UNNAMED HERV-H PROTEIN
1874	14859	27807	1.88	8.0E-58	11434921	NT	UNNAMED HERV-H PROTEIN
1874	14859	27808	1.88	8.0E-58	11434921	NT	Homo sapiens putative protein Osmuonocyl/enfense (POMT2), mRNA
2507	10045		2.65	8.0E-58	7706132	NT	Homo sapiens DHHG1 protein (LOC513394), mRNA
7449	20475	33769	0.65	7.0E-58	BE351971.1	EST_HUMAN	80134670471 NIH_JGCG 30 Homo sapiens cDNA clone IMAGE:3867577 5'
12303	24197		4.98	7.0E-58	5174642	NT	Homo sapiens MAD3 box transcription enhancer factor 2, polypeptide 5 (myocyte enhancer factor 2B) (MEF2B) mRNA
11278	24227	37753	2.79	7.0E-58	AW504109.1	EST_HUMAN	UHF-BN-ang-10-Q-UT1 NIH_JGCG 30 Homo sapiens cDNA clone IMAGE:3076867 5'
11278	24227	37754	2.79	7.0E-58	AW504109.1	EST_HUMAN	UHF-BN-ang-10-Q-UT1 NIH_JGCG 30 Homo sapiens cDNA clone IMAGE:3076867 5'
2385	15363	28419	4.05	6.0E-58	AI130689.1	EST_HUMAN	AL130689 12BP3 Homo sapiens cDNA clone NT2P53007285 5'
2012	15970	28803	1.62	6.0E-58	BE242150.1	EST_HUMAN	TOAAPT1219 Pediatric acute myelogenous leukemia cell (FAB M1) Bayle-HGSC projectFOAA Homo sapiens cDNA clone TOAAPT1219
2012	15970	28804	1.62	6.0E-58	BE242150.1	EST_HUMAN	TOAAPT1219 Pediatric acute myelogenous leukemia cell (FAB M1) Bayle-HGSC projectFOAA Homo sapiens cDNA clone TOAAPT1219
6294	19260	32005	1.16	6.0E-58	AF108911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10072	23364	37091	1.02	6.0E-58	11434748	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (p114N21), mRNA
12529	25316		1.41	6.0E-58	11506291	NT	Homo sapiens hypothetical protein FL20654 (FL20654), mRNA
300	13394	26321	4.35	5.0E-58	4607334	NT	Homo sapiens synapobegm 1 (STNU1), mRNA
1171	13773	28707	7.83	5.0E-58	BE76984.1	EST_HUMAN	RC4H1057-106000-016-003 NT1057 Homo sapiens cDNA
1199	14339	27195	3.77	5.0E-58	AW707948.1	EST_HUMAN	CNG-UM0045-24000-127-407 UM0045 Homo sapiens cDNA
1199	14339	27196	3.77	5.0E-58	AW707948.1	EST_HUMAN	CNG-UM0045-24000-127-407 UM0045 Homo sapiens cDNA

Table 4

Single Exon Probe Expressed in Bone Marrow

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Max Similar ELAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1300	14239	27193	3.1	5.0E-58	AW767948.1	EST_HUMAN	CH8-UM0043-20300-127-407 UM0043 Homo sapiens cDNA
1301	14239	27193	3.1	5.0E-58	AW767948.1	EST_HUMAN	CH8-UM0043-20300-127-407 UM0043 Homo sapiens cDNA
3334	13593	26036	3.95	5.0E-58	AA098183.1	EST_HUMAN	cb8967.at NC1_GGAP_Luf Homo sapiens cDNA clone IMAGE:1603968 3'
4287	17316	30105	0.65	5.0E-56	AB39746.1	EST_HUMAN	U89944 PROLIN II
5710	18804	30105	0.65	5.0E-56	AB39746.1	EST_HUMAN	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6302	18873	32612	5.21	5.0E-58	U149282	NT	h19187.71 Sources infant brain IN1B Homo sapiens cDNA clone IMAGE:52071 5'
6302	18873	32612	5.21	5.0E-58	U149282	NT	Homo sapiens chromosome 21 segment HS210088
6534	19873	32650	0.64	5.0E-58	AL182832.2	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
6616	19873	32651	1.16	5.0E-58	AL182832.2	NT	Homo sapiens nuclear (NUS) mRNA, complete cds
6645	20169	33492	0.7	5.0E-58	AF551334.1	NT	Homo sapiens nuclear (NUS) mRNA, complete cds
6948	20169	33492	0.7	5.0E-58	AF551334.1	NT	Homo sapiens nuclear (NUS) mRNA, complete cds
7313	20284	33625	0.8	5.0E-58	AB95408	NT	Homo sapiens fibrocytoma 2 synthesis (fibrocytoma 2) (FIB2), mRNA
8302	21271	34683	7.52	5.0E-58	8022063	NT	Homo sapiens fibrocytoma 2 synthesis (fibrocytoma 2) (FIB2), mRNA
8598	21684	35088	0.78	5.0E-58	AB349833.1	NT	Homo sapiens fibrocytoma 2 synthesis (fibrocytoma 2) (FIB2), mRNA
8598	21684	35088	0.78	5.0E-58	AB349833.1	NT	Homo sapiens fibrocytoma 2 synthesis (fibrocytoma 2) (FIB2), mRNA
8965	22648	36103	1.34	5.0E-58	5231227	NT	Homo sapiens mRNA for NKA101 protein, partial cds
9265	22648	36104	1.34	5.0E-58	5231227	NT	Homo sapiens mRNA for NKA101 protein, partial cds
10218	23411	36029	1.01	5.0E-58	11430647	NT	Homo sapiens fibrocytoma 2 synthesis (fibrocytoma 2) (FIB2), mRNA
10482	23411	36001	1.89	5.0E-58	AL183216.2	NT	Homo sapiens fibrocytoma 2 synthesis (fibrocytoma 2) (FIB2), mRNA
10789	23637	37183	0.51	5.0E-58	AB914611.1	NT	Homo sapiens fibrocytoma 2 synthesis (fibrocytoma 2) (FIB2), mRNA
10789	23637	37184	0.51	5.0E-58	AB914611.1	NT	Homo sapiens fibrocytoma 2 synthesis (fibrocytoma 2) (FIB2), mRNA
12352	25897	37164	2.17	5.0E-58	11520263	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
12701	25904	37164	2.17	5.0E-58	11520263	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
13016	25904	37164	2.17	5.0E-58	11520263	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
373	13439	26368	1.85	4.0E-58	4502202	NT	Homo sapiens cat eye syndrome chromosome region, candidate 3 (CEG3), mRNA
797	13588	26603	1.42	4.0E-58	4504834	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
1484	14497	27471	1.14	4.0E-58	4505840	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
2539	15538	28501	2.02	4.0E-58	U39251.1	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
3335	16307	28505	1.11	4.0E-58	D16470.1	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
3735	17139	28705	1.02	4.0E-58	5931860	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
4130	17037	34454	0.89	4.0E-58	BE438957.1	EST_HUMAN	h19180.ct NC1_GGAP_G08 Homo sapiens cDNA clone IMAGE:3107642 3'
1193	17037	34454	0.89	4.0E-58	BE438957.1	EST_HUMAN	Homo sapiens E1B-58kDa-associated protein 5 (E1B-58), mRNA
335	15424	38164	0.84	3.0E-58	U17978.1	EST_HUMAN	h19180.ct NC1_GGAP_G08 Homo sapiens cDNA clone IMAGE:3107642 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Max Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1300	14424	27393	2.32	3.0E-59	4736891	NT	Homo sapiens peptide YY (PYY) mRNA
3182	16248	29165	2.57	3.0E-59	BF569948.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
3183	16248	29166	2.57	3.0E-59	BF569948.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
6300	19458	32703	0.61	3.0E-59	BE048506.1	EST_HUMAN	CYC-810702-17040-104-09 BT0102 Homo sapiens cDNA
6897	18647	32916	0.79	3.0E-59	F07056.1	EST_HUMAN	HSC-T10891 normalized infant brain cDNA Homo sapiens cDNA clone c-11018
6797	19847	33136	3.62	3.0E-59	AV71297.1	EST_HUMAN	AV71297 DCA Homo sapiens cDNA clone DCA2604 5'
639	13962	25944	8.85	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
1294	14329						ribosomal protein L8 (HUMAN); gb:381887 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5409	18512	31390	8.41	2.0E-58	BE298532.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
5431	26938	31413	3.28	2.0E-58	BE507186.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
5431	26938	31441	3.28	2.0E-58	BE507186.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
6176	19290	32493	1.09	2.0E-58	BF514488.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
6244	19317	32547	1.85	2.0E-58	AF124974.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
6278	19330	32548	0.83	2.0E-58	BF52467.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
712	20332	33348	0.83	2.0E-58	AF124974.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
7884	20334	33993	2.69	2.0E-58	AF124974.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
7884	20334	33994	2.69	2.0E-58	AF124974.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
11093	20053	37776	18.24	2.0E-58	BF07745.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
11312	24952	37768	1.48	2.0E-58	AF077249.1	EST_HUMAN	60216576P7 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:490643 5'
729	13785	26719	0.68	1.0E-58	085134.1	NT	Human complement component C5 mRNA, 3' end
1009	14114	27064	5.86	1.0E-58	62714546	NT	Homo sapiens MADH dehydrogenase (ubiquinone) 1 beta subcomplex, 0 (22d, B22) (NDUFB9) mRNA
1330	14395	27353	2.03	1.0E-58	AF057162.1	EST_HUMAN	EST1399252 IMAGE:490643 Homo sapiens cDNA
1330	14395	27354	2.03	1.0E-58	AF057162.1	EST_HUMAN	EST1399252 IMAGE:490643 Homo sapiens cDNA
1397	14431	27340	0.98	1.0E-58	AF123809.1	NT	Homo sapiens partial AF-1 gene, exons 2 to 7 and 8A repeat elements
1672	14704	27881	0.95	1.0E-58	BE46132.1	EST_HUMAN	hy10093.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:3106953 3'
2814	15806	28625	1.21	1.0E-58	4759169	NT	Homo sapiens 3' end regulatory element binding transcription factor 2 (REBP2) mRNA
3548	19594	29520	1.19	1.0E-58	4759081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSFG2) mRNA
3548	19594	29521	1.19	1.0E-58	4759081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSFG2) mRNA
3733	19775	29587	0.7	1.0E-58	4807628	NT	Homo sapiens transition protein 1 (during fibroblast to plasma replacement) (TFP1) mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Even SEQ ID NO:	ORF SEQ ID NO:	Exon Signal Value	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5009	18020	30008	5.17	1.0E-50	A1141053.1	EST_HUMAN	Scavenger, NRP1L2P1, S1 Homo sapiens cDNA clone IMAGE:1678128.3
5941	19047	32221	1.18	1.0E-50	BE001880.1	EST_HUMAN	RC149-10254-2001-00-015-401 B102634 Homo sapiens cDNA
7040	20068	33574	0.64	1.0E-50	11420301.1	EST_HUMAN	Homo sapiens hypoxanthine phosphoribosyl transferase cDNA (LOC51260). mRNA
8451	21187		0.6	1.0E-50	A01973537.1	EST_HUMAN	Homo sapiens myosin (M-protein) 2 (B680) (MYO2B). mRNA
9221	21267	33619	0.59	1.0E-50	4605314.1	EST_HUMAN	Homo sapiens myosin (M-protein) 2 (B680) (MYO2B). mRNA
6033	22340	38727	0.94	1.0E-50	A01760011.1	EST_HUMAN	A01760011 NPC Homo sapiens cDNA clone NPAC4309.5
9430	22400	38537	0.95	1.0E-50	A01412397.1	EST_HUMAN	2590605.7 Scavenger, beta1, N1T Homo sapiens cDNA clone IMAGE:730497.5
9430	22400	38538	0.95	1.0E-50	A01412397.1	EST_HUMAN	2590605.7 Scavenger, beta1, N1T Homo sapiens cDNA clone IMAGE:730497.5
0546	23468	38663	0.95	1.0E-50	AA4112397.1	EST_HUMAN	Homo sapiens cDNA, large (Drosophila) homolog 2 (charybdom 1) (DL02). mRNA
12059	24522		2.61	1.0E-50	X03332.1	NT	Homo sapiens immunoglobulin kappa light chain, variable region 1.14
2238	14552	28270	21.09	8.0E-59	X03332.1	NT	Homo sapiens TATA box binding protein (TBP) mRNA
7015	20141	33498	0.71	8.0E-59	A0302991.1	EST_HUMAN	EST196683 Testis1 Homo sapiens cDNA 5' end
7015	20141	33498	0.71	8.0E-59	A0302991.1	EST_HUMAN	EST196683 Testis1 Homo sapiens cDNA 5' end
8521	21469	34004	3.74	8.0E-59	A0191663.1	EST_HUMAN	EST466531 T1 NC1, CGAP, XG11 Homo sapiens cDNA clone IMAGE:3362066.5
1179	18504		3.9	8.0E-59	BF033327.1	EST_HUMAN	cont1404.41 NC1, CGAP, XG8 Homo sapiens cDNA clone IMAGE:3362066.5
8161	20389	34489	1.94	6.0E-50	A065431.1	EST_HUMAN	SA GENIE PRODUCT PRECURSOR. 3' similar to TRQ13732 Q13732
8538	21556	34972	0.56	6.0E-50	A1762070.1	EST_HUMAN	cnb902.2 Normal Human Tissue Culture Bone Cells Homo sapiens cDNA clone N1BTEC, cm08042 random.
1788	14707	27762	1.19	5.0E-50	A0157281.1	EST_HUMAN	ad0095.1 Schneider cell strain 00054 Homo sapiens cDNA clone IMAGE:2783885.3 similar to TR0505.575769 T6d transduced DIFFERENTIATION ASSOCIATED PROTEIN 1 ;
1788	14707	27762	1.19	5.0E-50	A0157281.1	EST_HUMAN	ad0095.1 Schneider cell strain 00054 Homo sapiens cDNA clone IMAGE:2783885.3 similar to TR0505.575769 T6d transduced DIFFERENTIATION ASSOCIATED PROTEIN 1 ;
1708	14737	28112	1.19	5.0E-50	A0157281.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2783885.3 similar to TR0505.575769 T6d transduced DIFFERENTIATION ASSOCIATED PROTEIN 1 ;
3144	18021	29172	7.03	5.0E-50	A007481.1	EST_HUMAN	45486.1134 Scavenger, N1T, C8G, S1T Homo sapiens cDNA clone IMAGE:2305556.3
4937	17708	30001	7.38	5.0E-50	X33497.1	NT	Homo sapiens cDNA, large (Drosophila) homolog 2 (charybdom 1) (DL02). mRNA
5796	18648	32070	0.58	5.0E-50	B005508	NT	Homo sapiens alpha 2 (u) chain protein (A2.2). mRNA
7182	18413	31216	7.91	5.0E-50	A016204.1	EST_HUMAN	ad0095.1 Schneider cell strain 00054 Homo sapiens cDNA clone IMAGE:2781228.3 similar to b-catalin
9158	22124	33555	0.56	5.0E-50	11421778.1	EST_HUMAN	different TARI, repetitive element
10033	22600	39459	1.64	5.0E-50	A0176295.1	EST_HUMAN	Homo sapiens polyomavirus RNA III (DNA director) (3800) (PPC39). mRNA
11250	24206	37728	3.31	5.0E-50	A11434908.1	EST_HUMAN	A0176295.1 MOS Homo sapiens cDNA clone M05EG12.5
7394	13933	29801	3.22	4.0E-50	B00006.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase cDNA (LOC517143). mRNA
1242	14278	27239	0.75	4.0E-50		NT	Human mRNA for KIAA1818d gene, partial cds
							Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PI5K52B) mRNA, and translated products

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Med. Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1242	14278	27240	0.75	4.0E-59	4595618	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
5515	18711	51859	1.04	4.0E-59	11034810	NT	Homo sapiens estrogen (cathelin)-associated protein, delta 2 (neural plakophilin-related arm-repeat protein) (NPLOC2) mRNA
12107	24877	38575	1.5	4.0E-59	7827426	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog) like (ORC5L) mRNA
12422	25410		2.98	4.0E-59	AF597720.1	NT	Homo sapiens T3-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	19130		6.8	3.0E-59	AI195582.1	EST HUMAN	EST137562 MAGE sequences, MAGI Homo sapiens cDNA
228	13327	26750	4.47	3.0E-59	7822427	NT	Homo sapiens KIA0080 gene product (KIA0080) mRNA
1723	14753	27758	11.42	3.0E-59	4505960	NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA
1723	14753	27758	11.42	3.0E-59	4505960	NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA
2139	15168	28171	6.05	3.0E-59	AB026035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3146	16203	28171	6.05	3.0E-59	AB026035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3146	16203	28171	2.91	3.0E-59	4820214	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1) mRNA
3838	16876	28781	1.29	3.0E-59	4920214	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1) mRNA
4712	17732	30026	1.4	3.0E-59	4505944	NT	Homo sapiens zona pellucida glycoprotein 2 (spERM receptor) (ZP2) mRNA
4678	17895	30785	1.66	3.0E-59	7427522	NT	Homo sapiens chromodomain 2, segment HS21084
5019	18101		1.05	3.0E-59	AB5991.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRK) mRNA
6348	19415	32695	1.99	3.0E-59	8924074	NT	Human prothrombin converting enzyme (NEC2) gene, exon 2
7594	20645	33006	2.12	3.0E-59	6454137	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741) mRNA
8283	21232	34454	1.5	3.0E-59	X12550.1	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOAR1) mRNA
8283	21232	34454	1.5	3.0E-59	X12550.1	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOAR1) mRNA
10404	23326	36690	0.84	3.0E-59	X70251.1	NT	Human mRNA for dbi proto-oncogene
10404	23326	36690	0.84	3.0E-59	X70251.1	NT	Human mRNA for dbi proto-oncogene
12470	25219		1.37	3.0E-59	11477868	NT	H. sapiens CCL11 alpha gene
12672	25811		7.97	3.0E-59	11477868	NT	H. sapiens CCL11 alpha gene
5985	19070	32298	0.82	2.0E-59	F506353.1	EST HUMAN	Homo sapiens gamma-glutamyl/phenylalanine-lyase-like activity 1 (GGT11) mRNA
5985	19070	32298	0.82	2.0E-59	F506353.1	EST HUMAN	Homo sapiens gamma-glutamyl/phenylalanine-lyase-like activity 1 (GGT11) mRNA
6979	20202		0.91	2.0E-59	AA140073	EST HUMAN	UHL-BL16-32-Q11.11 N17 CGAP, SAGE Homo sapiens cDNA clone IMAGE398522.3'
7272	20007		0.67	2.0E-59	AB131351	EST HUMAN	AB0305.13 SAGE, testis, N177 CGAP, SAGE Homo sapiens cDNA clone IMAGE398522.3'
8532	21019		0.91	2.0E-59	F51350.1	EST HUMAN	Homo sapiens nucleosome-located protein 128 (N128) gene, complete cds
8532	21019		0.91	2.0E-59	F51350.1	EST HUMAN	Homo sapiens nucleosome-located protein 128 (N128) gene, complete cds
10080	22813		0.45	2.0E-59	A332974.1	EST HUMAN	MR0-F10144-26970-002-af10 F10144 Homo sapiens cDNA
10080	22813		0.45	2.0E-59	A332974.1	EST HUMAN	EST130133 Jukal T-cells Y Homo sapiens cDNA 5' end
10080	22813		1.56	2.0E-59	B260554.1	EST HUMAN	RC9-NT10356-10070-103-ae7 NT10358 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11180	24138	37697	2.34	2.0E-56	AW140698.1	EST - HUMAN	h07104x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE2691854 5'
11180	24138	37698	2.34	2.0E-56	AW140698.1	EST - HUMAN	h07104x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE2691854 5'
12373	25150	31897	6.86	2.0E-56	AB31906.1	EST - HUMAN	w38c12.x1 NCI_COAP_K011 Homo sapiens cDNA clone IMAGE260182 3' similar to TRQ8542
12684	25836	31426	4.02	2.0E-50	L17646.1	NT	Q88542 RTVL-H PROTEIN, contains LTR7 b1 LTR7 repetitive element ;
1594	13267		18.92	1.0E-50	BE29411.1	EST - HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
2025	19624		3.89	1.0E-50	AA748468.1	EST - HUMAN	ca58h11.s1 NCI_COAP_G051 Homo sapiens cDNA clone IMAGE351627 5'
7612	20761	34137	1.18	1.0E-50	AI130894.1	NT	Q13937 MER37 TRANSCRIPTIONAL ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
7585	20325	34319	1.07	1.0E-50	BE26814.1	EST - HUMAN	Homo sapiens mRNA for transcription factor
7585	20325	34320	1.07	1.0E-50	BE26814.1	EST - HUMAN	h0111185f1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE332662 5'
9740	22768	36222	0.85	1.0E-50	BE26814.1	EST - HUMAN	Homo sapiens zinc finger protein, ZF7 (ZNF270), mRNA
9833	22850	36351	0.54	1.0E-50	11419830.1	NT	Homo sapiens 3-hydroxyacyl-Coenzyme A hydratase (HCH), mRNA
9833	22850	36352	0.54	1.0E-50	11428549.1	NT	Homo sapiens mRNA for transcription factor
11201	20794	32332	2.55	8.0E-50	AI17846.1	EST - HUMAN	ES138854 IMAGE:neurospine, UACO Homo sapiens cDNA
784	18234	26786	2.55	8.0E-50	AI17846.1	EST - HUMAN	Homo sapiens alpha-tubulin ribonucleoprotein L3 polypeptide (6.0) (SNRPD3) mRNA
1467	15097	26217	2.65	8.0E-50	5174659.1	NT	Homo sapiens alpha-tubulin ribonucleoprotein L3 polypeptide (6.0) (SNRPD3) mRNA
2182	15107	26218	2.65	8.0E-50	5174659.1	NT	Homo sapiens alpha-tubulin ribonucleoprotein L3 polypeptide (6.0) (SNRPD3) mRNA
6094	10173	32389	0.94	8.0E-50	AB220041.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6053	19710	32907	1.01	8.0E-50	S93182.1	NT	hyaluronan-binding protein-hyalocyte growth factor activator homolog (human, spleen, mRNA, 2408 nt)
7552	20043	34265	0.99	8.0E-50	11428841.1	NT	Homo sapiens phosphatidylchyltransferase 1, choline beta isozyme (PCYT1B), mRNA
8298	21267	34676	2.37	8.0E-50	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8298	21267	34687	2.58	8.0E-50	11428949.1	NT	Homo sapiens S-antigen, retina and adrenal gland (erastin) (SAG), mRNA
8820	22675	36130	1.2	8.0E-50	11417119.1	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8820	22675	36131	1.2	8.0E-50	11417119.1	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10938	23959	37379	0.98	8.0E-50	5453907.1	NT	Homo sapiens EAN binding protein 7 (RANBP7), mRNA
11182	24138	37670	4.65	8.0E-50	AL163204.1	NT	Homo sapiens chromosome 21 segment H8321C004
11182	24138	37671	4.65	8.0E-50	AL163204.1	NT	Homo sapiens chromosome 21 segment H8321C004
755	19818	28760	30.34	7.0E-40	AF056068.1	NT	Homo sapiens MHC class 1 region
755	19818	28760	30.34	7.0E-40	AF056068.1	NT	Homo sapiens MHC class 1 region
818	19874	28922	1.17	7.0E-40	460483.1	NT	Homo sapiens interferon 10 receptor, beta (IL10RB), mRNA
2138	15185	28170	1.04	7.0E-40	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds

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Probe ID	SEQ ID	Exon	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source
2768	16796	28066		1.18	7.0E-60	AJ011453.1	NT
4208	12707	30314		3.1	7.0E-60	AF498498	NT
4008	12707	30515		0.12	7.0E-60	AJ294759.1	NT
6762	22703	36161		3.66	7.0E-60	H80411.1	EST_HUMAN
11602	24657	38235		1.57	7.0E-60	H50411.1	EST_HUMAN
21969	12024	28224		0.91	8.0E-60	BE56407.12	EST_HUMAN
81958	21084	34463		0.95	8.0E-60	I471735.1	EST_HUMAN
8760	21747			8.33	8.0E-60	H5248.1	EST_HUMAN
84	13200	29124		1.13	5.0E-60	AJ007917.1	EST_HUMAN
84	13200	29124		1.13	5.0E-60	AJ007917.1	EST_HUMAN
2244	15258	28264		1.25	4.0E-60	AJ503028.1	EST_HUMAN
2244	15258	28264		1.25	4.0E-60	AJ503028.1	EST_HUMAN
2244	15258	28285		1.31	4.0E-60	AJ4260037.1	EST_HUMAN
2084	16042			0.91	4.0E-60	BF18968.1	EST_HUMAN
7576	20594	33897		0.91	4.0E-60	BF18968.1	EST_HUMAN
9482	22446			0.59	4.0E-60	AJ182782.2	NT
11628	24656	38128		1.7	4.0E-60	AJ183597	NT
11628	24656	38128		1.7	4.0E-60	AJ183597	NT
1876	1461	27900		4.44	3.0E-60	BE56281.1	EST_HUMAN
1876	14601	27901		4.44	3.0E-60	BE56281.1	EST_HUMAN
1868	14670			1.88	3.0E-60	G531190	NT
4485	17570	30398		2.21	3.0E-60	AJ271733.1	EST_HUMAN
5452	18185	31485		2.11	3.0E-60	AJ271733.1	EST_HUMAN
9724	18816	31597		2.11	3.0E-60	AJ283195.1	EST_HUMAN
7143	18375	31283		0.55	3.0E-60	AJ72981.4	EST_HUMAN
8746	21713	35135		5.92	3.0E-60	F147484	NT
8745	21713	35135		5.22	3.0E-60	S174844	NT
8930	21866	35324		0.58	3.0E-60	AJ040283.1	EST_HUMAN
9064	22460	35455		1.2	3.0E-60	F147484	NT

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Ht BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10017	22544	35411	0.42	3.0E-40	BF102612.1	EST_HUMAN	501646227 NIH_MGC_50 Homo sapiens cDNA clone IMAGE300600 6'
12970	25871		1.53	3.0E-40	AA485268.1	EST_HUMAN	4077044.1 Swine lung (BS7216) Homo sapiens cDNA clone IMAGE540161 6' similar to contains LTR101.1 LTR101 negative element.
33	13153	26054	1.7	2.0E-40	AY008265.1	NT	Homo sapiens scute carrier (SC254.1) mRNA, complete cds, nuclear gene for mitochondrial product
1421	14454	27128	2.76	2.0E-40	M11694.1	NT	Hsp70 heat shock protein (HSP70) mRNA, complete cds, nuclear gene for mitochondrial product
1734	14764	27147	1.34	2.0E-40	M214603.1	NT	Hsp70 heat shock protein (HSP70) mRNA, complete cds, nuclear gene for mitochondrial product
1743	14773	27758	1.01	2.0E-40	AY008265.1	NT	Homo sapiens scute carrier (SC254.1) mRNA, complete cds, nuclear gene for mitochondrial product
2482	15955	28520	1.76	2.0E-40	AW350450.1	EST_HUMAN	RC1-H170265-012169-012-052 HT2088 Homo sapiens cDNA
2614	15962	28537	1.38	2.0E-40	B677229.1	NT	Homo sapiens interleukin 17 receptor (IL17R) mRNA
2721	15715	28133	0.94	2.0E-40	AW678005.1	EST_HUMAN	EST380114 IMAGE resequencing, IMAGE Homo sapiens cDNA
2721	15715	28133	0.94	2.0E-40	4757867.1	NT	Homo sapiens scute carrier (SC254.1) mRNA, complete cds, nuclear gene for mitochondrial product
3026	16051	28507	1.49	2.0E-40	AF237016.1	EST	Hsp70 heat shock protein (HSP70) mRNA, complete cds, nuclear gene for mitochondrial product
3026	16051	28507	0.83	2.0E-40	AF237016.1	EST	Hsp70 heat shock protein (HSP70) mRNA, complete cds, nuclear gene for mitochondrial product
4151	17162		0.65	2.0E-40	P0731458.1	EST_HUMAN	U4H-BMT1-145-406-5-01-1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE3070652 3'
6433	19450	32762	0.6	2.0E-40	AF071022.1	EST_HUMAN	miR127, NCI CGAP_C08 Homo sapiens cDNA clone IMAGE1076485 6' similar to contains THR11 THR12 repetitive element;
6640	19469	32764	1.48	2.0E-40	AF071022.1	EST_HUMAN	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6674	19427	33224	0.62	2.0E-40	AF187176.1	NT	Homo sapiens DNA polymerase beta catalytic subunit (REV3) mRNA, complete cds
7027	18329	31279	2.05	2.0E-40	4500244.1	EST_HUMAN	Homo sapiens cathepsin releasing hormone receptor 2 (CRHR2) mRNA
7027	18329	31280	2.05	2.0E-40	4500244.1	NT	Homo sapiens cathepsin releasing hormone receptor 2 (CRHR2) mRNA
7317	20293	33620	0.6	2.0E-40	A4311150.1	EST_HUMAN	EST181949 IMAGE resequencing, IMAGE Homo sapiens cDNA 3' and similar to af1491 to prothymosin, alpha
7317	20293	33620	0.6	2.0E-40	A4311150.1	EST_HUMAN	EST181949 IMAGE resequencing, IMAGE Homo sapiens cDNA 3' and similar to af1491 to prothymosin, alpha
7317	20280	33631	6.6	2.0E-40	A4311108.1	EST_HUMAN	0224009.2 NCI CGAP_K123 Homo sapiens cDNA clone IMAGE206186 3' similar to SW-GAUR_RAT
7434	20401	33755	0.53	2.0E-40	A3081124.1	EST_HUMAN	0224009.2 NCI CGAP_K123 Homo sapiens cDNA clone IMAGE206186 3' similar to SW-GAUR_RAT
7894	20367		1.06	2.0E-40	AF167268.1	EST_HUMAN	U4H-BMT1-145-406-5-01-1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE307210 3'
8338	21307	34722	1.09	2.0E-40	356597.1	EST_HUMAN	HS1BES1 human adult testis Homo sapiens cDNA clone cAN_1E5110
8219	22185	35518	4.86	2.0E-40	360303.1	NT	Human pro-B cell stimulating factor homologue (SDFBT) mRNA, complete cds
10337	22391	36740	2.2	2.0E-40	11951658.1	NT	Homo sapiens scute carrier (SC254.1) mRNA, complete cds, nuclear gene for mitochondrial product
10337	22391	36741	2.2	2.0E-40	11951658.1	NT	Homo sapiens scute carrier (SC254.1) mRNA, complete cds, nuclear gene for mitochondrial product
12304	24953	35581	1.9	2.0E-40	AW1751161.1	EST_HUMAN	CXCR-CT0013-250568-017-03 CT0013 Homo sapiens cDNA
12304	24953	35582	1.9	2.0E-40	AW1751161.1	EST_HUMAN	CXCR-CT0013-250568-017-03 CT0013 Homo sapiens cDNA

Single Exon Probes Expressed in Bone Marrow

Probe ID	Exon No.	Seq ID	ORF Seq ID	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description	
12347	28330			1.38	2.0E-60	U114182	NT	Homo sapiens non-histone chromatin protein 2 (S. cerevisiae) like 1 (NHPCL1), mRNA	
12348	28331			1.82	2.0E-60	U098673	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cist	
12371	25900			5.84	2.0E-60	U113088	NT	Homo sapiens similar to HSP6022 protein (Ht. sapiens) (LOC83349), mRNA	
12378	25421			2.47	2.0E-60	A001390.1	NT	Homo sapiens gene for AIF-4, complete cds	
523	13934			25.91	1.0E-60	A01390.1	EST_HUMAN	PMS-1/H0065/217020-201-405 H00605 Homo sapiens cDNA	
3920	10004			2.37	1.0E-60	A017856.1	EST_HUMAN	U413380/796A11 Homo sapiens cDNA clone Y76A11/001864 5	
4953	30895			0.975	1.0E-60	AU143383.1	EST_HUMAN	Homo sapiens chromosome 21 segment H527C088	
4953	30895			1.34	1.0E-60	AU143263.2	EST_HUMAN	RC4-BT0311-1417169-071-H05 B10311 Homo sapiens cDNA	
5280	12149			34.661	1.0E-60	BC094410.1	EST_HUMAN	nc412121 NC1 CGAP_F11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1, L1, L1 repetitive element	
9108	27201			3.08	1.0E-60	A42424041.1	EST_HUMAN	ATP5A081 TP Homo sapiens cDNA clone TFGAED905 5	
9134	22100			39.528	1.0E-60	AU174081.1	EST_HUMAN	U118344/HB.MB1 Homo sapiens cDNA clone HBMA1/00568 5	
11001	14215			27.095	1.95	9.0E-61	AU119344.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9031	22027			39.450	4.48	9.0E-61	48855446	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9031	22027			34.945	1.47	9.0E-61	48855446	NT	W0551031 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:2160555 3
2078	16574			23.994	0.16	8.0E-61	AU006478.1	EST_HUMAN	W0551031 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:2160555 3
2078	16574			23.994	0.17	8.0E-61	AU006478.1	EST_HUMAN	W0551031 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:2160555 3
2078	16574			26.995	1.96	8.0E-61	X07147.1	NT	Human endogenous centric PHE1, 155bp cDNA clone IMAGE:1068213 3
2092	10020			36.025	1.73	8.0E-61	A493968.1	EST_HUMAN	mdg9p5.1 NC1 CGAP_F11 Homo sapiens cDNA clone IMAGE:1068213 3
8227	21195			34.604	0.73	8.0E-61	A493968.1	EST_HUMAN	mdg9p5.1 NC1 CGAP_F11 Homo sapiens cDNA clone IMAGE:1068213 3
11926	24607			39.400	1.47	8.0E-61	H1725.1	EST_HUMAN	ATP5A081 TP Homo sapiens cDNA clone TFGAED905 5
11926	24607			39.401	1.47	8.0E-61	H1725.1	EST_HUMAN	ATP5A081 TP Homo sapiens cDNA clone TFGAED905 5
128	20163			29.163	0.87	7.0E-61	7708670	NT	SP-CA0H11.C50109 OVARIAN PROTEIN
128	13234			29.164	0.87	7.0E-61	7708670	NT	SP-CA0H11.C50109 OVARIAN PROTEIN
265	13361			28.255	0.21	DE0038.1	EST_HUMAN	Homo sapiens PXR2b protein (PXR2b), mRNA	
265	13361			28.255	0.21	DE0038.1	EST_HUMAN	Homo sapiens PXR2b protein (PXR2b), mRNA	
812	13870			28.519	0.31	DE0038.1	EST_HUMAN	Homo sapiens PXR2b protein (PXR2b), mRNA	
1324	14350			11.5	9.0E-61	AJ119800.1	NT	0013005681 NH IMG_C 21 Homo sapiens cDNA clone IMAGE:3933440 5	
1634	27652			27.652	1.15	9.0E-61	BE237400.1	EST_HUMAN	0013005681 NH IMG_C 21 Homo sapiens cDNA clone IMAGE:3933440 5
1634	27652			27.652	1.15	9.0E-61	BE237400.1	EST_HUMAN	Homo sapiens PRO2011 mRNA, complete cds
1655	14657			27.652	2.33	6.0E-61	AA595033.1	EST_HUMAN	0013005681 NH IMG_C 21 Homo sapiens cDNA clone IMAGE:3933440 5
2137	15154			28.199	0.97	6.0E-61	AU006826.1	NT	Homo sapiens solute carrier (SLC23A18) mRNA, complete cds; nuclear gene for mitochondrial product
3317	17607			29.290	0.87	6.0E-61	AU130598.1	EST_HUMAN	Homo sapiens cDNA clone NT294007283 5
6147	16222			33.652	1.93	6.0E-61	5782449.1	NT	Igfbp5-B58-CD76s (alternatively spliced) transcript, H. sapiens
7565	20528			33.897	1.58	6.0E-61	U24498.1	NT	Igfbp5-B58-CD76s (alternatively spliced) transcript, H. sapiens
7565	20528			33.897	1.58	6.0E-61	U24498.1	NT	Human autosomal dominant polytopic tumor disease protein 1 (POTD1) gene, 3'UTR

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7878	20822	34186	1.87	6.0E-61	AF03737.1	NT	Homo sapiens general transcription factor 2-1 (GTF2D) mRNA, complete cds
221	13321	28247	1.14	5.0E-61	8622660	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ1316), mRNA
1088	14710	27666	3.18	5.0E-61	8622660	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ1316), mRNA
3048	10108	28200	1.98	5.0E-61	4690008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
1724	17243	27768	1.87	5.0E-61	AL18379.2	NT	Homo sapiens chromosome 21 segment H82T0076
1724	17243	27768	1.87	5.0E-61	AL18379.2	NT	Homo sapiens chromosome 21 segment H82T0076
6518	18903	32180	0.51	4.0E-61	AU140307.1	EST_HUMAN	Homo sapiens B9G10 contig between AML1 and CBR1 on chromosome 21q22; segment T13
12348	26143	38164	2.27	4.0E-61	AF151401.1	EST_HUMAN	Homo sapiens DKF2P668B023 protein (DKF2P668B023), mRNA
8794	21731	38164	2.27	4.0E-61	AF151401.1	EST_HUMAN	Homo sapiens DKF2P668B023 protein (DKF2P668B023), mRNA
489	13571	26180	1.25	3.0E-61	AF151401.1	EST_HUMAN	AF151401 HTF Homo sapiens cDNA clone HTFA801.6
1217	14255	27213	3.74	2.0E-61	BE18410.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11028 (FLJ1028), mRNA
1217	14255	27214	3.4	2.0E-61	BE18410.1	EST_HUMAN	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA
1874	14708	27884	1.34	2.0E-61	NS3039.1	EST_HUMAN	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA
2849	15946		1.25	2.0E-61	188397.1	EST_HUMAN	Y6391.L1 Scars cell liver spleen NF1L3 Homo sapiens cDNA clone IMAGE246483 3' similar to
6566	18828	32651	0.92	2.0E-61	11428166	EST_HUMAN	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
8369	22334	35765	1.07	2.0E-61	AW84317.1	EST_HUMAN	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
9020	22741		1.27	2.0E-61	AB011108.1	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
10282	22207	36062	1.81	2.0E-61	AW80298.1	EST_HUMAN	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
10512	23534	37031	2.89	2.0E-61	11421776	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
11290	24188		0.91	2.0E-61	11419729	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
13042	25593	31701	1.39	2.0E-61	AW655328.1	EST_HUMAN	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
435	13509		1.85	1.0E-61	AL183103.2	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
774	13833	26779	0.98	1.0E-61	6453829	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
1784	14813		0.95	1.0E-61	133267.1	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
1875	14900	27699	4.59	1.0E-61	6005683	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
2248	15221	28241	1.52	1.0E-61	AW627281.1	EST_HUMAN	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
2949	15906	28831	1.58	1.0E-61	BE398883.1	EST_HUMAN	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
3337	16438	26593	0.97	1.0E-61	7682219	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
4288	17317	30168	1	1.0E-61	MB840.1	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to
4488	17444	30381	1.02	1.0E-61	4759249	NT	Q13H10513-300000-47-401 HT0813 Homo sapiens cDNA clone IMAGE246483 3' similar to

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3395	16444		4.9	6.0E-62	11418235	NT	Homo sapiens CGI-58 protein (CGI-58), mRNA
7887	20351	34209	3.27	6.0E-62	AI762801.1	EST_HUMAN	W64402.X1 NCI-DGAP-CLL1 Homo sapiens cDNA clone IMAGE:2389261 3'
7887	20351	34210	3.27	6.0E-62	AI762801.1	EST_HUMAN	W64402.X1 NCI-DGAP-CLL1 Homo sapiens cDNA clone IMAGE:2389261 3'
8425	21331		0.72	6.0E-62	AW501124.1	EST_HUMAN	UHF-8P05-41-09-03-UT1 NH ₂ MG-63 Homo sapiens cDNA clone IMAGE:3072833 5'
8500	21360	34884	1.4	8.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51009), mRNA
9709	22652	38118	4.02	6.0E-62	AW814333.1	EST_HUMAN	MR3-5T0203-130100-005-009 5T0203 Homo sapiens cDNA
416	13469	26424	2.28	5.0E-62	AI950528.1	EST_HUMAN	w651407.X1 NCI-DGAP-Lu28 Homo sapiens cDNA clone IMAGE:2847204 3' similar to SW_G085_HUMAN
2416	15423	28448	3.61	5.0E-62	JA27735.1	NT	Q08379 GOLGIN-66, contains element MER22 repetitive element;
2416	15423	28447	3.61	5.0E-62	JA27735.1	NT	Homo sapiens Xq pseudocentromeric region, segment 1/2
2416	15423	28447	3.61	5.0E-62	JA27735.1	NT	Homo sapiens Xq pseudocentromeric region, segment 1/2
2416	15423	28447	3.61	5.0E-62	JA27735.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
2416	15423	28447	3.61	5.0E-62	JA27735.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
2416	15423	28447	3.61	5.0E-62	JA27735.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3430	18478	26397	2.85	5.0E-62	4503738	NT	Homo sapiens tyrosine receptor 2 (TYR2) mRNA
4355	17382	30264	1.91	5.0E-62	AA431093.1	EST_HUMAN	AT7245A1801.1531; Homo sapiens cDNA clone IMAGE:78244 3' similar to SW_NDCC_RAT
4355	17382	30264	1.91	5.0E-62	AA431093.1	EST_HUMAN	AT7245A1801.1531; Homo sapiens cDNA clone IMAGE:78244 3' similar to SW_NDCC_RAT
8894	21600	35283	0.64	5.0E-62	AW065897.1	EST_HUMAN	SG2-NT108-10350-021-403 NH ₂ Homo sapiens cDNA
8894	21600	35283	0.64	5.0E-62	AW065897.1	EST_HUMAN	Homo sapiens paracatalin receptor 3 (PR3) mRNA
9675	22626	36282	8.13	5.0E-62	AW141087.1	EST_HUMAN	Homo sapiens muscle specific gene (MS), mRNA
11595	24534	39300	2.18	5.0E-62	11423574	NT	Homo sapiens muscle specific gene (MS), mRNA
11596	24534	39301	2.18	5.0E-62	11423574	NT	Homo sapiens muscle specific gene (MS), mRNA
841	13888	28933	2.29	4.0E-62	AW161479.1	EST_HUMAN	aw17403.Y1 Schneider f6d1 brain 0004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:A37104
841	13888	28954	2.29	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
842	13888	28953	1.27	4.0E-62	AW161479.1	EST_HUMAN	aw17403.Y1 Schneider f6d1 brain 0004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:A37104
842	13888	28954	1.27	4.0E-62	AA311281.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1468	14491		1	4.0E-62	AA311281.1	EST_HUMAN	aw17403.Y1 Schneider f6d1 brain 0004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:A37104
2464	15408	28491	2.85	4.0E-62	AI927900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2464	15408	28492	2.85	4.0E-62	AI927900.1	EST_HUMAN	aw17403.Y1 Schneider f6d1 brain 0004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:A37104
3470	18459		8.46	4.0E-62	451782	NT	EST180046 Jurkat T cells Y Homo sapiens cDNA, 3' end
							WT2008.X1 Sorensen_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2560359 3' similar to
							gb:A37104; mnt HISTONE H2B 2 (HUMAN);
							WT2008.X1 Sorensen_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2560359 3' similar to
							gb:A37104; mnt HISTONE H2B 2 (HUMAN);
							Homo sapiens keratin 18 (KRT18) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6092	19115	32316	1.83	4.0E-42	4508978	NT	Homo sapiens solute carrier family 13 (potassium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
6426	16495	32748	2.83	4.0E-42	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9A), mRNA
7377	20347	33068	2.08	4.0E-42	11427041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PPSS2), mRNA
7895	20389	34210	2.89	4.0E-42	7897097	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 38kD) (EIF2B2), mRNA
7896	20389	34220	2.89	4.0E-42	7897097	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 38kD) (EIF2B2), mRNA
8511	21479	34693	0.83	4.0E-42	11428973	NT	Homo sapiens 28S pre-ribosomal-associated factor 1 homolog (POT1), mRNA
9198	22184	35594	5.85	4.0E-42	45033080.1	NT	Homo sapiens mRNA for KIAA1253 protein, partial cds
11353	24303	37830	3.05	4.0E-42	45033080.1	NT	Homo sapiens mRNA for KIAA1253 protein, partial cds
11353	24303	37831	3.05	4.0E-42	45033080.1	NT	Homo sapiens mRNA for KIAA1253 protein, partial cds
11358	24396	38563	3.05	4.0E-42	45033080.1	NT	Homo sapiens mRNA for KIAA1253 protein, partial cds
12267	25304	38716	3.38	4.0E-42	45033080.1	NT	Homo sapiens mRNA for KIAA1253 protein, partial cds
12491	25624	39109	1.96	4.0E-42	11418322	NT	Homo sapiens mRNA for KIAA1253 protein, partial cds
12491	25624	39109	1.96	4.0E-42	11418322	NT	Homo sapiens mRNA for KIAA1253 protein, partial cds
13024	25500	31703	10.77	4.0E-42	11417862	NT	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13024	25500	31704	10.77	4.0E-42	11417862	NT	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
12977	25542	31717	3.07	4.0E-42	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
76	13102	26114	0.88	3.0E-42	4557784	NT	Homo sapiens neurofascin 2 (bilateral sciatic neuroma) (NF2), mRNA
3059	18116	29029	1.02	3.0E-42	AB040006.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3059	18116	29030	1.02	3.0E-42	AB040006.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3712	18755	29089	3.52	3.0E-42	X52858.1	NT	Human cyclophilin-related processed pseudogene wa3SR-LX1 NC_004947.1 Homo sapiens cDNA clone IMAGE-2296603 3' similar to contains THR12
8895	21681	35272	4.85	3.0E-42	AB023783.1	EST_HUMAN	THR12 repetitive element
1235	14272	27232	2.78	2.0E-42	AL163284.2	NT	Homo sapiens chromosome 21 segment H621084
8142	21079	34478	0.86	2.0E-42	AA07490.1	EST_HUMAN	EST1178377 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and
9127	22083	35520	4.47	2.0E-42	BF339911.1	EST_HUMAN	RCO-BN0284-300000-031-426 BN0284 Homo sapiens cDNA
9127	22093	35521	4.47	2.0E-42	BF339911.1	EST_HUMAN	RCO-BN0284-300000-031-426 BN0284 Homo sapiens cDNA
10533	23455		4.95	2.0E-42	AF224595.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2B) genes, complete cds
11690	24873		20.8	2.0E-42	BF330978.1	EST_HUMAN	C747-B1025/4381108-017-403 B10257 Homo sapiens cDNA
1046	14091	27044	1.88	1.0E-42	AF245403.1	NT	Homo sapiens intercalin 2 (INC2) mRNA, complete cds
1547	14690	27652	12.74	1.0E-42	78810.1	NT	Homo sapiens ADP-ATP carrier protein (ANT-2) gene, complete cds

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Table 4
Isotypes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1815	14842	27633	1.45	1.0E-42	AA625207.1	EST_HUMAN	af067117 Source: NHNPd_51 Homo sapiens cDNA clone IMAGE:404744.5 similar to WP_K01412.1
2025	15583	29809	1.48	1.0E-42	AL038944.1	EST_HUMAN	DKF25569F107.1 5691 (c-mycint, h1422) Homo sapiens cDNA clone DKF25569F104.5
3433	14559	34555	1.41	1.0E-42	AB040811.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
4659	17579	30470	1.13	1.0E-42	882320.1	NT	Homo sapiens hypothetical protein FL20212 (FL20212), mRNA
5159	18178	31055	0.88	1.0E-42	AA148822.1	EST_HUMAN	258506.1 Source: J999991.U9999, NHNPd Homo sapiens cDNA clone IMAGE:491611.5 similar to SW6506.1
5188	12005	31079	0.94	1.0E-42	U33503.1	NT	Homo sapiens B-ovine 193709 Cytokeratin 8B61.1
6401	16408	32736	2.84	1.0E-42	U05111.2	NT	Homo sapiens X28 region near ALD locus containing adult specificity phosphatase 9 (DUSP9), disomeric protein (CDM), adrenoleukodystrophy protein >
7421	26321	33553	0.91	1.0E-42	AA040909.1	EST_HUMAN	405052.01 Strategene fetal retina 879250 Homo sapiens cDNA clone IMAGE:839006.3
7432	26332	33565	2.48	1.0E-42	AA722878.1	EST_HUMAN	598070.01 Source: fetal_liver1, NHNPd Homo sapiens cDNA clone IMAGE:406771.3
7433	26332	33570	2.48	1.0E-42	AA722878.1	EST_HUMAN	598070.01 Source: fetal_liver1, NHNPd Homo sapiens cDNA clone IMAGE:406771.3
8110	20739	33502	1.93	1.0E-42	AA263061.1	EST_HUMAN	258507.01 NIH CGAP, GC031 GC031 Homo sapiens cDNA clone IMAGE:705095.5
8413	22378	33516	1.93	1.0E-42	78622898	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
8413	22378	33517	1.92	1.0E-42	78622898	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
8437	22421	33583	1.97	1.0E-42	U15933.1	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
9497	29415	35169	1.97	1.0E-42	U15933.1	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
9951	27278	35180	3.42	1.0E-42	AA681701.1	EST_HUMAN	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
11654	24659	35237	1.98	1.0E-42	U15933.1	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
12648	29529	35279	2.22	1.0E-42	U70801.1	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
23207	23507	37220	2.22	1.0E-42	U70801.1	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
2333	15392	37241	3.25	1.0E-42	11418322.1	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
2333	15392	37242	2.94	1.0E-42	AA1819403.1	EST_HUMAN	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
4071	17107	30000	1.91	9.0E-43	C1H181.9	EST_HUMAN	QV4510294.181192307.65 S1024 Homo sapiens cDNA clone GEN455010.5
4071	17107	30001	9.29	9.0E-43	AB020482.2	NT	CH181 Homo sapiens cDNA (Fujisawa) Homo sapiens cDNA clone GEN455010.5
4071	17107	30001	9.29	9.0E-43	AB020482.2	NT	Homo sapiens mRNA for KIAA0359 protein, partial cds
4315	18331	38814	1.77	9.0E-43	AB020482.2	NT	Homo sapiens KIAA0359 protein, partial cds
5315	18331	38814	1.77	9.0E-43	11418183.1	NT	Homo sapiens acyl-CoA oxidase 2, mitochondrial (ACOX2), mRNA
5451	18831	31578	1.31	9.0E-43	U15056.1	NT	Homo sapiens mRNA for PIB Vase
7388	20357	33709	3.43	9.0E-43	11429593.1	NT	Homo sapiens nucleoporin 8820 (NUP88), mRNA
8159	21037	34719	0.73	9.0E-43	4985544.1	NT	Homo sapiens pyruvate dehydrogenase kinase, isozyme gamma 3 (PDHX3), mRNA
8695	21037	35060	1.58	9.0E-43	11421160.1	NT	Homo sapiens Rta association (RA/GOS/AF-6) domain family 2 (RASSF2), mRNA
11248	21699	37119	1.54	9.0E-43	78622898	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA
11248	21699	37120	1.54	9.0E-43	78622898	NT	Homo sapiens KIAA0765 gene product (KIAA0765), mRNA

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Table 4
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2351	15300	28382	1.1	8.0E-63	4657724.NT	EST_HUMAN	Homo sapiens luciferase oxidase A (MAGO), nuclear gene encoding mitochondrial protein, mRNA
2353	15301	28383	2.49	8.0E-63	5031810.NT	EST_HUMAN	Homo sapiens IL2-inducible T cell kinase (ITK), mRNA
3475	16351	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16352	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16353	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16354	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16355	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16356	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16357	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16358	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16359	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16360	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16361	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16362	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16363	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16364	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16365	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16366	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16367	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16368	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16369	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16370	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16371	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16372	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16373	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16374	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16375	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16376	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16377	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16378	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16379	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16380	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16381	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16382	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16383	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16384	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16385	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16386	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16387	32618	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3476	16388	32619	3.42	8.0E-63	AF198246.1	NT	Gallus gallus Dact3 protein (Dact3), mRNA, complete cds
3475	16389	32618	3.42	8.0E-6			

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Table 4
Cytokines Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3525	16865	29878	3.64	2.0E-63	336891.1	NT	Homo sapiens polyoma: idiotype disease-associated protein (PID1) gene, complete cds
4901	17618	33810	0.95	2.0E-63	AF111187.2	NT	Homo sapiens Jun deimination protein genes, partial cds, cDNA, complete cds, and unknown gene
5168	18587	31170	1.19	2.0E-63	BE146938.1	EST_HUMAN	U4447010222-01169-18-01-01 H10222 Homo sapiens cDNA
5232	18240	31072	1.17	2.0E-63	EF972617	EST_HUMAN	Homo sapiens glutamine-peptide cyclodextrinase (glutaminyl cyclase) (GCPT), mRNA
5334	26635	31182	0.57	2.0E-63	EF972617	EST_HUMAN	Homo sapiens similar to acromucoidase pyrophosphatase (H. sapiens) (LOC63214), mRNA
5688	10071	32270	2.49	2.0E-63	EF973541.1	EST_HUMAN	U4170107044070-385-c03 F10710 Homo sapiens cDNA
5983	10071	32271	2.48	2.0E-63	EF973541.1	EST_HUMAN	Homo sapiens protein kinase, CAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
8310	18381	32620	0.53	2.0E-63	11421640	NT	Homo sapiens protein kinase, CAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
8310	18381	32621	0.53	2.0E-63	11421640	NT	Homo sapiens protein kinase, CAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
8980	10913	33209	1.23	2.0E-63	J60999.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRVY, TRV3, TCORBV2751P, TCORBV2251A2NT, TCORBV651AT, TCORBV751A12NT, TCORBV651AT1, TCORBV1433, TCORBV651P, TCORBV753A2T, TCORBV1433A2T, TCORBV652A2P, TCORBV752A1NT, TCORBV135913S
8911	10933	33209	0.81	2.0E-63	J60999.1	NT	Homo sapiens MIST mRNA, partial cds
8911	10933	33260	0.81	2.0E-63	A030268.1	NT	Homo sapiens MIST mRNA, partial cds
7278	20212	33315	1.49	2.0E-63	8910356	NT	Homo sapiens Carboxic anhydrase-related protein 10 (LOC66834), mRNA
7278	20212	33316	1.48	2.0E-63	8910356	NT	Homo sapiens Carboxic anhydrase-related protein 10 (LOC66834), mRNA
8058	20925	34391	0.82	2.0E-63	A040484.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8818	17845	32567	3.6	2.0E-63	AF183701.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9409	22774	35610	1.95	2.0E-63	11420948	NT	Homo sapiens protein family member 35 (KIF35), mRNA
9409	22774	35611	1.95	2.0E-63	11420948	NT	Homo sapiens protein family member 35 (KIF35), mRNA
10259	23224	38707	0.98	2.0E-63	AF183216.2	NT	Homo sapiens chaperone family member 35 (KIF35), mRNA
11068	24058	37882	13.74	2.0E-63	NT9646.1	EST_HUMAN	spB0654.9 Sarcos, fetal lung, NCBI 19870111, HSC 10316
11127	24057	37814	2.32	2.0E-63	AF069610.1	NT	spA1700.405 RIBOSOMAL PROTEIN S4 (HUMAN),
11127	24057	37815	2.32	2.0E-63	AF069610.1	NT	Homo sapiens neuramin II-abeta gene, partial cds
12381	25747	37616	8.02	2.0E-63	11418183	NT	Homo sapiens acyl-coA 2, mitochondrial (ACQ2), mRNA
1516	14547	2716	0.83	1.0E-63	F04681.1	EST_HUMAN	HSQZD70111 normalized infant brain cDNA Homo sapiens cDNA clone s-z0d11
1515	14547	2719	0.83	1.0E-63	F04681.1	EST_HUMAN	HSQZD70111 normalized infant brain cDNA Homo sapiens cDNA clone s-z0d11
4370	17367	30270	3.4	1.0E-63	F04681.1	EST_HUMAN	HSQZD70111 normalized infant brain cDNA Homo sapiens cDNA clone s-z0d11
4370	17367	30271	3.4	1.0E-63	F04681.1	EST_HUMAN	HSQZD70111 normalized infant brain cDNA Homo sapiens cDNA clone s-z0d11
5428	18529	31403	1.66	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11358	16198	29105	1.73	8.0E-64	AW028446.1	EST_HUMAN	WT3303.31 NC1 CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2926438.3
11358	16198	29108	1.73	6.0E-64	AW028446.1	EST_HUMAN	WT3303.31 NC1 CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2926438.3
12368	27162	31118	9.26	8.0E-64	11528198.UT	EST_HUMAN	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA
821	13879	28829	3.69	5.0E-64	AF231916.1	NT	Homo sapiens chromosome 21 unknown mRNA
821	13879	28830	3.66	5.0E-64	AF231916.1	NT	Homo sapiens chromosome 21 unknown mRNA
1341	14378	27345	0.93	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
1341	14378	27346	0.93	5.0E-64	AB020710.1	NT	Human (9) mitral protein homolog mRNA, complete cds
2637	14509	27483	3.32	5.0E-64	7862205.UT	EST_HUMAN	Homo sapiens mRNA for KIAA0693 protein, partial cds
2637	14509	27484	3.32	5.0E-64	7862205.UT	EST_HUMAN	Homo sapiens mRNA for KIAA0693 protein, partial cds
3983	17023	26534	7.14	5.0E-64	AF071493.1	EST_HUMAN	Homo sapiens putative transcription factor CBR3 (CBR3), mRNA, partial cds
4132	17104	30053	0.63	5.0E-64	AB071493.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
8125	21062	34480	0.67	4.0E-64	BE714007.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
11164	24121	37660	1.65	4.0E-64	AW191378.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
11164	24121	37661	1.65	4.0E-64	AW191378.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2208	18223	28243	6.32	3.0E-64	CI18865.1	EST_HUMAN	Homo sapiens mRNA for KIAA0693 protein, partial cds
3288	18322	29244	0.72	3.0E-64	BE714381.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3467	18503	29422	1.85	3.0E-64	AF117114.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4203	19274	32608	1.35	3.0E-64	236231.1	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4203	19274	32609	1.35	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32716	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32717	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32718	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32719	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32720	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32721	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32722	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32723	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32724	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32725	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32726	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32727	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32728	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32729	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32730	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32731	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32732	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32733	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32734	0.94	3.0E-64	AF150368.1	EST_HUMAN	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8639	21776	32735	0.94	3.0E-64	AF150368.1		

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2530	15593		2.05	2.0E-64	AB927030.1	EST_HUMAN	wb7501.x1 NCL CGAP_3011 Homo sapiens cDNA clone IMAGE2462281 3' similar to contains element L1 repetitive element;
2539	15598	28590	3.13	2.0E-64	AF15246.2	NT	Homo sapiens chromosome 21 segment HS21C546
2539	15598	28591	3.13	2.0E-64	AF15246.2	NT	Homo sapiens chromosome 21 segment HS21C546
3801	16841	29748	0.87	2.0E-64	AF168145.1	EST_HUMAN	EST170215 IMAGE ressequencing, IMAGE Homo sapiens cDNA
3801	16841	29749	0.87	2.0E-64	AF168145.1	EST_HUMAN	EST170215 IMAGE ressequencing, IMAGE Homo sapiens cDNA
6121	19199	32424	2.2	2.0E-64	AF1124387.1	EST_HUMAN	AF124387 NT26022 Homo sapiens cDNA clone N1ZRN2602213 5'
6370	19438	32691	1.38	2.0E-64	AF113708.1	NT	Homo sapiens endoprotein 4 (ANG4) mRNA, partial cds
6652	19690	32699	4.02	2.0E-64	BF66557.1	EST_HUMAN	6021247 AF1 NH JMGC 35 Homo sapiens cDNA clone IMAGE2480394 5'
8745	19800	33060	1.5	2.0E-64	AF078387.1	EST_HUMAN	0226033.x1 Scarsa, Daria, 1993, 1602 HFE gene, Homo sapiens cDNA clone IMAGE-1676717 3'
6859	19912	33298	3.88	2.0E-64	MF7185.1	NT	H. sapiens cDNA clone D13365.1, partial cds
8109	21043	34442	0.57	2.0E-64	11451934	NT	Homo sapiens cDNA clone 143BP1.1, mRNA
8764	21102	34501	0.96	2.0E-64	AF169785.1	EST_HUMAN	Q17410.1 (13.010200-859-173) F10413 Homo sapiens cDNA
9019	21882	35400	5.89	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytochrome protein 1 (Lcyctin) (LCP1), mRNA
9019	21882	35401	5.89	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytochrome protein 1 (Lcyctin) (LCP1), mRNA
9065	22459	35699	0.43	2.0E-64	11423508	NT	Homo sapiens hypothetical protein SB5187 (LOC57119), mRNA
9065	22459	35699	0.43	2.0E-64	AF115361.1	EST_HUMAN	AF115361 NT26214 Homo sapiens cDNA clone NT2621400109 5'
11114	24074	37587	3.94	2.0E-64	BE528114.1	EST_HUMAN	8020-2828F1 NCL CGAP_ Bin77 Homo sapiens cDNA clone IMAGE2180556 5'
11381	24337	37893	3.78	2.0E-64	AF192201.1	EST_HUMAN	w811053.x1 NCL CGAP_ UH1 Homo sapiens cDNA clone IMAGE2452211 3'
11381	24337	37893	3.78	2.0E-64	AF192201.1	EST_HUMAN	w811053.x1 NCL CGAP_ UH1 Homo sapiens cDNA clone IMAGE2452211 3'
11381	24337	37893	3.78	2.0E-64	AF192201.1	EST_HUMAN	601185078F1 NH JMGC 8 Homo sapiens cDNA clone IMAGE3542922 5'
11381	24337	37893	3.78	2.0E-64	BE226690.1	EST_HUMAN	601185078F1 NH JMGC 8 Homo sapiens cDNA clone IMAGE3542922 5'
12319	25122	38302	1.89	2.0E-64	BE226690.1	EST_HUMAN	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12319	25122	38302	1.89	2.0E-64	8597387	NT	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
12319	25122	38302	1.89	2.0E-64	AF165192.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
2585	33555	28276	1.48	1.0E-64	AF12919.1	NT	gbl-271688_cds1 PROTHYMOSIN ALPHA (HUMAN) contains element MSR1, negative element ;
1794	14829	27807	17.02	1.0E-64	AF1920419.1	EST_HUMAN	Homo sapiens transcription factor (SYN1), mRNA
3924	18081	29004	0.81	1.0E-64	4507334	NT	Homo sapiens transcription factor (SYN1), mRNA
3522	18986	29492	5.73	1.0E-64	AF16978.1	NT	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophycin genes, complete cds, and L-type calcium channel alpha
3596	18943	29582	1.38	1.0E-64	AF128527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3596	18943	29583	1.38	1.0E-64	AF128527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3917	18997	29870	2	1.0E-64	6622529	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10424	23346	36931	0.88	1.0E-64	AA424973.1	EST HUMAN	235908.s1 Soares_jmgreatn_uteru_NHRPU Homo sapiens cDNA clone IMAGE:48597.3
12288	23104	2821	2.03	1.0E-44	AA103442.2	NT	Homo sapiens chromosome 21 segment HS21048
2234	12397	28231	1.84	9.0E-45	X82211.1	NT	H sapiens DNA for endogenous retroviral like element
2234	12397	28232	1.84	9.0E-45	X82211.1	NT	H sapiens DNA for endogenous retroviral like element
11833	24745		33.25	9.0E-45	BF330976.1	EST HUMAN	GV42410257.0811695-571-403 B10357 Homo sapiens cDNA
11837	24720	38905	7.27	8.0E-35	AB26244.1	EST HUMAN	end907.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2918005.3 similar to
10515	23437	38938	2.13	7.0E-45	BC31653.1	EST HUMAN	SV-FL21 HUMAN-146778 6068 B10658 Homo sapiens cDNA
10515	23437	38938	2.13	7.0E-45	BC31653.1	EST HUMAN	GV2-B10655-240405-162-322 B10658 Homo sapiens cDNA
10515	23437	38938	2.13	7.0E-45	AV121848.1	EST HUMAN	AV721888 HTB Homo sapiens cDNA clone HTB2C08.5
1938	14692		12.23	6.0E-45	AA550926.1	EST HUMAN	186810.1 NCL CGAP P111 Homo sapiens cDNA clone IMAGE:396379 similar to ge-K00002.605
6721	18777	33956	0.87	8.0E-45	AA530862.1	EST HUMAN	1857807.51 NCL CGAP P18 Homo sapiens cDNA clone IMAGE:564557
9098	22054	35468	2.49	8.0E-45	AW083232.1	EST HUMAN	X67309.s1 NCL CGAP CG01 Homo sapiens cDNA clone IMAGE:268346.3 similar to TR-063308 Q83309
9355	22330	35759	4.18	6.0E-45	AA427278.1	EST HUMAN	LONG INTERSPERSED REPEITIVE DNA CONTAINING 7 ORF.3, contains 1.1 k2.11 repetitive element;
9355	22330	35760	4.18	6.0E-45	AA427278.1	EST HUMAN	236308.s1 Soares_spld_fovs_N23145 Sw Homo sapiens cDNA clone IMAGE:173147.3
9429	22393	35832	1.08	6.0E-45	AB05314.1	EST HUMAN	236308.s1 Soares_spld_fovs_N23145 Sw Homo sapiens cDNA clone IMAGE:173147.3
9429	22393	35833	1.08	6.0E-45	AB05314.1	EST HUMAN	4718035.x1 NCL CGAP Bm28 Homo sapiens cDNA clone IMAGE:1750428.3
11220	24173	37699	2.59	6.0E-45	BF367616.1	EST HUMAN	4718035.x1 NCL CGAP Bm28 Homo sapiens cDNA clone IMAGE:1750428.3
11378	24325	37694	1.51	6.0E-45	BF400235.1	EST HUMAN	602150.468F1 NHR_MGC_53 Homo sapiens cDNA clone IMAGE:393277.5
11625	24708	36531	1.8	6.0E-45	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
632	13697	26617	1.92	5.0E-45	AF094804.1	NT	Homo sapiens KEX3 protein mRNA, partial cds
1355	14590	27559	1.22	5.0E-45	7861951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1355	14590	27560	1.22	5.0E-45	7861951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2164	15180	28200	1.51	5.0E-45	AB033708.1	NT	Homo sapiens IPAD colony10 mRNA for peptidylarginine deiminase type I, complete cds
3269	16323	29245	2.13	5.0E-45	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase 1-3) (USP13) mRNA
3269	16323	29246	2.13	5.0E-45	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase 1-3) (USP13) mRNA
7052	20074	33381	1.18	5.0E-45	4504008	NT	Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA
10833	23754	37853	1.28	5.0E-45	AF090688.1	NT	Multiple sclerosis associated retrovirus polyprotein 1 (RFD1), mRNA
1895	13288	26224	2.33	4.0E-45	AL120116.1	EST HUMAN	DKFZP181G108.11 181 (synonym: hamy2) Homo sapiens cDNA clone DKFZP781G108.5
747	13808	26748	1.29	4.0E-45	AL209468.1	EST HUMAN	qm14601.x1 Soares_jlecenta_gushweka_2NHP869W Homo sapiens cDNA clone IMAGE:1851800.3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13808	28749	1.29	4.0E-65	A1264468.1	EST_HUMAN	gm46d1.x1 Scores: placenta, 20kweeks_20kweeks_Homo sapiens cDNA clone IMAGE:189160.3'
1080	14124	27077	1.51	4.0E-65	4838735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FMR1), mRNA
1482	14151	27489	15.65	4.0E-65	4509586	NT	Homo sapiens ribosomal protein L34 (RPL34), mRNA
3071	17011	28925	0.97	4.0E-65	A15603185.1	EST_HUMAN	RC2-BN033-16020-013-03 BN033 Homo sapiens cDNA
8279	18351	32595	4.17	4.0E-65	A8030983.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
8279	19351	32595	4.17	4.0E-65	A8030983.1	NT	Homo sapiens oyster binding protein-related protein 3 (ORP3) mRNA, complete cds
7289	20351	33595	0.62	4.0E-65	A17008372.1	NT	Human cabitrin-2 gene, exons 10 and 11, and 1' and 3' UTR repeats
7324	20395	33638	0.84	4.0E-65	M18676.1	NT	Homo sapiens hypothetical protein FLJ2287 (FLJ2287), mRNA
7429	20395	33748	2.48	4.0E-65	11545780	NT	Human 3' 5' cyclic nucleotide phosphodiesterase (HSPDCE3A) mRNA, partial cds
7797	20749	34124	0.58	4.0E-65	U40372.1	NT	Human 3' 5' cyclic nucleotide phosphodiesterase (HSPDCE3A) mRNA, partial cds
7797	20749	34125	0.58	4.0E-65	U40372.1	NT	Human MAP kinase kinase 2 (MAPKK2) mRNA, complete cds
8718	21055	34452	0.81	4.0E-65	U36956.1	NT	Homo sapiens mit (chicken)-like 2 (MEL2), cDNA
8714	21144	34549	0.78	4.0E-65	5453795	NT	Homo sapiens mit (chicken)-like 2 (MEL2), cDNA
8714	21144	34550	0.78	4.0E-65	5453795	NT	Homo sapiens mit (chicken)-like 2 (MEL2), cDNA
9501	22485	35903	1.34	4.0E-65	11428127	NT	Homo sapiens Janus kinase 2 (6 protein, tyrosine kinase) (JAK2), mRNA
10945	23865		2.65	4.0E-65	AJ27546.2	NT	Homo sapiens WEE1, gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
11301	24251	37777	2.99	4.0E-65	AJ738704.1	EST_HUMAN	AJ738704.08 Homo sapiens cDNA clone GBCCE05.5'
11434	24378	37918	6.02	4.0E-65	A1118463.1	NT	Homo sapiens PRK1474 mRNA, complete cds
12606	14124	27077	1.76	4.0E-65	4838735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FMR1), mRNA
13091	13390	26224	1.6	4.0E-65	A112341.1	EST_HUMAN	DKFZ791G105.1T.761 (synonym: henn2) Homo sapiens cDNA clone DKFZ791G105.5'
97	13214	28139	3.16	3.0E-65	5031978	NT	Homo sapiens pta-8-cell colony-enhancing factor (PEEF) mRNA
98	13214	28139	6.32	3.0E-65	5031978	NT	Homo sapiens pta-8-cell colony-enhancing factor (PEEF) mRNA
1226	13519		22.15	3.0E-65	U76923.1	NT	H sapiens HZF5 mRNA for zinc finger protein
1840	14897	27866	1.7	3.0E-65	A0008921.1	EST_HUMAN	02303.x1 Scores: testis, NHT Homo sapiens cDNA clone IMAGE:198173.3' similar to contains element
3053	16951	28929	0.74	3.0E-65	D87078.2	NT	MSR1 repetitive element
3263	18343	29264	0.65	3.0E-65	4844590	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3794	16776	29988	1.61	3.0E-65	A000692.1	EST_HUMAN	Homo sapiens laminin, beta 1 (LAMB1), mRNA
4679	17700	30598	1.33	3.0E-65		NT	02303.x1 Scores: testis, NHT Homo sapiens cDNA clone IMAGE:198173.3' similar to contains element
10439	23351	36835	1.42	3.0E-65	BE797368.1	EST_HUMAN	MSR1 repetitive element
						NT	Homo sapiens tRNA-GTPase activating protein (GAP and centrosome-associated) (GAPCEN), mRNA
						EST_HUMAN	601475696F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE388495.5'

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
17119	23916	37403	8.57	3.0E-65	AA430006.1	EST_HUMAN	IG25506.1 Source, testis, NIH, Homo sapiens cDNA clone IMAGE:781042 5'
3415	16465	26284	6.08	2.0E-65	BF680284.1	EST_HUMAN	IG2115052F1 NIH, JGCG, 38 Homo sapiens cDNA clone IMAGE:429566 5'
6866	19743		4.55	2.0E-65	BE28373.1	EST_HUMAN	IG0119385F1 NIH, JGCG, 7 Homo sapiens cDNA clone IMAGE:353741 5'
7339	20310	33653	27.84	2.0E-65	BF578622.1	EST_HUMAN	IG2114335F1 NIH, JGCG, 81 Homo sapiens cDNA clone IMAGE:429526 5'
9197	22163	35592	1.26	2.0E-65	AK024483.1	EST_HUMAN	Homo sapiens mRNA for L-200556 protein, partial cds
9197	22163	35593	1.26	2.0E-65	AK024483.1	NT	Homo sapiens mRNA for L-200556 protein, partial cds
12288	25066					EST_HUMAN	EST1178195 Ocan sarcoma (HOC) cell line Homo sapiens cDNA 5' end similar to endogenous
12708	25726		2.76	2.0E-65	AA307604.1	EST_HUMAN	retrovirus
3402	13611	26530	1.96	2.0E-65	BF260596.1	EST_HUMAN	IG0185403F1 NIH, JGCG, 37 Homo sapiens cDNA clone IMAGE:407399 5'
2638	15073	28035	1.54	1.0E-65	7687408	NT	Homo sapiens putative Rab3 GDP/GTP exchange factor homologue (RABEX3), mRNA
3389	17634	28031	1.07	1.0E-65	AB040948.1	NT	Homo sapiens mRNA for KIAA1913 protein, partial cds
4023	17391	28032	0.61	1.0E-65	BE46861.1	EST_HUMAN	IG244693.1 NCI, COGAP, GCB Homo sapiens cDNA clone IMAGE:320688 3'
4234	17265	28032	1.71	1.0E-65	4540082	NT	Homo sapiens giprotein-4 (GPC4) mRNA
4234	17265	30147	2.4	1.0E-65	AI102804.1	EST_HUMAN	Homo sapiens giprotein-4 (GPC4) mRNA
4234	17265	30148	2.4	1.0E-65	AI102804.1	EST_HUMAN	Homo sapiens giprotein-4 (GPC4) mRNA
5395	18463	31332	0.54	1.0E-65	BE206569.1	EST_HUMAN	IG0403702-1 T0405-194-69 B10702 Homo sapiens cDNA
5395	18463	31333	0.54	1.0E-65	BE206569.1	EST_HUMAN	IG0403702-1 T0405-194-69 B10702 Homo sapiens cDNA
5554	18851	31595	0.61	1.0E-65	AI243734.1	EST_HUMAN	IG0807.21 Source, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR-007623
5597	21865	34630	5.47	1.0E-65	AV632491.1	EST_HUMAN	QV2510385-140200-04212 S10288 Homo sapiens cDNA
5597	21865	34631	5.47	1.0E-65	AV632491.1	EST_HUMAN	QV2510385-140200-04212 S10288 Homo sapiens cDNA
5623	21861	35006	2.16	1.0E-65	BE732118.1	EST_HUMAN	IG01569124F1 NIH, JGCG, 21 Homo sapiens cDNA clone IMAGE:3841012 5'
5623	21861	35010	2.16	1.0E-65	BE732118.1	EST_HUMAN	IG01569124F1 NIH, JGCG, 21 Homo sapiens cDNA clone IMAGE:3841012 5'
5692	21830	35050	2.14	1.0E-65	AI14286.1	EST_HUMAN	IG0141295 THYROT1 Homo sapiens cDNA clone THYRO1000356 5'
5692	21830	35051	2.14	1.0E-65	AI14286.1	EST_HUMAN	IG0141295 THYROT1 Homo sapiens cDNA clone THYRO1000356 5'
9192	22150	35598	1.84	1.0E-65	BF686707.1	EST_HUMAN	IG2116239F1 NIH, JGCG, 36 Homo sapiens cDNA clone IMAGE:4293313 5'
9874	22933	35769	2.25	1.0E-65	AI102904.1	EST_HUMAN	IG0126040 NT-29P-2 Homo sapiens cDNA clone NT-29P-2004714 5'
9874	22933	35770	2.25	1.0E-65	AI102904.1	EST_HUMAN	IG0126040 NT-29P-2 Homo sapiens cDNA clone NT-29P-2004714 5'
9886	22951		2.52	1.0E-65	11431894	NT	Homo sapiens insulin-like growth factor receptor, type 1 (IGF1R), mRNA
9882	22951	36138	5.48	1.0E-65	AI191716.1	EST_HUMAN	IG01602.21 Source, testis, NIH, Homo sapiens cDNA clone IMAGE:1733460 3' similar to gp-25561 ZINC
10455	23170	36659	1.26	1.0E-65	AI151581.1	EST_HUMAN	IG013780 NT-29P3 Homo sapiens cDNA clone NT-29P3-2004016 5'
10685	23591	37055	0.54	1.0E-65	AI006569.1	EST_HUMAN	IG015424.1 Source, gland, NIH, JGCG, Homo sapiens cDNA clone IMAGE:382734 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meat Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10935	23855	37371	1.02	1.0E-06	AB207832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11011	23970	37501	7.57	1.0E-06	N26167.1	NT	Human p145 factor 4 variation 1 (PF145) gene, complete cds
11131	24091	37620	10.37	1.0E-06	4509060	NT	Homo sapiens thymosin protein L76 (RPL7A) mRNA
11465	24408	37656	2.43	1.0E-06	BF498707.1	EST_HUMAN	00212029P1 NIH_XLOC_59 Homo sapiens cDNA clone IMAGE428319.5
11545	24488	38040	1.89	1.0E-06	AB21017.1	EST_HUMAN	187606.x1 NCL CGAG_C08 Homo sapiens cDNA clone MAGE23719.3 similar to gbl.15533_maf
12269	25106	38140	3.13	1.0E-06	11489041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 (PACAPAR1) HUMAN
12391	25168	31615	7.2	1.0E-06	1148322	NT	Homo sapiens TNF-inhibitor protein CG121 (CT21) mRNA
12759	25427	37620	1.87	1.0E-06	1148248	NT	Homo sapiens cadherin EGF-Like domain 1 (CELSR1) mRNA
72	13160	26110	0.94	9.0E-06	AL160311.1	NT	Homo sapiens gene mapping to chromosome 22
72	13160	25111	0.94	9.0E-06	AL160311.1	NT	Novel human gene mapping to chromosome 22
1336	14391	27591	0.83	9.0E-06	6031863	NT	Homo sapiens SRS proteinase-associated pad1 homolog (POT1) mRNA
1336	14391	27592	0.83	9.0E-06	6031863	NT	Homo sapiens SRS proteinase-associated pad1 homolog (POT1) mRNA
1480	14513	29583	0.74	9.0E-06	AF7268.1	NT	Human transposon-like element, partial
3916	19356	29686	0.74	9.0E-06	U72363.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3916	19356	29686	0.74	9.0E-06	U72363.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3719	17739	30831	0.73	9.0E-06	AL137033.1	NT	Novel human gene mapping to chromosome X
4717	17737	30528	1.58	8.0E-06	AA24204.1	EST_HUMAN	z98055.1 Soares, NHHPUL_ST Homo sapiens cDNA clone IMAGE767048.5
11676	24641		1.48	7.0E-06	BE094410.1	EST_HUMAN	RCA-BT0311-141192-01-H06 BT0311 Homo sapiens cDNA
4393	17421	30304	1.01	9.0E-06	AB24653.1	EST_HUMAN	wn57907.x1 NCL_LGAP_Lu10 Homo sapiens cDNA clone MAGE2446987.3 similar to WPF15G6-4A
4393	17421	30305	1.01	9.0E-06	AB24653.1	EST_HUMAN	CE18595
4393	17421	30306	1.01	9.0E-06	AB24653.1	EST_HUMAN	wn57907.x1 NCL_LGAP_Lu10 Homo sapiens cDNA clone MAGE2446987.3 similar to WPF15G6-4A
4393	17421	30307	1.01	9.0E-06	AB24653.1	EST_HUMAN	CE18595
8777	21744	30308	0.82	6.0E-06	BE17653.1	EST_HUMAN	wn57907.x1 NCL_LGAP_Lu10 Homo sapiens cDNA clone MAGE2446987.3 similar to WPF15G6-4A
11493	24436	37652	4.16	9.0E-06	BE09181.1	NT	H sapiens mRNA for thymosin protein L31
1366	14403	27375	1.84	5.0E-06	BE094410.1	EST_HUMAN	RCA-BT0311-141192-01-H06 BT0311 Homo sapiens cDNA
8048	22593	30541	15.84	5.0E-06	11420657	NT	Homo sapiens tyrosine kinase receptor binding protein (IKB3) mRNA
791	19350	26797	1.39	4.0E-06	6078818	EST_HUMAN	Novel human gene mapping to chromosome X
1790	14779	27764	1.15	4.0E-06	AW897798.1	EST_HUMAN	Novel human gene mapping to chromosome X
2288	15301	28326	1.84	4.0E-06	AB2211.1	NT	Human DNA topoisomerase II (HMG2) mRNA
2481	15405		2.82	4.0E-06	AJ22394.1	NT	Homo sapiens beta-galactosidase (HMG2) mRNA
4823	17840		3.19	4.0E-06	9333467	NT	Human integrase retrovirus, complete genome

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Probe SEQ ID NO.	Exon SEQ ID NO.	Off Seq ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11838	24721	38306	6.1	3.0E-66	5458946	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B59), alpha isoform (PPP2R5A), mRNA
13109	25529	31947	1.38	3.0E-66	11417862	NT	Homo sapiens calcineurin binding protein 1 (CABP330), mRNA
53	13173	20062	1.64	2.0E-66	7957334	NT	Homo sapiens Mitochondrial NDK-related kinase (MINK), mRNA
53	13173	20063	1.84	2.0E-66	7957334	NT	Homo sapiens Mitochondrial NDK-related kinase (MINK), mRNA
422	13117	20015	0.7	2.0E-66	4056524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L), mRNA, and translated products
422	13117	20016	0.7	2.0E-66	4056524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L), mRNA, and translated products
1643	14898	27667	2.18	2.0E-66	AL103012	NT	Homo sapiens chromosome 21 segment H53C101
2241	15235	26278	2.35	2.0E-66	AF035581	NT	Homo sapiens pseudogene for the low density lipoprotein receptor
2241	15235	26279	2.35	2.0E-66	AF035581	NT	Homo sapiens pseudogene for the low density lipoprotein receptor
3432	16578	20501	0.39	2.0E-66	8822369	NT	Homo sapiens Myotubularin protein FL20309 (FL20309), mRNA
3777	16519	20727	0.9	2.0E-66	AL117233	NT	Novel human gene mapping to chromosome 1
4895	17708	30564	36.82	2.0E-66	AI133297	2	Homo sapiens HLA-B gene for human leukocyte antigen B
4895	17708	30565	36.82	2.0E-66	AI133297	2	Homo sapiens HLA-B gene for human leukocyte antigen B
5914	19000	32161	0.82	2.0E-66	AW166854	1	ES1306930 IMAGE resequences, MAGI Homo sapiens cDNA
5914	19000	32162	0.82	2.0E-66	AW166854	1	ES1306930 IMAGE resequences, MAGI Homo sapiens cDNA
9109	22105	35565	2.86	2.0E-66	N44548.1	EST_HUMAN	W59602.1 Soares, multiple sclerosis, ZNF418P Homo sapiens cDNA clone IMAGE:277628 5'
12514	25041		2.91	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phases expressed 1 (GTSE1), mRNA
2004	15903	29865	1.98	1.0E-66	AV171817	1	AV171817 DOB Homo sapiens cDNA clone DCBADC07 5'
2004	15903	29866	1.98	1.0E-66	AV171817	1	AV171817 DOB Homo sapiens cDNA clone DCBADC07 5'
4412	15903	29866	3.59	1.0E-66	AV171817	1	AV171817 DOB Homo sapiens cDNA clone DCBADC07 5'
4412	15903	29866	3.59	1.0E-66	AV171817	1	AV171817 DOB Homo sapiens cDNA clone DCBADC07 5'
5455	18094	37168	5.82	1.0E-66	BF07308.1	EST_HUMAN	60213296F1 NH ₂ MG-81 Homo sapiens cDNA clone IMAGE:728418 5'
5875	18094	37168	5.82	1.0E-66	BF07308.1	EST_HUMAN	60213296F1 NH ₂ MG-81 Homo sapiens cDNA clone IMAGE:728418 5'
5875	18094	37168	5.82	1.0E-66	BF07308.1	EST_HUMAN	60213296F1 NH ₂ MG-81 Homo sapiens cDNA clone IMAGE:728418 5'
7125	20798	33394	1.09	1.0E-66	BF23823.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
8801	21798	33592	1.2	1.0E-66	AA668868.1	EST_HUMAN	RC5-ENG193-010000-004-006 BN0188 Homo sapiens cDNA
9781	22722	39176	0.7	1.0E-66	AA018828.1	EST_HUMAN	aa00604.1 NC ₂ CGAP CG81 Homo sapiens cDNA clone IMAGE:827282 3'
10737	23059	37153	0.9	1.0E-66	AV148749	1	AV148749 NPC Homo sapiens cDNA clone NPC03V005 5'
10737	23059	37153	0.9	1.0E-66	AV148749	1	AV148749 NPC Homo sapiens cDNA clone NPC03V005 5'
10893	23913	37429	0.41	1.0E-66	BE049561	EST_HUMAN	h047602.2t Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:304863 3'

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (%) HIT EAST E Value	Top HIT Accession No.	Top HIT Database Source	Top HIT Descriptor
11290	24240	37767	2.47	1.0E-96	AF111697.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cDNA clone, complete cds, and unknown gene
11653	24795	38322	1.89	1.0E-98	AW098744.1	EST_HUMAN	HS180020 IMAGE retrotransposon, MAGU Homo sapiens cDNA
12398	26170		2.75	9.0E-67	11416177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
390	13495	39426	2.51	7.0E-67	AW192232.1	EST_HUMAN	hs176022.1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gh1437104 ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
1362	14415	27386	1.29	7.0E-67	AF383418.1	EST_HUMAN	EST198872 Testis 1 Homo sapiens cDNA 5' and similar to C. elegans hypothetical protein, csmid ZK355
1558	14590	27951	1.19	7.0E-67	W63947.1	EST_HUMAN	ZK550371 Scoring, fetal, liver, spleen, INFLS 5' Homo sapiens cDNA clone IMAGE:218049 5'
1558	14590	27952	1.19	7.0E-67	W63947.1	EST_HUMAN	ZK550371 Scoring, fetal, liver, spleen, INFLS 5' Homo sapiens cDNA clone IMAGE:218049 5'
2048	15007	28086	1.02	7.0E-67	7687243	NT	Homo sapiens insulin 1,3,4,4-tetrasubstituted kinase (INS1), mRNA
2048	15007	28087	1.02	7.0E-67	7687243	NT	Homo sapiens insulin 1,3,4,4-tetrasubstituted kinase (INS1), mRNA
2621	13495	28405	2.76	7.0E-67	AW192232.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
6109	19273	32537	0.98	7.0E-67	01090696	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6401	19469	32716	1.82	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6401	19469	32717	1.82	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6885	19937	33233	1.14	7.0E-67	4885564	NT	Homo sapiens ATPase, H ⁺ translocating, lysosomal (vesicular proton pump) non-catalytic accessory protein 1A (110/1160) (ATP5HA), mRNA
7850	20836	34216	1.13	7.0E-67	11416212	NT	Homo sapiens mitochondrial carrier family protein (LOC56972), mRNA
7850	20836	34217	1.13	7.0E-67	11416212	NT	Homo sapiens mitochondrial carrier family protein (LOC56972), mRNA
6969	21834	35055	0.99	7.0E-67	4597332	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6284	22250	35681	0.73	7.0E-67	10835044	NT	Homo sapiens retinohyaline dehydrogenase 2 (RALDH2), mRNA
11995	24862	38455	2.45	7.0E-67	U82466.1	NT	Human cytochrome oxidase subunit VIIa (COX6A1P) pseudogene, complete cds
12189	25019	38919	1.62	7.0E-67	11430469	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12189	25019	38920	1.62	7.0E-67	11430469	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12839	25223	37179	1.09	7.0E-67	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
13009	26591		1.44	7.0E-67	11421827	NT	H sapiens calcium channel, voltage-dependent, alpha 2delta subunit 1 (CACNA2D1), mRNA
591	13381	26546	1.19	6.0E-67	W68965.1	NT	H sapiens mRNA for acyl-CoA carboxylase
796	13555	26902	1.7	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1278	14313	27274	2.06	6.0E-67	Y14320.1	NT	Homo sapiens PMP39 gene, exons 3,4,5,6 & 7
3183	16238	29156	1.16	6.0E-67	4995434	NT	Homo sapiens rethoblastoma 1 (including osteosarcoma) (RET1) mRNA
3431	16487	29414	1.33	6.0E-67	4907332	NT	Homo sapiens Syngap II (SYNS) mRNA, and transcribed products
3431	16487	29415	1.33	6.0E-67	4907332	NT	Homo sapiens Syngap III (SYNS) mRNA, and transcribed products

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4162	17163	30069	0.79	6.0E-47	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4162	17163	30070	0.79	6.0E-47	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4734	17754	30647	3.55	6.0E-47	7857020	NT	Homo sapiens DKFZP454P211 protein (DKFZP454P211), mRNA
4734	17754	30648	3.55	6.0E-47	7857020	NT	Homo sapiens DKFZP454P211 protein (DKFZP454P211), mRNA
5242	18250	31121	0.59	6.0E-47	AF016884.1	NT	Homo sapiens B-ATF gene, complete cds
5242	18250	31122	0.59	6.0E-47	AF016884.1	NT	Homo sapiens B-ATF gene, complete cds
3235	18250	25212	2.22	5.0E-47	AF096660.1	NT	Homo sapiens 1 cell receptor beta locus, TORBY753A2 to TORBY753A2 region
11328	24279		13.19	5.0E-47	BC010038.1	EST_HUMAN	PM3-BN0176-10000-0071-g04 BN0176 Homo sapiens cDNA
1331	14365	27335	2.25	4.0E-47	BC0816.1	EST_HUMAN	PM3-BN0176-10000-0071-g04 BN0176 Homo sapiens cDNA
8345	21324	34750	0.85	4.0E-47	A173032.1	EST_HUMAN	Q26655.x3 NCL CGAP_1083 Homo sapiens cDNA clone IMAGE:1482288 3' similar to SW_253A_HUMAN
8745	21653		1.18	4.0E-47	BF357321.1	EST_HUMAN	Q60790 ZINC FINGER PROTEIN SJA-1
11403	24347		1.46	4.0E-47	AAT14284.1	EST_HUMAN	NC049017.1 NCL CGAP_351 Homo sapiens cDNA clone IMAGE:128472 3' similar to TR_O10385 O10385
2824	13959	20520	1.18	3.0E-47	A433378.1	EST_HUMAN	XP-010-OUTP48-80 PROTEIN 1, cDNA 5' and 3' ends
4723	17743	30634	2.52	3.0E-47	AY66156.1	EST_HUMAN	XP-010-OUTP48-80 PROTEIN 1, cDNA 5' and 3' ends
4733	17773		1.08	3.0E-47	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
8522	21490	34905	1.15	3.0E-47	BF190988.1	EST_HUMAN	H0195.v1 NCL CGAP_1081 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW_RHOP_MOUSE
11598	24528		15.35	3.0E-47	A4627874.1	EST_HUMAN	Q61983 GTP-RHO BINDING PROTEIN 1.1
190	13291	26217	0.97	2.0E-47	BC548354.1	EST_HUMAN	om18007.at Source: NCL CGAP_351 Homo sapiens cDNA clone IMAGE:147355 3'
846	13802	26860	6.48	2.0E-47	AW819405.1	EST_HUMAN	om18007.at Source: NCL CGAP_351 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW_RHOP_MOUSE
1107	14151		1.26	2.0E-47	AF187460.1	NT	CE09817.1
1801	14025	27922	1.26	2.0E-47	BC30307.1	EST_HUMAN	QV4-S10234-18108-037-008 S10234 Homo sapiens cDNA
1901	14925	27923	1.26	2.0E-47	BC30307.1	EST_HUMAN	QV4-S10234-18108-037-008 S10234 Homo sapiens cDNA
2281	15295	28291	0.93	2.0E-47	BE303037.1	EST_HUMAN	Homo sapiens double stranded RNA activated protein kinase (PKA) gene, exon 2a, 2, 3, and 4
2291	15295	28292	1.18	2.0E-47	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2603976 5' similar to TR_O94892 O94892
2394	15401	28426	0.61	2.0E-47	AF030961.1	NT	KIAA0788 PROTEIN ;
2438	15445	28465	1.36	2.0E-47	4759795	NT	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2603976 5' similar to TR_O94892 O94892
3481	16527	29452	3.78	2.0E-47	AA62795.1	EST_HUMAN	KIAA0788 PROTEIN ;
4027	17005	28665	2.7	2.0E-47	AL163300.2	NT	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2603976 5' similar to TR_O94892 O94892

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Table 4
Antibodies Expressed in Bone Marrow

[illegible]

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
820	13678	29827	4.72	5.0E-48	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	13678	29826	4.72	5.0E-48	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2791	16783	26769	1.28	5.0E-48	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3182	16218	20133	3.06	5.0E-48	AB027852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4210	17239		0.8	5.0E-48	4828667	NT	Homo sapiens retinol-binding protein 2 (RBP2) mRNA
4516	17543	30429	0.76	5.0E-48	AL157643.1	EST - HUMAN	DKFZ470207.1 J147 (synonym: h1c1) Homo sapiens cDNA clone DKFZ470207.1
6989	19941	33236	0.67	5.0E-48	7018512	NT	Homo sapiens RUS3A, interacting protein (RUS3) like 1 (RUS3L1), mRNA
8889	19941	33237	0.67	5.0E-48	7018512	NT	Homo sapiens RUS3A, interacting protein (RUS3) like 1 (RUS3L1), mRNA
2532	15535	25555	0.84	4.0E-48	11427388	NT	Homo sapiens RUS3A, interacting protein (RUS3) like 1 (RUS3L1), mRNA
2532	15535	25555	0.84	4.0E-48	11427388	NT	Homo sapiens RUS3A, interacting protein (RUS3) like 1 (RUS3L1), mRNA
3011	18026		7.83	4.0E-48	PD4408	SWISSPROT	Homo sapiens RUS3A, interacting protein (RUS3) like 1 (RUS3L1), mRNA
6075	21198	32363	0.67	4.0E-48	AF127033.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
8639	21198	32363	0.67	4.0E-48	AF127033.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
8639	21198	32363	0.67	4.0E-48	AF127033.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
7046	21837	34273	0.72	4.0E-48	7881883	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSPG1), mRNA
8325	22240	35793	5.91	4.0E-48	DS4470.2	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSPG1), mRNA
8325	22240	35793	5.91	4.0E-48	DS4470.2	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSPG1), mRNA
9533	24268	39444	2.83	4.0E-48	AB040818.1	NT	Homo sapiens mRNA for KIAA0148 protein, partial cds
11346	24268	39444	2.83	4.0E-48	AB040818.1	NT	Homo sapiens mRNA for KIAA0148 protein, partial cds
11346	24268	39444	2.83	4.0E-48	AB040818.1	NT	Homo sapiens mRNA for KIAA0148 protein, partial cds
3673	16718	26930	1.55	4.0E-48	4502382	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
3673	16718	26930	1.55	4.0E-48	4502382	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
5209	18303	31164	0.93	3.0E-48	AF236952.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
8812	21195		5.47	3.0E-48	AI342323.1	EST - HUMAN	q3802.x1 Sueres, fugal, lung, NHL, 19W Homo sapiens cDNA clone IMAGE:1950287.3 similar to contains
10866	23788	37286	2.01	3.0E-48	AF26784.1	EST - HUMAN	THRL2 THR repetitive element
13012	25725		1.99	3.0E-48	AW03485.1	EST - HUMAN	HSPD16718 IM3 Homo sapiens cDNA clone c300023D9
2873	18321		27.5	2.0E-48	DD0322.1	NT	QY1-DT072-01020-056-106 DT072 Homo sapiens cDNA
4095	17092	29897	0.75	2.0E-48	BEF19768.1	EST - HUMAN	Glicetulus longicaudatus mRNA for EF-1 alpha, complete cds
4708	17729	30825	1.86	2.0E-48	AB00891.1	NT	HYPOHETICAL 88.8 KD PROTEIN
7099	20081		9.21	2.0E-48	R40098.1	EST - HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
7285	20020	33299	4.51	2.0E-48	BF03516.1	EST - HUMAN	Yp3gdp1.1 Saccharomyces infant strain TNB Homo sapiens cDNA clone IMAGE:34868.3
7425	20392		0.91	2.0E-48	1162373	NT	BM145894F1 TNH, JMG, 86 Homo sapiens cDNA clone IMAGE:382034.5
							Homo sapiens UTP-4-acyl-alpha-D-glucosaminyl-polypeptide 4-acyl-galactosaminyltransferase 6 (GALNACT-1B) (GALNT1), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7586	20556	33918	0.81	2.0E-48	BF338746.1	EST_HUMAN	IL3-CT0684-18000-279-401 CT0634 Homo sapiens cDNA
6301	22286	35908	0.97	2.0E-48	Q93859	SWISSPROT	FORMIN 4 (LIMB DEFORMITY PROTEIN)
80	13196	28120	0.78	1.0E-48	4503222	NT	Homo sapiens meningioma (disrupted in balanced translocation) T (MNT), mRNA
298	13390	28318	17.84	1.0E-48	AW619405.1	EST_HUMAN	QV4-CT0234-181199-097-005 S10234 Homo sapiens cDNA
2263	15277	28301	1.27	1.0E-48	AB011148.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2263	15277	28301	1.27	1.0E-48	AB011148.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2767	15756	28781	1.04	1.0E-48	AW441832.1	EST_HUMAN	UHH-B03-alc-01-01-01 NCI Q03AP_S005 Homo sapiens cDNA clone IMAGE362344 5'
4037	17075	28974	1.01	1.0E-48	BE269032.1	EST_HUMAN	00177002P7.NH.JGCC_17 Homo sapiens cDNA clone IMAGE362344 5'
5069	18076	30957	0.90	1.0E-48	AW997443.1	EST_HUMAN	041717.AT Source_NFL_1_GENC_S1 Homo sapiens cDNA clone IMAGE148018 3'
5395	19498	31378	1.13	1.0E-48	7023239	NT	Homo sapiens cell recognition molecule Casp2 (KIA00865), mRNA
7338	20360	34270	0.98	1.0E-48	11430776	NT	Homo sapiens actinin-5/SMO-specific protease (SERP-1), mRNA
11188	24103	37884	1.48	1.0E-48	11418855	NT	Homo sapiens phosphoprotein 75 (PDE7B), mRNA
11350	24268	37935	3.49	1.0E-48	11418869	NT	Homo sapiens phosphoprotein 75 (PDE7B), mRNA
11350	24268	37935	3.49	1.0E-48	11418869	NT	Homo sapiens phosphoprotein 75 (PDE7B), mRNA
11531	24588	38113	2.13	1.0E-48	U5318.1	NT	Human protein kinase C subunit beta (PKCB), gene exon 4-5
11531	24588	38113	2.13	1.0E-48	U5318.1	NT	Human protein kinase C subunit beta (PKCB), gene exon 4-5
11675	24862	39448	1.73	1.0E-48	11418431	NT	Homo sapiens CGL-18 protein (LGG51832), mRNA
11763	24862	39448	1.73	1.0E-48	11418431	NT	Homo sapiens CGL-18 protein (LGG51832), mRNA
12700	31168	28120	2.19	1.0E-48	4503222	NT	Homo sapiens meningioma (disrupted in balanced translocation) T (MNT), mRNA
13005	25698	31419	2.07	1.0E-48	11430400	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13057	25698	31419	1.81	1.0E-48	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
22	13142	29040	5.15	9.0E-60	5031078	NT	Homo sapiens pre-B cell colony-enhancing factor (PBCE) mRNA
22	13142	29041	5.15	9.0E-60	5031078	NT	Homo sapiens pre-B cell colony-enhancing factor (PBCE) mRNA
10261	14075	27026	0.78	9.0E-60	5031860	NT	Homo sapiens 20S proteasome-associated peptidyl homology (POH1) mRNA
10261	14075	27026	0.78	9.0E-60	5031860	NT	Homo sapiens 20S proteasome-associated peptidyl homology (POH1) mRNA
4155	17185	30074	0.97	9.0E-60	4157857	NT	Homo sapiens v-src murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4179	17209	30092	1.02	9.0E-60	4604010	NT	Homo sapiens glutamate-tryptophan lyase (tryptophan synthetase), regulatory (30.8kD) (GLULR) mRNA
5241	18249	31120	0.83	9.0E-60	AF57177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
11238	24189		5.51	9.0E-60	AU117241.1	EST_HUMAN	AU117241 HEMBAT Homo sapiens cDNA clone HEMBAT1000966 5'
3397	19448		1.77	8.0E-49	AJ237744.1	NT	Homo sapiens RIBR1 gene (partial), exon 12
8467	19552	33802	5.05	7.0E-48	9689572	NT	Homo sapiens actin-related protein 3-isoa (ARP3BETA), mRNA
8106	21185	34574	15.42	8.0E-46	A192764.1	EST_HUMAN	q6201.x1 Source_NHL Lung_NHL19W Homo sapiens cDNA clone IMAGE1743801 3' similar to pBL11066-005 NUCSOMAL PROTEIN L18 (HUMAN).

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe Seq ID NO.	Exon Seq ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8195	21165	34795	18.42	6.0E-09	AI192784.1	EST HUMAN	qez2101.x1 Soares_fetal_lung_NHL-19W Homo sapiens cDNA clone IMAGE:1743807 3' similar to gp-11666 a05 RIBOSOMAL PROTEIN L18 (HUMAN);
9325	22220	35720	1.04	5.0E-09	AA82038.1	EST HUMAN	000603.x1 NO1 CGAP CGST Homo sapiens cDNA clone IMAGE:197280 3'
821	13502		1.27	4.0E-09	AB79350.1	EST HUMAN	wn26111.x1 NO1 CGAP CGST Homo sapiens cDNA clone IMAGE:2831748 3'
9335	23848	32130	1.38	4.0E-09	BE01083.1	EST HUMAN	00734705T1 NIH_XGC_B Homo sapiens cDNA clone IMAGE:3678419 3'
5943	19029	32223	5	4.0E-09	AI764973.1	EST HUMAN	wn57508.x1 NO1 CGAP K1611 Homo sapiens cDNA clone IMAGE:2364919 3' similar to TRC5137
8783	19838	33122	2.77	4.0E-09	AI764973.1	EST HUMAN	085137 AC11-CCO1 THOES12P4-05L Homo sapiens cDNA clone IMAGE:2364919 3' similar to TRC5137
8783	19838	33122	2.77	4.0E-09	AB57732	NT	Homo sapiens least transacting growth factor beta binding protein 2 (LFBP-2) mRNA
9285	22231	33657	0.85	4.0E-09	AJ11654.1	EST HUMAN	Homo sapiens least transacting growth factor beta binding protein 2 (LFBP-2) mRNA
988	13499	28432	3.2	3.0E-09	BE23507.1	EST HUMAN	001161801 NIH_XGC_18 Homo sapiens cDNA clone IMAGE:1096283 3'
614	13970	26595	2.86	3.0E-09	AF227172.1	EST HUMAN	001161801 NIH_XGC_18 Homo sapiens cDNA clone IMAGE:1096283 3'
2388	15394		0.53	3.0E-09	AF227172.1	EST HUMAN	Homo sapiens Smad4 and Olf-interacting zinc finger protein mRNA, partial cds
4818	17839		0.53	3.0E-09	AF227172.1	EST HUMAN	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
5286	17839	38813	0.83	3.0E-09	AF227172.1	EST HUMAN	044804.1 Soares_fetal_liver spleen NHL-S Homo sapiens cDNA clone IMAGE:121016 5'
5314	18330		0.83	3.0E-09	AF227172.1	EST HUMAN	044804.1 Soares_fetal_liver spleen NHL-S Homo sapiens cDNA clone IMAGE:121016 5'
5712	18806	31953	0.54	3.0E-09	U41761.1	NT	Homo sapiens acyltransferase 2, mitochondrial (ACOT2) mRNA
8072	20195		0.59	3.0E-09	AJ277557.1	NT	Human type II L-1 receptor gene, exon 1B
7036	16370	31267	0.6	3.0E-09	U41761.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleoside (dNT-2 gene), exons 1-4
7597	20558	33916	0.82	3.0E-09	AF05703.1	NT	Homo sapiens sperm surface protein (SPS), mRNA
7551	20611	33977	1.52	3.0E-09	U52351.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSO) gene, nuclear gene
7800	20762	34128	8.4	3.0E-09	AF28075.1	NT	encoding mitochondrial protein, complete cds
8715	21693	35111	1.05	3.0E-09	AJ138646.1	EST HUMAN	Homo sapiens TRAF3-binding protein TRBP mRNA, complete cds
9120	22096		1.38	3.0E-09	AA475306.1	EST HUMAN	UI-HB1-4evy-D1-04UI-51 NO1 CGAP Subt Homo sapiens cDNA clone IMAGE:271840 3'
9328	22096	35722	0.5	3.0E-09	AF227172.1	EST HUMAN	ES198807 HSC172 cell II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S16
9788	22709	36164	1.94	3.0E-09	AJ15225.1	NT	Homo sapiens hypochlorite protein HJ2275 (HJ2275) mRNA
8891	22844	36901	59.4	3.0E-09	X06233.1	NT	H1 sapiens mRNA for Nucleocytoplasmic beta-1-4-galactosyltransferase
10188	23113	36907	0.71	3.0E-09	AF227172.1	NT	Human mRNA for calcium-binding protein in macrophage (hMCP-1) macrophage migration inhibitor factor (MIP-related protein)
11003	23999	37463	3.26	3.0E-09	AF227172.1	NT	Homo sapiens SEC10 (S. cerevisiae) like 1 (SEC10L1) mRNA
11190	24148		12.51	3.0E-09	AA475306.1	EST HUMAN	Homo sapiens HSC172 cell II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S16
12300	25111		7.34	3.0E-09	U41761.1	NT	Homo sapiens HSC172 cell II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S16

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NC:	Exon Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
129	13477	28411	1.00	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0555 protein gene, complete cds, and alpha1b protein gene, partial cds
129	13477	28411	1.00	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0555 protein gene, complete cds, and alpha1b protein gene, partial cds
404	13477	28411	4.79	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0555 protein gene, complete cds, and alpha1b protein gene, partial cds
1802	14820	27624	1.48	2.0E-69	BE27657.1	EST_HUMAN	Homo sapiens KIAA0555 protein gene, complete cds, and alpha1b protein gene, partial cds
2890	16916		3.8	2.0E-69	AA431157.1	EST_HUMAN	B01106444F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:330074.5
8900	21598	35289	0.97	2.0E-69	AA114270.1	EST_HUMAN	2w71602.F1 Soares, Jastis, NIH Homo sapiens cDNA clone IMAGE:781682.5
1714	14744	27728	2.89	1.0E-69	AF033768.1	NT	Ratna nonreducing brain specific corticotropin-binding protein CBP80 mRNA, partial cds
5059	18059		0.73	1.0E-69	BE40094.1	EST_HUMAN	0013017284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:363576.5
6168	19243	32474	0.78	1.0E-69	BE002501.1	EST_HUMAN	001676768F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3698932.5
6768	19812	32475	0.78	1.0E-69	BE002501.1	EST_HUMAN	QVQ-1T0010-03T189-045-045-037 T10010 Homo sapiens cDNA
8922	20216	33544	4.09	1.0E-69	AW393998.1	EST_HUMAN	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8922	20216	33544	1.4	1.0E-69	7662283	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8922	20216	33544	1.4	1.0E-69	7662283	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7011	2037	33483	2.78	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7011	2037	33483	2.78	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7059	20307	33336	0.62	1.0E-69	BE331007.1	EST_HUMAN	001276832F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3610314.5
7659	20307	33397	0.62	1.0E-69	BE331007.1	EST_HUMAN	001276832F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3610314.5
10334	23456	36952	4.31	1.0E-69	BE245070.1	EST_HUMAN	Human p15 cell acute lymphoblastic leukemia Bayles-HQSG project/NT CBA Homo sapiens cDNA clone T36AP-2019
10834	23456	36953	4.31	1.0E-69	BE245070.1	EST_HUMAN	Human p15 cell acute lymphoblastic leukemia Bayles-HQSG project/NT CBA Homo sapiens cDNA clone T36AP-2019
10831	23456	37053	1.48	1.0E-69	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
11719	23700	37188	0.83	1.0E-69	BF526428.1	EST_HUMAN	002437768F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4181325.5
11719	23700	37188	2.78	1.0E-69	45049748	NT	Homo sapiens KIAA0716 protein, partial cds
12284	25066	39167	1.89	1.0E-69	BF125887.1	EST_HUMAN	001762002F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025765.5
12284	25331		6.78	1.0E-69	AA006994.1	EST_HUMAN	wf64023.x1 Soares, NPLT, GBC_351 Homo sapiens cDNA clone IMAGE:296930.3 similar to contains Alu repetitive element/contains element MIR repetitive element
2339	15980	28370	1.61	8.0E-70	AA233035.1	EST_HUMAN	nc1341217 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1008023
4401	17428	30314	2.11	8.0E-70	L77598.1	NT	Homo sapiens DGS-3 mRNA, 3' end
1830	14857	27654	2.26	7.0E-70	AA977007.1	EST_HUMAN	008901.x1 NCI_CGAP_Bn28 Homo sapiens cDNA clone IMAGE:2769304.3
1830	14857	27655	2.26	7.0E-70	AA977007.1	EST_HUMAN	008901.x1 NCI_CGAP_Bn28 Homo sapiens cDNA clone IMAGE:2769304.3
1647	14671	27669	1.87	7.0E-70	AA282956.1	EST_HUMAN	2180471 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:713239.5
2078	16095		2.97	7.0E-70	8001688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DCC-IR) mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source
1593	14825	27699	1.56	3.0E-70	BE071798.1	EST_HUMAN
1593	14825	27699	1.56	3.0E-70	BE071798.1	EST_HUMAN
5701	18796	31970	0.83	3.0E-70	11430988	NT
5701	18796	31971	0.83	3.0E-70	11430988	NT
6956	19136	32346	1.1	3.0E-70	AI831976.1	EST_HUMAN
6959	19573	32826	1.27	3.0E-70	BF685283.1	EST_HUMAN
6959	19573	32827	1.27	3.0E-70	BF685283.1	EST_HUMAN
10467	23389	39883	0.55	3.0E-70	BE502973.1	EST_HUMAN
40	13100	29083	2.14	2.0E-70	AF101872.1	NT
590	13793	26680	14.23	2.0E-70	N42181.1	EST_HUMAN
590	13793	26681	14.23	2.0E-70	N42181.1	EST_HUMAN
703	13796	29104	1.38	2.0E-70	AI248895.1	EST_HUMAN
1023	14226	27020	1.23	2.0E-70	8626069	NT
1089	14228	27184	1.73	2.0E-70	7281983	NT
1188	14228	27185	1.73	2.0E-70	7281983	NT
1594	14896	27671	1.53	2.0E-70	A4180093.1	EST_HUMAN
1694	14996	27672	1.53	2.0E-70	A4180093.1	EST_HUMAN
1757	14769	27771	1.79	2.0E-70	AL183292.2	NT
2328	15339	29500	5.47	2.0E-70	AA054010.1	EST_HUMAN
3641	16984	29700	1.05	2.0E-70	H07698.1	EST_HUMAN
3643	16973	29774	0.86	2.0E-70	AL13207.2	NT
4079	17114	30010	5.63	2.0E-70	M09161.1	NT
4221	17260	30135	0.96	2.0E-70	L78810.1	NT
4221	17260	30139	0.96	2.0E-70	L78810.1	NT
5593	16686	31658	9.14	2.0E-70	X72692.1	NT
5593	16686	31659	9.14	2.0E-70	X72692.1	NT
6528	19186	32640	1.1	2.0E-70	AF110105.1	NT
6700	19444	33128	3.84	2.0E-70	D12625.1	NT
8524	19878	33167	11.3	2.0E-70	AF120041.1	NT
<p>Top Hit Description</p> <p>RCO-B10322-071269-011-12 B10522 Homo sapiens cDNA</p> <p>RCO-B10322-071269-011-12 B10522 Homo sapiens cDNA</p> <p>Homo sapiens placophilin 4 (PKP4), mRNA</p> <p>W86003.X1 NCL CGAP_CELT Homo sapiens cDNA clone IMAGE:2389005.3</p> <p>032141661F1 NH MGCC 48 Homo sapiens cDNA clone IMAGE:4302809.5</p> <p>032141661F1 NH MGCC 48 Homo sapiens cDNA clone IMAGE:4302809.5</p> <p>h281192.X1 NCL CGAP_LJ24 Homo sapiens cDNA clone IMAGE:3214119.3</p> <p>Homo sapiens phosphatidylinositol 4-kinase 2B0 (p4K2B0) mRNA, complete cds</p> <p>Y07470.11 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270522.6 similar to SW-620.H1 RAT P26265 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;</p> <p>Y07470.11 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270522.6 similar to SW-620.H1 RAT P26265 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;</p> <p>052101.1 X1 NCL CGAP_Fant Homo sapiens cDNA clone IMAGE:2004913.5</p> <p>Homo sapiens 12S ribosomal protein L220B (L220B) mRNA</p> <p>Homo sapiens KJ431019.3 gene product (KJ431019.3) mRNA</p> <p>Homo sapiens KJ431019.3 gene product (KJ431019.3) mRNA</p> <p>TR-G 041260 G104/1263 D2085.5 ;</p> <p>2549105.1 Singapore HeLa cell c3 897216 Homo sapiens cDNA clone IMAGE:612441.5 similar to</p> <p>TR-G 041260 G104/1263 D2085.5 ;</p> <p>Homo sapiens chromosome 21 segment HS21C002</p> <p>245604.1 Soares retina N24HR Homo sapiens cDNA clone IMAGE:340214.5 similar to SW_GAG_HTL1A</p> <p>P03345 GAG POLYPROTEIN ;</p> <p>Y08004.1 Soares fetal liver spleen 1N6LS Homo sapiens cDNA clone IMAGE:191599.5</p> <p>Novel human gene mapping to chromosome X</p> <p>Human normosule myosin heavy chain-B (MYH10) mRNA, partial cds</p> <p>Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds</p> <p>Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds</p> <p>H sapiens gene for schwanomin (C58)</p> <p>H sapiens gene for schwanomin (C58)</p> <p>Homo sapiens NALP1 mRNA, complete cds</p> <p>Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds</p> <p>Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds</p>						

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Table 4
Single Exon Probe Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8824	19878	33108	11.3	2.0E-70	AF122074.1	NT	Homo sapiens cytoplasmic dyshin intermediate chain 1 mRNA, complete cds
7930	19421	31223	1.44	2.0E-70	11422842	NT	Homo sapiens alpha-1-mannosidase alpha 2,9-sialyltransferase (SIA70), mRNA
7930	20583	33566	0.56	2.0E-70	AF288207.1	NT	Homo sapiens cytoplasmic RNA synthetase mRNA, complete cds, internal very 5' splice
8251	21220	34626	5.38	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-Subunit), exons 4 and 5
8854	21832	34932	0.45	2.0E-70	11423599	NT	Homo sapiens myo-1b-glucosylase, 4-ephe-glucantransferase (glycogen branching enzyme, glycogen storage disease type III) (AGLI), mRNA
9007	21973		0.76	2.0E-70	H47593.1	EST_HUMAN	hp7802.r1 Soares fetal liver spleen, N15.S1 Homo sapiens cDNA clone IMAGE:106882.5
9504	22487	39535	0.95	2.0E-70	11526355	NT	Homo sapiens dyshin p22 subunit (LOC101914), mRNA
10497	23419	39181	1.42	2.0E-70	AF123093.1	NT	Homo sapiens calcium channel gamma 1 subunit protein, partial cds
10953	23983	37386	0.49	2.0E-70	AB033042.1	NT	Homo sapiens myo-1b-glucosylase, 4-ephe-glucantransferase (glycogen branching enzyme, glycogen storage disease type III) (AGLI), mRNA
11408	24352	37884	3.11	2.0E-70	8623420	NT	Homo sapiens dyshin p22 subunit (LOC101914), mRNA
11408	24352	37884	3.11	2.0E-70	8623420	NT	Homo sapiens dyshin p22 subunit (LOC101914), mRNA
11956	24635	38431	11.5	2.0E-70	4933520	NT	Homo sapiens dyshin p22 subunit (LOC101914), mRNA
12037	25321	31788	2.94	2.0E-70	11433460	NT	Homo sapiens dyshin p22 subunit (LOC101914), mRNA
12837	25321	31787	2.94	2.0E-70	11433460	NT	Homo sapiens dyshin p22 subunit (LOC101914), mRNA
3404	16483		3.08	1.0E-70	4807476	NT	Homo sapiens dyshin p22 subunit (LOC101914), mRNA
9835	23579		0.78	1.0E-70	U65794.1	EST_HUMAN	213505.r1 Soares, fetal, liver, spleen, N15.S1 Homo sapiens cDNA clone IMAGE:410024.5
10158	23083		0.84	1.0E-70	AA12282.1	EST_HUMAN	245403.r1 Soares, testis, N1T Homo sapiens cDNA clone IMAGE:79744.5
11281	24231	37757	8.6	1.0E-70	AF175838.1	EST_HUMAN	AV758358 CB Homo sapiens cDNA clone CBGB05.0
9854	19135	32344	7.1	9.0E-71	AF143870.1	EST_HUMAN	9Q0401.x1 Soares, testis, N1T Homo sapiens cDNA clone IMAGE:1738009.3 similar to TR014646
9054	19135	32345	7.1	9.0E-71	AF143870.1	EST_HUMAN	9Q0401.x1 Soares, testis, N1T Homo sapiens cDNA clone IMAGE:1738009.3 similar to TR014646
7251	20253	33887	1.98	9.0E-71	AF54903.1	EST_HUMAN	W55203.x1 NO1, CGAP, G08 Homo sapiens cDNA clone IMAGE:2300288.3 similar to TR097213
11852	20253	33887	3.97	9.0E-71	AF54903.1	EST_HUMAN	W55203.x1 NO1, CGAP, G08 Homo sapiens cDNA clone IMAGE:2300288.3 similar to TR097213
9425	22389		3.92	8.0E-71	AA171451.1	EST_HUMAN	W55203.x1 NO1, CGAP, G08 Homo sapiens cDNA clone IMAGE:2300288.3 similar to TR097213
10927	23887	37658	0.45	8.0E-71	AF173820.1	EST_HUMAN	W55203.x1 NO1, CGAP, G08 Homo sapiens cDNA clone IMAGE:2300288.3 similar to TR097213
7891	20562	33523	8.17	7.0E-71	AA442230.1	EST_HUMAN	W55203.x1 NO1, CGAP, G08 Homo sapiens cDNA clone IMAGE:2300288.3 similar to TR097213

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF ID NO.	Expression Signal	Most Similar [Top] Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8789	2796	3978	4.40	1.0E-71	8822811	NT	Homo sapiens hypothetical protein FLJ10988 (FLJ10988), mRNA
8934	22548	39597	0.83	1.0E-71	S72935.1	NT	CSNK2A1-epsilon kinase II (CKII) subunit alpha [human, Genomic, 8882] [c]
10357	22360	39787	9.48	1.0E-71	AY076743.1	NT	Homo sapiens cytochrome c oxidase subunit VIIc-related protein gene, complete cds
10428	22360	39787	3.08	1.0E-71	AY78127.1	EST_HUMAN	AY78127 MDS Homo sapiens cDNA clone MDSE1003 5'
10534	22623	37336	1.52	1.0E-71	11435142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
11238	21181	37768	2.43	1.0E-71	AY76127.1	EST_HUMAN	AY76127 MDS Homo sapiens cDNA clone MDSE1003 5'
11238	21181	37768	2.43	1.0E-71	11416903	NT	Homo sapiens coagulation factor XII, AT polypeptide (FXII), mRNA
11481	24424	37768	2.12	1.0E-71	11417191	NT	Homo sapiens leucocyte/erythroid aminopeptidase (LNEP), mRNA
11481	24424	37768	2.27	1.0E-71	11417191	NT	Homo sapiens leucocyte/erythroid aminopeptidase (LNEP), mRNA
12381	25346	37764	3.13	1.0E-71	148011399.1	NT	Homo sapiens gene for 2F-5, complete cds
407	13480	28414	1.26	8.0E-72	U867655.1	EST_HUMAN	HYPOD1/NC1/CGAP J119 Homo sapiens cDNA clone IMAGE2523168 3' similar to TR-086705 086705
407	13480	28415	1.26	8.0E-72	U867655.1	EST_HUMAN	HYPOD1/NC1/CGAP J119 Homo sapiens cDNA clone IMAGE2523168 3' similar to TR-086705 086705
8222	19008	33268	0.89	8.0E-72	AF035792.1	EST_HUMAN	HYPOD1/NC1/CGAP J119 Homo sapiens cDNA clone IMAGE2523168 3' similar to TR-086705 086705
11444	24387	37628	2.55	8.0E-72	11424460	NT	HYPOD1/NC1/CGAP J119 Homo sapiens cDNA clone IMAGE2523168 3' similar to TR-086705 086705
11444	24387	37628	2.55	8.0E-72	11424460	NT	HYPOD1/NC1/CGAP J119 Homo sapiens cDNA clone IMAGE2523168 3' similar to TR-086705 086705
11444	24387	37628	2.55	8.0E-72	11424460	NT	HYPOD1/NC1/CGAP J119 Homo sapiens cDNA clone IMAGE2523168 3' similar to TR-086705 086705
4139	17170	30058	1.24	7.0E-72	4501866	NT	Homo sapiens scintase 2, mitochondrial (AC02), nuclear gene encoding mitochondrial protein, mRNA
4139	17170	30057	1.24	7.0E-72	4501866	NT	Homo sapiens scintase 2, mitochondrial (AC02), nuclear gene encoding mitochondrial protein, mRNA
4139	17170	30058	1.24	7.0E-72	4501866	NT	Homo sapiens scintase 2, mitochondrial (AC02), nuclear gene encoding mitochondrial protein, mRNA
7331	20302	33546	2.87	7.0E-72	S41884.1	NT	(cysteine) PTPase 2, polynuclear alpha [human, Genomic, 1182 nt, segment 2 of 3]
12800	25428		1.52	7.0E-72	262250.1	EST_HUMAN	HSPO13670 HM3 Homo sapiens cDNA clone s400007G02
8727	21895		4.9	8.0E-72	163248.2	NT	Homo sapiens chromosome 21 segment H321048
66	13184	28102	4.89	5.0E-72	BF333707.1	EST_HUMAN	QVC-C53001C-160000-388-e11 CS0010 Homo sapiens cDNA
66	13184	28103	4.89	5.0E-72	BF333707.1	EST_HUMAN	QVC-C53001C-160000-388-e11 CS0010 Homo sapiens cDNA
66	13184	28103	13.05	5.0E-72	BF333707.1	EST_HUMAN	QVC-C53001C-160000-388-e11 CS0010 Homo sapiens cDNA
66	13184	28103	13.05	5.0E-72	BF333707.1	EST_HUMAN	QVC-C53001C-160000-388-e11 CS0010 Homo sapiens cDNA
1141	14184		2.78	5.0E-72	L11945.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7738	20114	33427	1.66	5.0E-72	AU128584	EST_HUMAN	AU128584 NT2P22 Homo sapiens cDNA clone NT2P2203761 6'

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[illegible]

Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6711	19767	33947	1.24	1.0E-72	11321678	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6768	23668	33126	1.3	1.0E-72	AV751816.1	EST	HUMAN
7699	20842	34225	3.72	1.0E-72	BE179434.1	EST	HUMAN
7699	20842	34225	3.72	1.0E-72	BE179434.1	EST	HUMAN
7699	20842	34225	3.72	1.0E-72	BE179434.1	EST	HUMAN
9049	22076	36339	7.79	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein S22 (S22), mRNA, complete cds
9049	22076	36339	7.79	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein S22 (S22), mRNA, complete cds
1455	14488	27663	1.53	9.0E-73	AW374688.1	EST	HUMAN
6150	19231	32462	0.84	9.0E-73	11529883	NT	Homo sapiens membrane protein, apolipoprotein 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
11297	24247		18.46	9.0E-73	11424099	NT	Homo sapiens neuronal protein L15a (RPL15A), mRNA
1039	14084	27035	0.93	8.0E-73	AW071785.1	EST	HUMAN
5680	19785	31924	0.76	8.0E-73	4505798	NT	ves5680.1, NCI, COG, PRO, FGEN, M1986
6724	19782	33059	5.01	8.0E-73	11429469	NT	ves5680.1, NCI, COG, PRO, FGEN, M1986
8432	21401	34814	2.3	8.0E-73	AF113128.1	NT	Homo sapiens phosphoglucomutase 3, cytosolic, class 2, alpha polypeptide (PGC32A), mRNA
9708	22681	38117	7.24	8.0E-73	BE218900.1	EST	HUMAN
10097	23023	35497	2.34	8.0E-73	11528837	NT	Homo sapiens interferon 12 receptor, beta 1 (IL12RB1), mRNA
10097	23023	35498	2.34	8.0E-73	AF358428.1	NT	Homo sapiens interferon 12 receptor, beta 1 (IL12RB1), mRNA
12010	24897	35483	3.54	8.0E-73	AF358428.1	NT	Homo sapiens interferon 12 receptor, beta 1 (IL12RB1), mRNA
12785	28418	37135	3.48	8.0E-73	11418189	NT	Homo sapiens transferrin A-inhibitor guanine nucleotide-exchange protein 1 mRNA, complete cds
1136	14759	27130	1.3	7.0E-73	BE23280	NT	Homo sapiens lysosomal protein FLJ20309 (FLJ20309), mRNA
3312	18855	22555	1.74	7.0E-73	AI182303.2	NT	Homo sapiens hypodermal protein FLJ20309 (FLJ20309), mRNA
4681	17698		1.74	7.0E-73	AI182303.2	NT	Homo sapiens chromosome 21 segment HS21C08
159	13262		2.68	6.0E-73	BE166741.1	EST	HUMAN
7378	20348	35809	2.11	4.0E-73	11422146	NT	Homo sapiens chromosome 21 segment HS21C018
5325	19492	31148	1.16	3.0E-73	AV1843788.1	EST	HUMAN
1344	14578	27604	1.34	3.0E-73	11435613	NT	Homo sapiens HEL G protein (FAM44), mRNA
1679	14804	27604	1.34	3.0E-73	11435613	NT	Homo sapiens HEL G protein (FAM44), mRNA
1278	14804	27605	1.34	3.0E-73	11435613	NT	Homo sapiens HEL G protein (FAM44), mRNA
6865	19909	33204	0.86	3.0E-73	AA138403.1	EST	HUMAN
9111	22077	35503	0.54	3.0E-73	AV729428.1	EST	HUMAN

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORE SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9111	22077	36504	0.54	3.0E-73	AF729428.1	EST_HUMAN	homo sapiens cDNA clone HTCAAF071 5'
11047	24011		1.66	3.0E-73	X69660.1	NT	H sapiens SHQLP2 pseudogene, 6' and
13017	25567		1.35	3.0E-73	AL163243.2	NT	Homo sapiens chromosome 21: segment HS21C048
13021	25569		1.97	3.0E-73	AW690351.1	EST_HUMAN	RC3-NM0065-270400-011-024 NN0068 Homo sapiens cDNA
852	13608	26968	1.9	2.0E-73	AF139897.1	NT	Homo sapiens BASF1 (BASF1) mRNA, partial cds
1653	14685		2.85	2.0E-73	AW690351.1	EST_HUMAN	RC3-NM0065-270400-011-024 NN0068 Homo sapiens cDNA
2206	15318		1.58	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3196	16281	26770	3.89	2.0E-73	4592562	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3591	16807	26527	0.77	2.0E-73	7066539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3591	16807	26526	0.77	2.0E-73	7066539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
6377	19537	32593	0.7	2.0E-73	AF06624.1	NT	Nice muscular rhinovirus-interacting from Kinase (Cik) mRNA, complete cds
6377	19537	32593	0.7	2.0E-73	AF06624.1	NT	Nice muscular rhinovirus-interacting from Kinase (Cik) mRNA, complete cds
6377	19537	32593	0.38	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6869	19591	32594	1.32	2.0E-73	AF06624.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6869	19591	32597	1.43	2.0E-73	AF06624.1	NT	Homo sapiens interleukin 4 receptor (IL4R) mRNA
8092	21029	34427	0.59	2.0E-73	AB02049.1	NT	Human epithelial myelin protein 22 mRNA, complete cds
8092	21035	34435	0.77	2.0E-73	AB020760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
9550	22843	36506	0.65	2.0E-73	AF168349.1	NT	Galactosyl dihex2 protein (Dhx2) mRNA, complete cds
9550	22843	36506	0.65	2.0E-73	AF168349.1	NT	Galactosyl dihex2 protein (Dhx2) mRNA, complete cds
10788	23769	37211	1.12	2.0E-73	AF168349.1	NT	Galactosyl dihex2 protein (Dhx2) mRNA, complete cds
10853	23763	37284	1.89	2.0E-73	AF168349.1	NT	Homo sapiens sucrinase (SVL), transcript variant 1, mRNA
10853	23763	37285	1.69	2.0E-73	11466660	NT	Homo sapiens sucrinase (SVL), transcript variant 1, mRNA
11017	24657	37599	1.49	2.0E-73	11431598	NT	Homo sapiens KIAA1000 protein, GdpG-associated, gamma-actinin ear containing, ARF-binding protein 2 (KIAA1080), mRNA
11395	24341	37572	2.64	2.0E-73	4576162	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11395	24341	37573	2.64	2.0E-73	4576162	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11420	24354	37590	1.81	2.0E-73	AB026882.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12851	14665		1.81	2.0E-73	AW690351.1	EST_HUMAN	RC3-NM0065-270400-011-024 NN0068 Homo sapiens cDNA
1798	14827	27814	2.81	1.0E-73	AJ121586.1	EST_HUMAN	AJ121586 MAMMA1 Homo sapiens cDNA clone MAMMA100480 5'
6495	16559	32510	1.2	1.0E-73	BE151283.1	EST_HUMAN	GM1-H10282-11189-042-10 HT0282 Homo sapiens cDNA
9897	22789	36244	1.47	1.0E-73	AI147427.1	EST_HUMAN	qg51407.1 Sorensen, Jussis, NHT Homo sapiens cDNA clone IMAQIE: (839567) 5' similar to contains element MER32 repetitive element;

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11776	28024	37455	2.1	1.0E-73	BE38497.1	EST_HUMAN	BT276071.NH.MGC_20 Homo sapiens cDNA clone IMAGE:387105.5'
742	18803	26742	1.47	8.0E-74	457426	NT	Homo sapiens CD36-like 4 (CD36L4) mRNA
6021	19104	32035	1.84	8.0E-74	S83184.1	NT	Cdc-19/midlin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 5409 nt]
6021	19104	32035	1.84	8.0E-74	S83184.1	NT	Cdc-19/midlin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 5409 nt]
1068	14887	27685	4.43	7.0E-74	AJ001058.1	NT	Homo sapiens NKX2-2 gene, exon 10
3355	18360	29311	2.01	7.0E-74	AL165246.2	NT	Homo sapiens chromosome 21 segment HS70046
5568	22602	36001	2.25	7.0E-74	BE307452.1	EST_HUMAN	BT164234.F1.NF.MGC_73 Homo sapiens cDNA clone IMAGE:303267.5'
12784	28417	31724	4.84	7.0E-74	BE269305.1	EST_HUMAN	BT119257.F1.NF.MGC_73 Homo sapiens cDNA clone IMAGE:353865.5'
1124	14168	27120	5.19	6.0E-74	AF106907.1	NT	Homo sapiens ST6I gene, partial cds; P51 and hypothetical protein genes, complete cds, and S171 gene, partial cds
1631	14664	27639	1.03	6.0E-74	AW263177.1	EST_HUMAN	BT199721.Sunnae.NH.MGC_51 Homo sapiens cDNA clone IMAGE:270698.3'
2324	15355	28307	7.92	6.0E-74	BE388260.1	EST_HUMAN	BT283527.F1.NH.MGC_44 Homo sapiens cDNA clone IMAGE:380543.5'
2324	15355	28307	7.92	6.0E-74	BE388260.1	EST_HUMAN	BT283527.F1.NH.MGC_44 Homo sapiens cDNA clone IMAGE:380543.5'
2875	15361	28452	1.12	6.0E-74	AW014039.1	EST_HUMAN	U11810.amh.h29.2.JUL11.NCL.CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2706958.3'
2875	15361	28452	1.12	6.0E-74	AW014039.1	EST_HUMAN	U11810.amh.h29.2.JUL11.NCL.CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2706958.3'
3726	19768	28679	1.28	6.0E-74	BE048948.1	EST_HUMAN	BT54411.1.NCL.CGAP_K611 Homo sapiens cDNA clone IMAGE:312332.3'
3726	19768	28680	1.28	6.0E-74	BE048948.1	EST_HUMAN	BT54411.1.NCL.CGAP_K611 Homo sapiens cDNA clone IMAGE:312332.3'
5005	18075	30985	4.18	6.0E-74	4758135	NT	Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 11 (S cerevisiae CHL1-like helicase) (DOX11) mRNA
5065	18075	30985	4.18	6.0E-74	4758135	NT	Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 11 (S cerevisiae CHL1-like helicase) (DOX11) mRNA
5450	18941	31451	2.68	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP) mRNA
506	13981	28517	3.68	6.0E-74	AW02068.1	EST_HUMAN	df1608.y1.Morton.Feldi.Cochlea Homo sapiens cDNA clone IMAGE:2485704.5'
2713	15707	31462	1.78	6.0E-74	AW382765.1	EST_HUMAN	PMO-070289-27109-001-H07-070289 Homo sapiens cDNA
5481	18351	31462	12.05	6.0E-74	11034117	NT	Homo sapiens phosphatidyl-inositol 3-kinase, class I (PI3K) mRNA
5587	18975	32168	7.23	6.0E-74	X89870.1	NT	H sapiens mRNA for PCPRT18 protein
5938	19024	32218	7.23	6.0E-74	4507866	NT	H sapiens VAMP (vesicle-associated membrane protein)-associated protein A (VAPA) mRNA, and transferrin products
6013	19068	32266	2.71	6.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R) mRNA
6013	19068	32266	2.71	6.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R) mRNA
7080	20101	33412	2.18	6.0E-74	7692265	NT	Homo sapiens KIA00718 gene product (KIA00718) mRNA
7632	20101	33412	0.54	6.0E-74	7692265	NT	Homo sapiens KIA00718 gene product (KIA00718) mRNA
8371	21340	34751	3.05	6.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222) mRNA
11087	24048	37570	4.06	6.0E-74	Y09420.1	NT	H sapiens mRNA for HRP41

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12164	26012	38610	3.9	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12235	26057		7.14	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12948	26488		1.52	1.0E-74	AF040785.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
2652	15949		6.34	8.0E-75	AF176228.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12543	26298		1.81	8.0E-75	AF163022.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
2326	18340	28362	1.16	8.0E-75	AB174151.1	EST	Homo sapiens chromosome 21 segment HS21002
5391	18240	31094	0.91	5.0E-75	BE647035.1	EST	Homo sapiens chromosome 21 segment HS21002
8075	21012	34413	0.31	5.0E-75	AA053440.1	EST	Homo sapiens chromosome 21 segment HS21002
6296	22235	38654	1.13	5.0E-75	AF176228.1	NT	Homo sapiens chromosome 21 segment HS21002
6412	22436	38674	0.34	5.0E-75	AF176228.1	NT	Homo sapiens chromosome 21 segment HS21002
8546	22512	35961	0.89	5.0E-75	BE650465.1	EST	Homo sapiens chromosome 21 segment HS21002
9549	22512	35962	0.86	5.0E-75	BE650465.1	EST	Homo sapiens chromosome 21 segment HS21002
9728	22756	36209	1.42	5.0E-75	BE650465.1	EST	Homo sapiens chromosome 21 segment HS21002
10594	23510	37007	2.9	5.0E-75	AB386231.1	EST	Homo sapiens chromosome 21 segment HS21002
1112	13223	29147	1.68	4.0E-75	BE081333.1	EST	Homo sapiens chromosome 21 segment HS21002
459	13532	27765	2.69	4.0E-75	BE081333.1	EST	Homo sapiens chromosome 21 segment HS21002
1780	14809	27765	1.73	4.0E-75	AF07226.1	EST	Homo sapiens chromosome 21 segment HS21002
2891	15921	28941	4.5	4.0E-75	BE009464.1	EST	Homo sapiens chromosome 21 segment HS21002
3512	19568	29482	0.83	4.0E-75	8922807	NT	Homo sapiens chromosome 21 segment HS21002
9607	19703	31659	0.65	4.0E-75	11417848	NT	Homo sapiens chromosome 21 segment HS21002
9607	19703	31659	0.65	4.0E-75	11417848	NT	Homo sapiens chromosome 21 segment HS21002
9400	19498	32719	6.35	4.0E-75	5578457	NT	Homo sapiens chromosome 21 segment HS21002
8923	19973	33271	1.61	4.0E-75	11417848	NT	Homo sapiens chromosome 21 segment HS21002
8923	19973	33271	1.61	4.0E-75	11417848	NT	Homo sapiens chromosome 21 segment HS21002
11044	24008	37534	15.05	4.0E-75	7966563	NT	Homo sapiens chromosome 21 segment HS21002
10004	10855	27007	4.38	3.0E-75	AF157623.1	NT	Homo sapiens chromosome 21 segment HS21002
10083	14055	27007	3.22	3.0E-75	AF157623.1	NT	Homo sapiens chromosome 21 segment HS21002
2430	14879	27075	2.38	3.0E-75	AB011053.1	NT	Homo sapiens chromosome 21 segment HS21002
2633	15437	26864	5.12	3.0E-75	4789163	NT	Homo sapiens chromosome 21 segment HS21002
3034	10852	28210	1.06	3.0E-75	AF163022.2	NT	Homo sapiens chromosome 21 segment HS21002

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3303	16238	29177	1.13	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIA0081 protein, partial cds
3301	16411	29324	0.95	3.0E-75	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3301	16411	29324	0.95	3.0E-75	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3301	16411	29324	0.95	3.0E-75	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3732	16794	29705	0.78	3.0E-75	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4197	17228	30118	1.03	3.0E-75	DB0765.1	NT	Homo sapiens KIA00971 protein (KIA00971) mRNA
4465	17492	30379	0.71	3.0E-75	7602421	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (APB2), mRNA
5323	18429	31179	1.15	3.0E-75	11420966	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (APB2), mRNA
5323	18429	31180	1.15	3.0E-75	11420966	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (APB2), mRNA
6057	19714	32961	0.81	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6057	19714	32962	0.81	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6935	20159	33479	1.76	3.0E-75	11529319	NT	Homo sapiens HR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6935	20159	33480	1.76	3.0E-75	11529319	NT	Homo sapiens HR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7342	20313	33557	4.47	3.0E-75	76022208	NT	Homo sapiens KIA00533 gene product (KIA00533), mRNA
7342	20313	33557	4.47	3.0E-75	76022208	NT	Homo sapiens KIA00533 gene product (KIA00533), mRNA
7884	20828	34204	2.82	3.0E-75	4855532	NT	Homo sapiens Oncogene TM (TM) mRNA
7884	20828	34205	2.82	3.0E-75	4855532	NT	Homo sapiens Oncogene TM (TM) mRNA
8336	22301	35730	1.21	3.0E-75	11426054	NT	Homo sapiens zinc finger protein (ZNF11), mRNA
10037	22994	36431	0.65	3.0E-75	11426054	NT	Homo sapiens Zinc finger protein (ZNF11), mRNA
10068	23828	37941	4.16	3.0E-75	11426054	NT	Homo sapiens Zinc finger protein (ZNF11), mRNA
12085	24657	39552	1.73	3.0E-75	11426054	NT	Homo sapiens Zinc finger protein (ZNF11), mRNA
12085	24657	39553	1.73	3.0E-75	11426054	NT	Homo sapiens Zinc finger protein (ZNF11), mRNA
5759	18850		1.41	2.0E-75	AF174068.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone cDNA BE0202.9
9103	22068	35465	2.56	2.0E-75	AB011783.1	EST_HUMAN	AF091622 c1 NC1 CGAP_M05 Homo sapiens cDNA clone IMAGE:2832707 3' similar to contains PTRY.11
2311	15320	28945	7.79	1.0E-75	AW168135.1	EST_HUMAN	PTF7 repetitive element;
2311	15320	28945	7.79	1.0E-75	X22221.1	NT	H. sapiens ERCC22 gene, exons 1 & 2 (partial)
4719	19015	28643	3.35	1.0E-75	X22221.1	NT	H. sapiens ERCC22 gene, exons 1 & 2 (partial)
4719	19015	28643	3.35	1.0E-75	X22221.1	NT	H. sapiens ERCC22 gene, exons 1 & 2 (partial)
5204	18233	31107	0.67	1.0E-75	BE684192.1	EST_HUMAN	601197535F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3904275 5'
5204	18233	31107	0.67	1.0E-75	BE684192.1	EST_HUMAN	601197535F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922935 5'
7543	20760	34195	0.76	1.0E-75	BE052528.1	EST_HUMAN	RC5-B17054-020300-031-H03 B170540 Homo sapiens cDNA
7543	20760	34196	0.76	1.0E-75	BE052528.1	EST_HUMAN	RC5-B17054-020300-031-H03 B170540 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed In Bone Marrow

Probe NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description	
8787	21724		12.42	1.0E-76	AA598270.1	EST - HUMAN	257603 at Sarsra, testis. NHT Homo sapiens cDNA clone IMAGE:724486 3' similar to gbAI13932.40S	
8788	21724		12.42	1.0E-76	AA598270.1	EST - HUMAN	REBOSONAL PROTEIN S17 (HUMAN).	
8789	22734	38179	4.03	1.0E-75	BF131984.1	EST - HUMAN	19050022AFH1 NHT_MGC_19 Homo sapiens cDNA clone IMAGE:1126076 5'	
8790	22734	38180	4.03	1.0E-75	BF131984.1	EST - HUMAN	19050022AFH1 NHT_MGC_19 Homo sapiens cDNA clone IMAGE:1126076 5'	
8791	22734	38180	4.03	1.0E-75	BF131984.1	EST - HUMAN	19050022AFH1 NHT_MGC_19 Homo sapiens cDNA clone IMAGE:1126076 5'	
8792	21129	24182	3.79	1.0E-75	AA1650437.1	EST - HUMAN	6177608.31 Stragelung lung (6837210) Homo sapiens cDNA clone IMAGE:868596 3'	
8793	24372	37910	2.13	1.0E-76	AF223391.1	NT	Homo sapiens calcium channel aliphatic E subunit (CACNA1E) gene, exon 7-49, and partial cds, alternatively spliced	
8794	12438	18232	3107.	1.72	1.0E-76	BE894169.1	EST - HUMAN	4780317193F1 NHT_MGC_72 Homo sapiens cDNA clone IMAGE:3922203 5'
8795	48	13198	20070	2.23	9.0E-76	A1852948.1	EST - HUMAN	w630b10.1x1 NCL_GCAP_G03 Homo sapiens cDNA clone IMAGE:2207168 3' similar to TR-OT62935 076235
8796	44	13198	20071	2.23	9.0E-76	A1852948.1	EST - HUMAN	TRAP1.
8797	15432		2.23	9.0E-76	A1852948.1	EST - HUMAN	TRAP1.	
8798	10291	23198	30970	0.86	6.0E-76	AF155460.1	EST - HUMAN	268007 at Sarsra, testis. NHT_Homo sapiens cDNA clone IMAGE:474941 3'
8799	10291	23198	30970	0.86	6.0E-76	AF155460.1	EST - HUMAN	Human foetal Heavy subunit mRNA, complete cds
8800	937	13950	28841	0.98	8.0E-76	4504374.2	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA
8801	13870	28642	4.08	8.0E-76	4504374.2	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA	
8802	2921	18979	28804	1.28	8.0E-76	7709774.2	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA
8803	2921	18979	28804	1.28	8.0E-76	7709774.2	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA
8804	2921	18979	28804	1.28	8.0E-76	7709774.2	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA
8805	16337	32003	4.79	8.0E-76	11421442.1	NT	Homo sapiens LIM domain kinase 1 (LMK1). mRNA	
8806	7335	20388	34043	1.41	8.0E-76	11432512.1	NT	Homo sapiens serine/threonine kinase 2 (STK2). mRNA
8807	7315	20378	34141	0.97	8.0E-76	11432512.1	NT	Homo sapiens mitochondrial center family protein (COCS18972). mRNA
8808	21607	33330	3.84	8.0E-76	11419681.2	NT	Homo sapiens ALK1 protein (COCS1181). mRNA	
8809	1332	17137	39855	0.48	8.0E-76	AB546764.1	NT	Homo sapiens mRNA for KIAA1554 protein, partial cds
8810	10746	22686	37113	1.41	8.0E-76	MT37521.1	NT	Human adrenoleukodystrophy (ADA) gene, complete cds
8811	10746	22686	37113	1.41	8.0E-76	MT37521.1	NT	Human adrenoleukodystrophy (ADA) gene, complete cds
8812	10746	22686	37113	1.41	8.0E-76	MT37521.1	NT	Human adrenoleukodystrophy (ADA) gene, complete cds
8813	12797	24568	2.25	8.0E-76	10442622.1	NT	Homo sapiens baculoviral IAP repeat-containing 8 (BIRC8) mRNA	
8814	12797	24568	2.25	8.0E-76	11476822.1	NT	Homo sapiens cadherin binding protein 1 (X-AB0330). mRNA	
8815	13336	28762	1.41	7.0E-76	5019032.1	NT	Homo sapiens cyclophilin B dehydrogenase (c3 component of pyruvate dehydrogenase complex, 2-oxo-acyl-CoA dehydrogenase subunit) (CYC1B) mRNA	
8816	3355	19349	29277	28.95	7.0E-76	AF155460.1	NT	Homo sapiens cAMP response element-binding protein 1 (CREB1) mRNA
8817	3355	19349	29277	28.95	7.0E-76	AF155460.1	NT	Homo sapiens cAMP response element-binding protein 1 (CREB1) mRNA
8818	3355	19349	29277	28.95	7.0E-76	AF155460.1	NT	Homo sapiens cAMP response element-binding protein 1 (CREB1) mRNA
8819	4396	17427	30313	4.52	7.0E-76	4507184.2	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and isoforms
8820	4396	17427	30313	4.52	7.0E-76	4507184.2	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and isoforms
8821	4396	17427	30313	4.52	7.0E-76	4507184.2	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and isoforms
8822	4396	17427	30313	4.52	7.0E-76	4507184.2	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and isoforms
8823	4396	17427	30313	4.5				

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	OSF SEQ ID NO.	Expression Signal	Mod Similar (Top Hit) Blast E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1537	14570	27545	1.74	2.0E-76	4504028	NT	Human sapiens GM2 ganglioside activator protein (GM2A) mRNA
1945	14989	27967	1.03	2.0E-76	AA29394.1	EST_HUMAN	z680H1 rat <i>Stralagene scitro</i> brain S11 Homo sapiens cDNA clone IMAGE:701025 3'
2854	15914	28937	3.73	2.0E-76	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3308	16391	29291	1.87	2.0E-76	AA448692.1	EST_HUMAN	z64602.1 Sources, Jaisis, NHT Homo sapiens cDNA clone IMAGE:760988 3' similar to SW-ITB5_HUMAN
3308	16391	29292	1.87	2.0E-76	AA448692.1	EST_HUMAN	z64602.1 Sources, Jaisis, NHT Homo sapiens cDNA clone IMAGE:760988 3' similar to SW-ITB5_HUMAN
4931	17394	30478	1.01	2.0E-76	AL163832.2	NT	P16904 INTEGRIN BETA-3 SUBUNIT PRECURSOR ;
4934	17696	30888	7.8	2.0E-76	AW979818.1	EST_HUMAN	P16904 INTEGRIN BETA-3 SUBUNIT PRECURSOR ;
5332	18498	31969	0.97	2.0E-76	AF127943.1	NT	QY5-OT0026-220300-152.511 OT0028 Homo sapiens cDNA
5703	19793	31969	5.35	2.0E-76	AB26204.1	NT	Orilla gorilla olfactory receptor (GGO18) gene, partial cds
7063	20032	33963	0.95	2.0E-76	11421326	NT	Homo sapiens KIA04763 gene product (KIA04763), mRNA
7063	20032	33963	0.75	2.0E-76	11426938	NT	Homo sapiens KIA04763 gene product (KIA04763), mRNA
7063	20032	33963	0.75	2.0E-76	11427410	NT	Homo sapiens KIA04763 gene product (KIA04763), mRNA
10945	21657	37162	7.93	2.0E-76	11457211	NT	Homo sapiens KIA04763 gene product (KIA04763), mRNA
11289	24218	37143	2.84	2.0E-76	754660	NT	Homo sapiens KIA04763 gene product (KIA04763), mRNA
4339	17355	30243	3.37	1.0E-76	DC3874.1	NT	Homo sapiens KIA04763 gene product (KIA04763), mRNA
4339	17355	30243	3.37	1.0E-76	DC3874.1	NT	Homo sapiens KIA04763 gene product (KIA04763), mRNA
5523	16622	31557	6.74	1.0E-76	BE70637.1	EST_HUMAN	Human mRNA for HUG-1, complete cds
6372	16440	33445	0.94	1.0E-76	AA333207.1	EST_HUMAN	EST137201 Embryo, 8 week, Homo sapiens cDNA, 5' end
7109	20043	33445	4.09	1.0E-77	BE86625.1	EST_HUMAN	EST137201 Embryo, 8 week, Homo sapiens cDNA, 5' end
12023	25490		1.36	6.0E-77	BE410354.1	EST_HUMAN	EST137201 Embryo, 8 week, Homo sapiens cDNA, 5' end
189	13289	29215	1.35	8.0E-77	R83144.1	EST_HUMAN	Yp1102.1 Sources, Jaisis, NHT Homo sapiens cDNA clone IMAGE:187155 5' similar to
4550	17573	30463	1.26	8.0E-77	BF20518.1	EST_HUMAN	SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
5528	18827	31563	1.83	8.0E-77	4506230	NT	Human mRNA for HUG-1, complete cds
11716	24679	36257	1.82	8.0E-77	AA019770.1	EST_HUMAN	EST137201 Embryo, 8 week, Homo sapiens cDNA, 5' end
11716	24679	36258	1.82	8.0E-77	AA019770.1	EST_HUMAN	EST137201 Embryo, 8 week, Homo sapiens cDNA, 5' end
12800	25484	31732	4.86	8.0E-77	R00246.1	EST_HUMAN	Yp1102.1 Sources, Jaisis, NHT Homo sapiens cDNA clone IMAGE:187155 5' similar to
1946	14970	27969	2.43	7.0E-77	AA52766.1	EST_HUMAN	Yp1102.1 Sources, Jaisis, NHT Homo sapiens cDNA clone IMAGE:187155 5' similar to
2421	15428	29451	1.86	7.0E-77	4609944	NT	Human sapiens polyoma (RNA) (DNA directed) polypeptide E (28SD) (POLR2E) mRNA
2421	15428	29452	1.86	7.0E-77	4609944	NT	Human sapiens polyoma (RNA) (DNA directed) polypeptide E (28SD) (POLR2E) mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2600_13606	26021	26021	2.28	2.0E-77	AB037636.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4084_17100	25692	25692	1.25	2.0E-77	BC044316.1	EST_HUMAN	h43905.x1 Scavenger, NR1, T, GAG, S1 Homo sapiens cDNA clone IMAGE:3049113 3' similar to SW-GAG2_HUMAN P1026 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4442_17468	30357	30357	0.88	2.0E-77	AB133519.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
4442_17468	30358	30358	0.68	2.0E-77	AB133519.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
4802_17819	30713	30713	2.32	2.0E-77	AA630026.1	EST_HUMAN	h88912.x1 NCL_GGAP_P12 Homo sapiens cDNA clone IMAGE:1188838 similar to SW-RL20_HUMAN P4791.4 60S RIBOSOMAL PROTEIN L28, [1] contains element MSR1 repetitive element ;
5158_17468	30357	30357	0.65	2.0E-77	AB133519.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
5158_17468	30358	30358	0.65	2.0E-77	AB133519.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
6355_19748	32558	32558	2.08	2.0E-77	BE296940.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
6296_19388	32507	32507	1.82	2.0E-77	BE297433.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
7380_20350	33701	33701	14.21	2.0E-77	AA630033.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
8874_21841	35594	35594	0.75	2.0E-77	AB22707.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
5898_23830	36290	36290	5.94	2.0E-77	U5321.1	NT	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
5898_23830	36290	36290	5.94	2.0E-77	U5321.1	NT	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
10354_22278	38752	38752	0.5	2.0E-77	BF030349.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
10354_22278	38754	38754	0.5	2.0E-77	BF030349.1	EST_HUMAN	h22902.x1 NCL_GGAP_Bra52 Homo sapiens cDNA clone IMAGE:2260468 3' similar to TR063245
45_13163	29068	29068	0.94	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
45_13163	29069	29069	0.94	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
272_13388	20294	20294	1.33	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (probable neuro-II, Alzheimer disease) (APP), mRNA
272_13388	20295	20295	1.33	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (probable neuro-II, Alzheimer disease) (APP), mRNA
876_15853	20891	20891	2.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (probable neuro-II, Alzheimer disease) (APP), mRNA
876_15853	20892	20892	2.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (probable neuro-II, Alzheimer disease) (APP), mRNA

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Table 4
Single Evon Pmbas Expressed in Bone Marrow

Probe ID	Seq ID	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BUSSE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2450	15495	29477	1.79	1.0E-77	ABD20024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds	
3058	17481	29028	2.01	1.0E-77	4803300	NT	Homo sapiens 2,4-dienyl CoA reductase 1, muscle/borderline (BCGR1), mRNA	
4330	17408	30289	3.92	1.0E-77	7070626	NT	Homo sapiens C3orf60 protein (C3orf60), mRNA	
4350	17500	30438	3.92	1.0E-77	4795053	NT	Homo sapiens C3orf60 protein (C3orf60), mRNA	
4532	17575	30435	16.98	1.0E-77	1.220041.1	NT	Homo sapiens beta 2-microglobulin A.L.1 and C.B.1 on chromosome 21;22; segment 1/3	
4532	17575	30435	16.98	1.0E-77	1.220041.1	NT	Homo sapiens beta 2-microglobulin A.L.1 and C.B.1 on chromosome 21;22; segment 1/3	
4880	17701	30589	2.11	1.0E-77	6855232	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcribed variant BRCA1-exon4, mRNA	
4721	17741	30632	0.72	1.0E-77	UAZ70414.1	EST_HUMAN	3058454.1 NC_034747. Homo sapiens cDNA clone IMAGE:581110.3	
5000	17555	30438	0.95	1.0E-77	4796053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA	
5219	17566	30438	0.68	1.0E-77	4796053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA	
5248	18254	30438	1.12	1.0E-77	AL493247.2	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA	
6008	19120	32325	1.61	1.0E-77	AF068644.1	NT	Homo sapiens dyfuchin 1 (DYF1) gene, exons 27 and 28	
6165	19240	32471	1.39	1.0E-77	AF068644.1	NT	Homo sapiens dyfuchin 1 (DYF1) gene, exons 27 and 28	
6580	19565	33021	1.28	1.0E-77	U62884.1	NT	Human von Willebrand factor gene, exon 20	
7254	19889	33298	14.51	1.0E-77	5881412	NT	Homo sapiens alpha 1 (alpha1) globulin gene, exons 1 and 2	
7528	19931	34290	0.91	1.0E-77	11420159	NT	Homo sapiens alpha 1 (alpha1) globulin gene, exons 1 and 2	
8040	20077	34573	0.59	1.0E-77	X04571.1	NT	Human mRNA for kidney osteopontin growth factor (OGF) precursor	
8920	22884	39013	0.65	1.0E-77	Y04934.1	NT	Homo sapiens cDNA for core alpha-2(I)-globulin gene	
9620	23964	39014	0.65	1.0E-77	Y04934.1	NT	Homo sapiens cDNA for core alpha-2(I)-globulin gene	
10860	23910	37316	0.92	1.0E-77	AB02936.1	NT	Homo sapiens hCG-17.2 mRNA for glycoprotein/hormone, complete cds	
10860	23910	37316	0.92	1.0E-77	AB02936.1	NT	Homo sapiens hCG-17.2 mRNA for glycoprotein/hormone, complete cds	
10916	23836	37332	3	9.0E-78	AF073302.1	EST_HUMAN	RC3-C10352. Homo sapiens cDNA clone HEMBA100434.5	
6586	19846	32619	2.93	9.0E-78	AF047091.1	EST_HUMAN	RC2-C10352. Homo sapiens cDNA clone HEMBA100434.5	
6586	19846	32620	2.93	9.0E-78	AF047091.1	EST_HUMAN	RC2-C10352. Homo sapiens cDNA clone HEMBA100434.5	
6586	19846	32620	2.93	9.0E-78	AF047091.1	EST_HUMAN	RC2-C10352. Homo sapiens cDNA clone HEMBA100434.5	
86	13022	26126	2.14	6.0E-78	AF118786.1	EST_HUMAN	AF118786. Homo sapiens cDNA clone HEMBA100434.5	
86	13022	26127	2.14	6.0E-78	AF118786.1	EST_HUMAN	AF118786. Homo sapiens cDNA clone HEMBA100434.5	
3325	16376	29257	8.86	6.0E-78	BF344101.1	EST_HUMAN	6230166887. NCI C6397. Homo sapiens cDNA clone IMAGE:4182311.5	
6712	18768	30589	2.34	6.0E-78	11422700	EST_HUMAN	Homo sapiens C3orf60 protein (C3orf60), mRNA	
219	13319	26344	1.79	5.0E-78	11422468	NT	Homo sapiens dyfuchin 1 (DYF1) gene, exons 27 and 28	
2569	15570	28560	5.46	5.0E-78	AF673424.1	EST_HUMAN	CE22121.1	
3036	16445	29372	3.94	5.0E-78	M55880.1	NT	Human C3orf60 protein (C3orf60), mRNA	
5468	18586	31467	2.45	5.0E-78	AF053539.1	EST_HUMAN	Homo sapiens beta 2-microglobulin A.L.1 and C.B.1 on chromosome 21;22; segment 1/3	
5955	18751	31817	24.78	5.0E-78	11415885	NT	Homo sapiens transforming growth factor, beta-induced 68kD (TGFB1), mRNA	

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7961	20331	33691	2.22	5.0E-78	AW058120.1	EST_HUMAN	EST:905190 IMAGE resources, MACB Homo sapiens cDNA
9438	22402	35940	6.95	5.0E-78	U06889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
9439	22403	35941	3.51	5.0E-78	BE060838.1	EST_HUMAN	801548051F1 NF1_NGCG_32 Homo sapiens cDNA clone IMAGE:3881887.5
11614	24592	38112	1.94	5.0E-78	BE241639.1	EST_HUMAN	TCAP:IE00898 Pediatric acute myelogenous leukemia cell (FAB M1) Bcr/Myo-HGSC project/CAA Homo sapiens cDNA clone TCAP:IE00898
11614	24592	38113	1.94	5.0E-78	BE241639.1	EST_HUMAN	TCAP:IE00898 Pediatric acute myelogenous leukemia cell (FAB M1) Bcr/Myo-HGSC project/CAA Homo sapiens cDNA clone TCAP:IE00898
11938	14182	27133	1.86	4.0E-78	AL043414.2	EST_HUMAN	DKFZ543N0323.1 434 (synonym: Hs43) Homo sapiens cDNA clone DKFZ543N0323.5
1321	14553	27324	2.74	4.0E-78	AL368941.1	NT	Novel human gene mapping to chromosome 22
4636	14698	27893	1.11	4.0E-78	AB065094.1	EST_HUMAN	w87612.1 NCL GMAP_KD11 Homo sapiens cDNA clone IMAGE:348616.5 3' similar to SW-WAP_PIG
2338	15337	28263	3.31	4.0E-78	AF107403.1	NT	C46552 WHET ACIDIC PROTEIN PRECURSOR ; Homo sapiens pre-mRNA splicing factor (SPR55) mRNA, complete cds
4350	17377	30256	2.16	4.0E-78	763870.1	NT	Homo sapiens synovial (LOC308105) mRNA
4837	17634	30719	2.16	4.0E-78	450563.1	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4837	17634	30720	2.16	4.0E-78	450563.1	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5982	18651	33137	1.13	4.0E-78	11420713.1	NT	Homo sapiens K14A428 gene product (K14A428) mRNA
6237	19369	32663	0.81	4.0E-78	7862109.1	NT	Homo sapiens K14A428 gene product (K14A428) mRNA
6725	19791	33660	0.56	4.0E-78	45067368.1	NT	Homo sapiens ribosomal protein S6 isoform 200 (RPS6B1) mRNA
7733	20698	34052	0.58	4.0E-78	45067368.1	NT	Homo sapiens ribosomal protein S6 isoform 200 (RPS6B1) mRNA
9205	22171	36901	1.68	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 200 (PIK200) mRNA, complete cds
9205	22171	35902	1.96	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 200 (PIK200) mRNA, complete cds
9720	22751	36904	0.94	4.0E-78	11417291.1	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4) mRNA
10811	23752	37233	1.97	4.0E-78	11560151.1	NT	Homo sapiens hypothetical C2342 zinc finger protein FLJ22504 (FLJ22504) mRNA
10811	23752	37234	1.97	4.0E-78	11560151.1	NT	Homo sapiens hypothetical C2342 zinc finger protein FLJ22504 (FLJ22504) mRNA
11749	24634	38213	1.95	4.0E-78	AF169148.1	NT	Homo sapiens e-Cadherin (CDH1) mRNA, complete cds
11983	24754	38350	6.69	4.0E-78	X08844.1	NT	Human transforming growth factor-beta precursor gene exon 4-5 (and joined mature peptide)
12126	24955	38950	2.38	4.0E-78	1102371.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4) mRNA
12737	25428	31739	3.60	4.0E-78	AB011936.1	NT	Homo sapiens gene for AIF-4, complete cds
162	13265	26169	2.77	3.0E-78	AF069001.1	NT	Homo sapiens eRF1 gene, complete cds
162	13265	26169	2.77	3.0E-78	AF069001.1	NT	Homo sapiens eRF1 gene, complete cds
3778	18818		0.84	3.0E-78	AU140994.1	EST_HUMAN	AU140984 PLACE3 Homo sapiens cDNA clone PLACE30030373.5
3820	18899	26771	0.88	3.0E-78	4607834.1	NT	Homo sapiens synaplein 1 (SYN1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF BEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	16899	28771	0.79	3.0E-76	4507334	NT	Homo sapiens synaptobrevin 1 (SNCA1), mRNA
10569	23571		5.79	3.0E-76	BE14778.1	EST_HUMAN	OMD-10780-04-0089-035-07 HT1080 Homo sapiens cDNA
11328	24278	37804	1.8	3.0E-76	BE159318.1	EST_HUMAN	QVQ-01087-10200-114-003 HT1080 Homo sapiens cDNA
3138	16195		4.1	2.0E-76	U04489.1	NT	Homo sapiens type IV collagen alpha 3 chain (COL4A3) gene, exon 20
4042	17060		1.43	2.0E-76	AA311872.1	EST_HUMAN	EST162833 Jurkat T-cells V1 Homo sapiens cDNA 5' end
7705	20662	34027	1.24	2.0E-76	AA1402306.1	EST_HUMAN	UHF-800-04-5-10-04-111 Homo sapiens cDNA 3' end
7705	20662	34028	1.24	2.0E-76	AA1402306.1	EST_HUMAN	UHF-800-04-5-10-04-111 Homo sapiens cDNA 3' end
8003	20942	34335	3.2	2.0E-76	BF68800.1	EST_HUMAN	80216555-1 HT1080-04-18 Homo sapiens cDNA clone IMAGE:3064139.5
8375	21344	34785	2.54	2.0E-76	AV17177.1	EST_HUMAN	80216555-1 HT1080-04-18 Homo sapiens cDNA clone IMAGE:3064139.5
8795	21762	35183	1.51	2.0E-76	AI557509.1	EST_HUMAN	AV17177-1 Homo sapiens cDNA clone DGBAWF69.5
8795	21762	35184	1.51	2.0E-76	AI557509.1	EST_HUMAN	AV17177-1 Homo sapiens cDNA clone DGBAWF69.5
11416	24380	37895	2.5	2.0E-76	AI197937.1	EST_HUMAN	PC-1 (B-107) human B-cells Homo sapiens cDNA 3'
11450	24651	37949	2.03	2.0E-76	AI197937.1	EST_HUMAN	PC-1 (B-107) human B-cells Homo sapiens cDNA 3'
5718	19482	31357	3.22	1.0E-76	AI147204.1	NT	224872.1 Scavenger kinase-like protein (LOC251900), mRNA
7144	18476	31284	0.87	1.0E-76	AI147204.1	NT	224872.1 Scavenger kinase-like protein (LOC251900), mRNA
8496	21497	31847	2.85	1.0E-76	U23273.1	EST_HUMAN	AV148659 GLC Homo sapiens cDNA clone GLCBM001.3'
12233	25125	31847	3.81	1.0E-76	U23273.1	EST_HUMAN	Human cardiac/retrotransposon kinase (MSB) (mb) mRNA, complete cds
4727	17141	30538	3.81	1.0E-76	U23273.1	EST_HUMAN	Human cardiac/retrotransposon kinase (MSB) (mb) mRNA, complete cds
4868	17916	30538	3.81	1.0E-76	U23273.1	EST_HUMAN	Human cardiac/retrotransposon kinase (MSB) (mb) mRNA, complete cds
5507	18007	31527	16.13	9.0E-76	AB028070.1	NT	Homo sapiens peptide YY (PYY), mRNA
8474	19539	32785	2.48	9.0E-76	54651146	NT	RC2-BN007-4-00300-014-c12 BN007 Homo sapiens cDNA
6773	19327	33106	0.87	9.0E-76	11430322	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6773	19327	33106	0.87	9.0E-76	11430322	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
7573	20584	34150	0.84	9.0E-76	11424427	NT	Homo sapiens hypothetical protein FLJ11284 (FLJ11284), mRNA
7835	20773	34150	0.84	9.0E-76	11424427	NT	Homo sapiens hypothetical protein FLJ11284 (FLJ11284), mRNA
7835	20773	34151	0.84	9.0E-76	11424427	NT	Homo sapiens cAMP response element-binding protein CRE-BP1 (H_051668.1), mRNA
7875	20819	34197	0.55	9.0E-76	202056.1	NT	Homo sapiens cAMP response element-binding protein CRE-BP1 (H_051668.1), mRNA
8889	21667	35079	0.5	9.0E-76	11417260	NT	Human T-cell mRNA for glycyl RNA synthetase, complete cds
8889	21667	35080	0.5	9.0E-76	11417260	NT	Human T-cell mRNA for glycyl RNA synthetase, complete cds
9418	22383	35021	5.53	9.0E-76	U26853.1	NT	Homo sapiens threonyl-RNA synthetase (TARS), mRNA
9418	22383	35022	5.53	9.0E-76	U26853.1	NT	Homo sapiens threonyl-RNA synthetase (TARS), mRNA
8735	22763	30218	0.68	9.0E-76	U26853.1	NT	Homo sapiens capsin kinase II alpha subunit (PKA), complete cds
8735	22763	30218	0.68	9.0E-76	U26853.1	NT	Homo sapiens capsin kinase II alpha subunit (PKA), complete cds
10730	23652	37145	0.55	9.0E-76	11438543	NT	Homo sapiens DNA for myeloid leukemia protein, complete cds
10730	23652	37145	0.55	9.0E-76	11438543	NT	Homo sapiens DNA for myeloid leukemia protein, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
10784	23705	37204	1.53	9.0E-79	AF082448.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10784	23705	37205	1.53	9.0E-79	AF082448.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
11406	24350	37882	4.27	9.0E-79	AY00873.1	NT	Homo sapiens TRAF-1-regulated IKK activator 1 beta Uer1a mRNA, complete cds
11841	24724	38310	2.97	9.0E-79	11432827	NT	Homo sapiens suppressor of white apical homolog 2 (SWAP2), mRNA
11841	24724	38311	2.97	9.0E-79	11432827	NT	Homo sapiens suppressor of white apical homolog 2 (SWAP2), mRNA
12115	24985	38586	2.71	9.0E-79	7862491	NT	Homo sapiens KIAA1035 protein (KIAA1035), mRNA
13000	25558	31720	1.55	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3725	16787	28708	1.33	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21010
5195	16204	31078	0.96	8.0E-79	8597387	NT	Homo sapiens chromosome 21 segment HS21010
3235	15230	26242	7.24	7.0E-79	BE81948.1	EST HUMAN	50747276071 NH1_MGC_38 Homo sapiens cDNA clone IMAGE:462558 3' similar to
13170	25020		2.65	6.0E-79	AA099230.1	EST HUMAN	29446441 Soares_fetal_liver_spleen_1NF13_31 Homo sapiens cDNA clone IMAGE:3875657 3'
11824	24207	36290	4.37	3.0E-79	AL103422.1	NT	TRC151408 015408 NEUTRAL PROTEASE LARGE SUBUNIT
3104	18246		1.43	3.0E-79	11432828	NT	Homo sapiens chromosome 21 segment HS210082
313	13403	26331	1.43	3.0E-79	AF114438.1	NT	Homo sapiens hypodermic protein PL-10283 (PLN10283), mRNA
9719	14030	20884	2.02	3.0E-79	AF523708.1	NT	Homo sapiens Interleukin 30 (IL30) mRNA, complete cds
3115	16172	20682	1.82	3.0E-79	09510.3	NT	Homo sapiens cell cycle 218 (CC218) and rat cyclin D1 (CC1) gene, complete cds
5435	18337	31445	0.05	3.0E-79	AF10322.1	NT	Homo sapiens USTRP19 (USP19) mRNA, complete cds
5812	18902	32065	1.61	3.0E-79	0302069.1	NT	Homo sapiens mRNA for KIAA0302 protein, partial cds
5841	18931	32115	0.95	3.0E-79	BE786470.1	EST HUMAN	80148274351 NH1_MGC_38 Homo sapiens cDNA clone IMAGE:3844554 5'
5841	18931	32116	0.95	3.0E-79	BE786470.1	EST HUMAN	80148274351 NH1_MGC_38 Homo sapiens cDNA clone IMAGE:3844554 5'
5853	18952	32136	4.05	3.0E-79	BE786470.1	EST HUMAN	Homo sapiens retin 1 (NTN1), mRNA
5853	18952	32139	4.05	3.0E-79	11428770	NT	Homo sapiens retin 1 (NTN1), mRNA
5909	19991	33257	0.8	3.0E-79	BE25683.1	EST HUMAN	6011205551 NH1_MGC_18 Homo sapiens cDNA clone IMAGE:3352855 5'
7262	19997	33294	3.31	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0302 protein, partial cds
8504	21472	34496	1.59	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
9759	22869	35150	0.57	3.0E-79	10930306	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
10712	23834		0.64	3.0E-79	AY088115.1	EST HUMAN	Homo sapiens intracellular repeat domain 3 (ITIC3), mRNA
287	13382		2.05	2.0E-79	AB031261	EST HUMAN	AY088115.1 GK0 Homo sapiens cDNA clone GK0A0111 5'
635	13701	26022	1.29	2.0E-79	BE379626.1	EST HUMAN	Y4803.1 Soares fetal liver spleen 1NF15 Homo sapiens cDNA clone IMAGE:308541 3'
926	13981	26935	1.35	2.0E-79		EST HUMAN	601119041592 NH1_MGC_33 Homo sapiens cDNA clone IMAGE:3511107 5'
926	13981	26935	1.35	2.0E-79		EST HUMAN	Homo sapiens BCL-2-like 2 (BCL2L2) mRNA
945	14038	26990	4.78	2.0E-79	4895524	NT	Homo sapiens Gathrin-Rasheed filina sarcoma viral (v-fil) oncogene homolog (FGR) mRNA
995	14039	26991	4.78	2.0E-79	4895524	NT	Homo sapiens Gathrin-Rasheed filina sarcoma viral (v-fil) oncogene homolog (FGR) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1036	14082		1.02	2.0E-79	AB23747.1	EST_HUMAN	HTB97.XT NCL CGAP P-28 Homo sapiens cDNA clone IMAGE:211886.3'
1304	14833	27810	0.97	2.0E-79	7657024	NT	Homo sapiens Dokkopi gene 4 (DKK-4), mRNA
1304	14833	27820	0.97	2.0E-79	7657024	NT	Homo sapiens Dokkopi gene 4 (DKK-4), mRNA
1304	14833	27814	0.92	2.0E-79	7652255	NT	Homo sapiens KIAA0703 gene product (KIA0703), mRNA
2136	14918	27914	4.97	2.0E-79	4589603	NT	Homo sapiens phosphodiesterase 8A, cAMP-specific, rod, alpha (PDE8A), mRNA
2136	15174	28163	4.97	2.0E-79	4589603	NT	Homo sapiens phosphodiesterase 8A, cAMP-specific, rod, alpha (PDE8A), mRNA
2136	15174	28164	4.97	2.0E-79	4589603	NT	Homo sapiens phosphodiesterase 8A, cAMP-specific, rod, alpha (PDE8A), mRNA
2322	16277	28237	0.91	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fes-associated factor FAF1 (FAF1 gene)
2322	16277	28237	0.91	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fes-associated factor FAF1 (FAF1 gene)
3633	18073	29837	0.83	2.0E-79	AF170462.1	NT	Homo sapiens chloride channel CLCA1 (CLCA1), complete cds
4133	17224	30113	1.15	2.0E-79	AJ271408.1	NT	Homo sapiens chromosome 21 segment HS210306
4716	17736	30428	0.97	2.0E-79	AL163066.2	NT	EST110298 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, contig BC003.16
5754	18048		1.25	2.0E-79	AA31223.1	EST_HUMAN	Homo sapiens X transporter protein 3 (X3), mRNA
5815	18035	32088	0.86	2.0E-79	1181769	NT	Homo sapiens mRNA for KIA0030 protein, partial cds
6371	19439	32362	1.07	2.0E-79	AB020037.1	NT	Homo sapiens mRNA for KIA0030 protein, partial cds
7133	18385	31273	0.7	2.0E-79	AF260913.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7373	20343	33694	1.74	2.0E-79	732479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7373	20343	33695	1.74	2.0E-79	732479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
8437	21406	34618	1.73	2.0E-79	4594462	NT	Homo sapiens retinol dehydrogenase 1 (RDH1), mRNA
8662	21620	35262	2.55	2.0E-79	11471428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9116	22084	35512	0.48	2.0E-79	8623248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9116	22084	35513	0.48	2.0E-79	8623248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9357	22322	35749	1.1	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H ⁺ -transporting, lysosomal (vacuolar proton pump) membrane factor associated protein M8-9 (H sapiens) (LOC03981), mRNA
10452	23374	36695	3.12	2.0E-79	S72869.1	NT	HAD103170 putative cytochrome P-450 (CYP450), mRNA, 3011 nt
10452	23374	36696	3.12	2.0E-79	S72869.1	NT	HAD103170 putative cytochrome P-450 (CYP450), mRNA, 3011 nt
11366	24315	37640	3.68	2.0E-79	BE004398.1	EST_HUMAN	RC4-B1 (313b-110300-015-110) B' (313) Homo sapiens cDNA
11366	24315	37641	3.68	2.0E-79	BE004398.1	EST_HUMAN	RC4-B1 (313b-110300-015-110) B' (313) Homo sapiens cDNA
11366	24315	37641	3.68	2.0E-79	BE004398.1	EST_HUMAN	RC4-B1 (313b-110300-015-110) B' (313) Homo sapiens cDNA
11366	24315	37641	3.68	2.0E-79	BE004398.1	EST_HUMAN	RC4-B1 (313b-110300-015-110) B' (313) Homo sapiens cDNA
12007	16350	31295	3.21	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIA0879), mRNA
12007	16350	31295	3.21	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIA0879), mRNA
12263	25107	31894	4.68	2.0E-79	AB020440.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12263	25107	31894	4.68	2.0E-79	AB020440.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12263	25107	31894	4.68	2.0E-79	AB020440.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12263	25107	31894	4.68	2.0E-79	AB020440.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
6739	25666		3.26	1.0E-79	BF36307.1	EST_HUMAN	MRO-NN0087-356000-017-510 NN0087 Homo sapiens cDNA

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Probe Seq ID Seq ID No.	Exon Seq ID Seq ID No.	ORF SEQ ID NO.	Expression Signal	Mod Similar (% BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8852	18905	33200	0.51	1.0E-79	AI013480.1	EST_HUMAN	IG7605.x1 N1_QGAP_U2 Homo sapiens cDNA clone IMAGE:2281288 3' similar to TR-Q2623 Q26923
8852	18905	33201	0.51	1.0E-79	AI013480.1	EST_HUMAN	IG7605.x1 N1_QGAP_U2 Homo sapiens cDNA clone IMAGE:2281288 3' similar to TR-Q2623 Q26923
8907	21895	34971	0.73	1.0E-79	BF394211.1	EST_HUMAN	IG7605.x1 N1_QGAP_U2 Homo sapiens cDNA clone IMAGE:3632809 6'
11944	24824	38419	2.84	1.0E-79	BF087403.1	EST_HUMAN	IG7605.x1 N1_QGAP_U2 Homo sapiens cDNA clone IMAGE:3632809 6'
3181	16217	28131	0.23	9.0E-40	AA725943.1	EST_HUMAN	IG7605.x1 N1_QGAP_U2 Homo sapiens cDNA clone IMAGE:3632809 6'
3181	16217	28132	0.23	9.0E-40	AA725943.1	EST_HUMAN	IG7605.x1 N1_QGAP_U2 Homo sapiens cDNA clone IMAGE:3632809 6'
10373	22288	38772	1.02	9.0E-40	BE786053.1	EST_HUMAN	IG7605.x1 N1_QGAP_U2 Homo sapiens cDNA clone IMAGE:3632809 6'
11606	24544	38104	0.28	9.0E-40	11433924	NT	Homo sapiens sulfate carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
11606	24544	38105	0.28	9.0E-40	11433924	NT	Homo sapiens sulfate carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3816	16660		1.22	0.0E-40	U94307.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RSN) pseudogene mRNA, partial cds
7602	20009	34183	2.95	0.0E-40	11422847	NT	Homo sapiens KIA00724 gene product (KIA00724), mRNA
7602	20009	34184	2.95	0.0E-40	11422847	NT	Homo sapiens KIA00724 gene product (KIA00724), mRNA
9757	22598	38156	1.14	0.0E-40	600592	NT	Homo sapiens triple functional domain (TPFRF Interactin) (TRIC), mRNA
9757	22598	38156	1.14	0.0E-40	600592	NT	Homo sapiens triple functional domain (TPFRF Interactin) (TRIC), mRNA
7166	10397	31242	0.59	7.0E-40	AF127902.1	NT	Callithrix jacchus olfactory receptor (CJA80) gene, partial cds
901	13596	28913	0.7	0.0E-40	AI42197.1	EST_HUMAN	IG7605.x1 N1_QGAP_U2 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW-NUEM_HUMAN
1650	14482	27855	2.17	0.0E-40	U64988.1	NT	Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KO SUBUNIT PRECURSOR ;
2307	18319	28338	1.17	0.0E-40	6831054	NT	Homo sapiens NRD connective mRNA, complete cds
2307	18319	28339	1.17	0.0E-40	6831054	NT	Homo sapiens NRD connective mRNA, complete cds
4314	17343	30225	1.1	0.0E-40	AB032981.1	NT	Homo sapiens mitochondrial membrane maintenance deficient (S. cerevisiae) 3 (MOM3), mRNA
4314	17343	30226	1.1	0.0E-40	AB032981.1	NT	Homo sapiens mitochondrial membrane maintenance deficient (S. cerevisiae) 3 (MOM3), mRNA
8589	18988	32177	1.32	0.0E-40	11421469	NT	Homo sapiens mRNA for KIAA1156 protein, partial cds
8164	19288	32503	3.12	0.0E-40	AI04468.1	NT	Homo sapiens mRNA for KIAA1156 protein, partial cds
8355	19424	32966	3.81	0.0E-40	1143739	NT	Homo sapiens mRNA for KIAA1156 protein, partial cds
8403	19471	32770	0.93	0.0E-40	7892393	NT	Homo sapiens mRNA for KIAA1156 protein, partial cds
8403	19471	32770	0.93	0.0E-40	7892393	NT	Homo sapiens mRNA for KIAA1156 protein, partial cds
9455	19520	32770	0.93	0.0E-40	116533.1	NT	Homo sapiens mRNA for KIAA1156 protein, partial cds
9778	22142	35586	3.06	0.0E-40	11526484	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Stimler (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3176	22142	335669	3.06	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3373	22338	357069	1.50	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3714	22697	36125	0.94	6.0E-80	AF161495.1	NT	Homo sapiens HSPC166 mRNA, complete cds
3841	22777	36233	0.47	6.0E-80	AJ271735.1	NT	Homo sapiens X4 pseudotubercular region, segment 1/2
10220	23145	36934	1.85	6.0E-80	U2021.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exon 21
11289	24239	37766	2.43	6.0E-80	11427366	NT	Homo sapiens brainstem Kunitz domain guanine nucleotide-binding protein 1 (BG1), mRNA
11588	24498	38054	20.37	6.0E-80	AF228730.1	NT	Homo sapiens CYP19 mRNA, complete cds
12051	24824	38521	1.84	6.0E-80	AF10285.1	NT	Homo sapiens N-acetylglucosaminyl-6-phosphate sulfatase mRNA, complete cds
12304	26787		2.39	6.0E-80	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12505	26243		6.41	6.0E-80	AB029900.1	NT	Homo sapiens CRNA for cyclophilin sulfotransferase, exon 1, 2, 3, 4, 5
12994	28914		4.47	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGC12 gene)
590	13957	28572	2.89	6.0E-80	4568228	NT	Homo sapiens protein gene (proscama, macrophage) 28S subunit, non-A, P, alpha, 3 (P5MA03) mRNA
836	13883	20848	1.49	6.0E-80	AF108350.1	NT	Homo sapiens protein-tyrosine kinase (MNBB) mRNA, complete cds
836	13883	20849	1.49	6.0E-80	AF108350.1	NT	Homo sapiens protein-tyrosine kinase (MNBB) mRNA, complete cds
1193	14253		0.90	6.0E-80	X71547.1	NT	H. sapiens noni gene (noni 13)
1450	14463		2.21	6.0E-80	AL162268.2	NT	Homo sapiens chromosome 21 segment HS21C083
2369	15377	25400	1.92	6.0E-80	AF163395.1	NT	Human 13.9kb protein homolog mRNA, complete cds
2437	16444	28462	6.37	6.0E-80	AB375654.1	NT	Homo sapiens mRNA for KIAA1634 protein, partial cds
2850	15768	28818	5	6.0E-80	AB375654.1	NT	Homo sapiens H3 histone family, member 1 (H3F-1) mRNA
4059	17105	25958	1.28	6.0E-80	AB375654.1	NT	Homo sapiens HMT-1 mRNA for beta-1.4 mannose 6-phosphatase, complete cds
4059	17105	25959	1.28	6.0E-80	AB375654.1	NT	Homo sapiens HMT-1 mRNA for beta-1.4 mannose 6-phosphatase, complete cds
4951	18068	30594	1.53	6.0E-80	AL162268.2	NT	Homo sapiens chromosome 21 segment HS21C088
8700	21688	36601	1.14	6.0E-80	F59915.1	EST_HUMAN	Human muscicula keratin complex 2, gene 5q (K12-5q), mRNA
9613	22571	36069	15.3	6.0E-80	F59915.1	EST_HUMAN	Human muscicula keratin complex 2, gene 5q (K12-5q), mRNA
4738	17786	30663	9.37	6.0E-80	AB375654.1	EST_HUMAN	Human muscicula keratin complex 2, gene 5q (K12-5q), mRNA
4943	17861		3.11	6.0E-80	BE871465.1	EST_HUMAN	Human muscicula keratin complex 2, gene 5q (K12-5q), mRNA
5919	19005	32197	2.02	6.0E-80	AB375654.1	EST_HUMAN	Human muscicula keratin complex 2, gene 5q (K12-5q), mRNA
1314	14541	27632	4.7	6.0E-80	R33321.1	EST_HUMAN	Human muscicula keratin complex 2, gene 5q (K12-5q), mRNA
1577	14922	27632	1.49	6.0E-80	AB375654.1	EST_HUMAN	Human muscicula keratin complex 2, gene 5q (K12-5q), mRNA
2071	15988	28109	6.1	6.0E-80	AL043119.2	EST_HUMAN	Human muscicula keratin complex 2, gene 5q (K12-5q), mRNA
5574	19443	32884	0.60	6.0E-80	AB375654.1	EST_HUMAN	Human muscicula keratin complex 2, gene 5q (K12-5q), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	Q95 SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6374	19442	33885	0.69	2.0E-40	AB238172.1	EST_HUMAN	wb6d0.x1 NCI CGAP. C6e Homo sapiens cDNA clone IMAGE:2449786 3'
6977	20200	33859	1.01	2.0E-40	AA59862.1	EST_HUMAN	m6d01.x1 NCI CGAP. C6e Homo sapiens cDNA clone IMAGE:1000177 3'
7098	20032	33335	1.51	2.0E-40	11421930	NT	Homo sapiens GGP transport complex protein, (80 ID) (GT080), mRNA
7463	20429	33786	0.81	2.0E-40	178216.1	EST_HUMAN	y6881.2.1 Soares infant brain N1B Homo sapiens cDNA clone IMAGE:22881 5' similar to
8614	22477	35022	1.22	2.0E-40	AW664270.1	EST_HUMAN	SP K10R. XENLA P08802 KERATIN, TYPE I, CYTOSKELETAL ENDO B ;
10126	23032	36550	0.97	2.0E-40	AJ007375.1	NT	EST379343 IMAGE resequencing, MACH Homo sapiens cDNA
11216	24189	37897	8.05	2.0E-40	AA369882.1	EST_HUMAN	27012.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:272727 5' similar to TRG191316
340	13429	38506	2.11	1.0E-40	AF160352.2	EST_HUMAN	GP1315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
800	13889	28806	1.95	1.0E-40	AF231923.1	NT	Homo sapiens chromosome 21 segment HS21C103
1371	14692		2.82	1.0E-40	A123856.1	EST_HUMAN	m0112.x5 NCI CGAP. C6e Homo sapiens cDNA clone IMAGE:1076695 3' similar to contains ORF.11 ORF
4857	17874	30762	0.76	1.0E-40	N96520.1	EST_HUMAN	capillary domain 1 ;
5400	18503	33821	3.82	1.0E-40	BE368615.1	EST_HUMAN	24007.11 Soares fetal liver spleen N1F5.1 Homo sapiens cDNA clone IMAGE:284972 5' similar to contains
6035	19193	33276	8.24	1.0E-40	110347.1	NT	61274303F1 N1F1_UGG.20 Homo sapiens cDNA clone IMAGE:3815433 5'
6546	19704	32890	1.3	1.0E-40	5174540	NT	Human pro-alpha1(I) collagen (COL3A1) gene, exons 1-54, complete cds
7414	20391	33732	1.09	1.0E-40	AI224172.1	NT	Homo sapiens metal dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
7824	20772	34148	2.6	1.0E-40	AB48731.1	EST_HUMAN	Homo sapiens mRNA for leoplatin B
8573	21541	34691	1.17	1.0E-40	AB48731.1	EST_HUMAN	w62508.x1 NCI CGAP. K561 Homo sapiens cDNA clone IMAGE:2472364 3'
9048	22014	35437	0.92	1.0E-40	1142121	NT	w62503.x1 NCI CGAP. K561 Homo sapiens cDNA clone IMAGE:2472364 3'
9048	22014	35437	0.92	1.0E-40	1142121	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9048	22014	35437	0.92	1.0E-40	1142121	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9540	22684	36032	1.36	1.0E-40	AF245216.1	NT	Homo sapiens probable mitomycin binding C-type lectin DC-SIGNR mRNA, complete cds
9540	22684	36032	1.36	1.0E-40	AF245216.1	NT	Homo sapiens probable mitomycin binding C-type lectin DC-SIGNR mRNA, complete cds
10791	23712	37214	1.12	1.0E-40	DG479.2	NT	Homo sapiens similar to rat myomegalin (LOC54182), mRNA
11013	23978	37603	1.72	1.0E-40	11841276	NT	Homo sapiens similar to rat myomegalin (LOC54182), mRNA
11443	24396	37626	1.67	1.0E-40	8923609	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
12378	25287	31779	2.27	1.0E-40	11417601	EST_HUMAN	Homo sapiens myofibrillar (disrupted in balanced fertilization) 1 (MNT), mRNA
11488	24431	37960	9.7	8.0E-41	BE394625.1	EST_HUMAN	60131031F1 N1F1_UGG.24 Homo sapiens cDNA clone IMAGE:3652070 5'
7484	20430	33787	2.97	7.0E-41	AB22115.1	EST_HUMAN	2a61c08.x3 Soares, fetal lung, N6L16W Homo sapiens cDNA clone IMAGE:269518 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar EST BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11519	24460	30010	3.39	4.0E-41	4769095	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
11619	24460	30011	3.39	4.0E-41	4769096	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
12200	29883	31439	3.45	4.0E-41	11417892	NT	Homo sapiens calcineurin binding protein 1 (KIA00300) mRNA
12201	29883	31439	3.45	4.0E-41	11417892	NT	Homo sapiens calcineurin binding protein 1 (KIA00300) mRNA
12737	29389	31763	1.71	4.0E-41	11417871	NT	Homo sapiens beta-creb1-binding protein 1 (KIA00300) mRNA
12737	29389	31763	1.71	4.0E-41	11417871	NT	Homo sapiens beta-creb1-binding protein 1 (KIA00300) mRNA
12878	29472	31728	3.89	4.0E-41	11417974	NT	Homo sapiens transcobalamin II; megaloblastic anemia (TMC2) mRNA
1272	14307	27268	10.2	3.0E-41	115000.1	NT	Homo sapiens NF2 gene
1272	14307	27267	10.2	3.0E-41	115000.1	NT	Homo sapiens NF2 gene
2390	15398	28412	1.95	3.0E-41	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3004	18032	28986	5.18	3.0E-41	4592280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3004	18032	28981	5.19	3.0E-41	4592280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2844	15004	28638	2.48	2.0E-41	BE764363.1	EST_HUMAN	Homo sapiens NCL CGAP Bm82 Homo sapiens cDNA clone IMAGE:3677121 5'
2844	15004	28638	2.48	2.0E-41	BE764363.1	EST_HUMAN	Homo sapiens NCL CGAP Bm82 Homo sapiens cDNA clone IMAGE:3677121 5'
3737	18928	29733	0.96	2.0E-41	AW81154.1	EST_HUMAN	Homo sapiens NCL CGAP K411 Homo sapiens cDNA clone IMAGE:2952384 5'
6200	21269	34670	0.83	2.0E-41	8622839	NT	Homo sapiens NCL CGAP K411 Homo sapiens cDNA clone IMAGE:2952384 5'
13032	18928	29735	2.55	2.0E-41	AW81154.1	EST_HUMAN	Homo sapiens NCL CGAP K411 Homo sapiens cDNA clone IMAGE:2952384 5'
4543	17566	30453	3.12	1.0E-41	AA040370.1	EST_HUMAN	PIR-S53437 S82437 QDP-diacylglycerol synthase - full length
4675	17566	30583	9.34	1.0E-41	BE047096.1	EST_HUMAN	PIR-S53437 S82437 QDP-diacylglycerol synthase - full length
5308	18928	38611	3.31	1.0E-41	U67928.1	NT	Human acetylcholinesterase (AChE) gene, exon 3
5427	18530	31409	3.6	1.0E-41	11432069	NT	Homo sapiens polymerase (DNA directed), gamma (POLG) mRNA
5427	18530	31410	3.6	1.0E-41	11432069	NT	Homo sapiens polymerase (DNA directed), gamma (POLG) mRNA
5980	18978	31839	0.83	1.0E-41	AA056568.1	EST_HUMAN	Z65406.1 Soares, NHHMP, S11 Homo sapiens cDNA clone IMAGE:362475 5' similar to SW/PR12_HUMAN
5737	18931	32009	3.37	1.0E-41	U52351.1	NT	P-49483 DNA PMASE 58 KD SUBUNIT 1
5737	18931	32010	3.37	1.0E-41	U52351.1	NT	Homo sapiens arm-repeat protein NRPAP1/neurogranin (GTND2) mRNA, partial cds
5289	18942	32575	1.65	1.0E-41	BF74941.1	EST_HUMAN	Homo sapiens arm-repeat protein NRPAP1/neurogranin (GTND2) mRNA, partial cds
6959	19766	33032	0.86	1.0E-41	11420688	NT	G0213788-PT NMR_MSC_83 Homo sapiens cDNA clone IMAGE:4274555 5'
6959	19766	33032	0.86	1.0E-41	11420688	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (700D) (PDE1C) mRNA
8859	19768	33033	0.86	1.0E-41	11420688	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (700D) (PDE1C) mRNA
9602	19964	33261	1.26	1.0E-41	AJ133269.1	NT	Homo sapiens cavadin-1/2 locus, Oat1g1, D7S822, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)

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Probe Seq ID NO.	Exon Seq ID NO.	ORF Seq ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6049	20966	34382	7.93	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
10134	23090	36537	7.95	1.0E-81	BE562878.1	EST HUMAN	80184595.F11.NIH_MGC_391 Homo sapiens cDNA clone IMAGE:380228.6
10134	23090	36538	7.95	1.0E-81	BE562878.1	EST HUMAN	80184595.F11.NIH_MGC_391 Homo sapiens cDNA clone IMAGE:380228.6
10328	23352	36731	4.63	1.0E-81	BE564387.1	EST HUMAN	80134318.F11.NIH_MGC_331 Homo sapiens cDNA clone IMAGE:386483.9
10463	23395	36878	1.09	1.0E-81	AA630794.1	EST HUMAN	ac14408.at Stratagene HeLa cell c3 897210 Homo sapiens cDNA clone IMAGE:386427.3 similar to SW1Y806_YEAST Y98128.HYPOTHETICAL 60.9 KD PROTEIN IN RP101-RP513 INTERGENIC REGION
10465	23397	36900	3.01	1.0E-81	BE74456.1	EST HUMAN	801877338.F11.NIH_MGC_31 Homo sapiens cDNA clone IMAGE:3833260.5
10465	23397	36901	3.01	1.0E-81	BE74456.1	EST HUMAN	801877338.F11.NIH_MGC_31 Homo sapiens cDNA clone IMAGE:3833260.5
10674	23704	37299	1.7	1.0E-81	AA1897590.1	EST HUMAN	CM84NN055.124000-147412.133890 Homo sapiens cDNA
11425	24360	37605	2.9	1.0E-81	AA1844986.1	EST HUMAN	MRG-C110005.255959-13 CT10006 Homo sapiens cDNA
11425	24360	37606	2.9	1.0E-81	AA1844986.1	EST HUMAN	MRG-C110005.255959-13 CT10006 Homo sapiens cDNA
11429	24373	37911	6.85	1.0E-81	AA1798167.1	EST HUMAN	PC3-L110005.292200-311-093 UM0248 Homo sapiens cDNA
11429	24373	37912	6.85	1.0E-81	AA1798167.1	EST HUMAN	PC3-L110005.292200-311-093 UM0248 Homo sapiens cDNA
11851	24734	38321	2.11	1.0E-81	BF204283.1	EST HUMAN	801857714.F11.NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4110469.5
12414	25195	31822	4.59	1.0E-81	11418138	NT	Homo sapiens protein (similar to podocortin B mRNA coding protein) (D174219.2), mRNA
107	13133	26031	0.94	8.0E-82	AF161406.1	NT	Homo sapiens RSPC298 mRNA, partial cds
137	13133	26031	2.07	8.0E-82	AF161406.1	NT	Homo sapiens RSPC298 mRNA, partial cds
263	13399	28294	2.7	8.0E-82	U08586.1	NT	Human CRFB4 gene, partial cds
818	13873	28621	14.93	8.0E-82	U08586.1	NT	Human CRFB4 gene, partial cds
868	13943	28601	1.44	8.0E-82	U08586.1	NT	Human CRFB4 gene, partial cds
1487	14320	27493	1.36	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1865	14993	27674	1.7	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4114	17148	30040	0.82	8.0E-82	4804116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4272	17271	30161	0.75	8.0E-82	8622432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20481), mRNA
2777	19769	28769	2.83	7.0E-82	BF033327.1	EST HUMAN	80149535.F11.NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3862088.5
2823	20026	36524	1.8	7.0E-82	AA144050.1	EST HUMAN	AA1740950.HEB1A1 Homo sapiens cDNA clone HEB1A1000752.3
1885	14712	27960	25.07	4.0E-82	AA5653747.1	EST HUMAN	aa56504.at Stratagene schizoblast ST1 Homo sapiens cDNA clone IMAGE:96842.3
5974	18670	31842	0.89	4.0E-82	BF139189.1	EST HUMAN	Homo sapiens alpha-lubulin isoform 1 mRNA, complete cds
5974	18670	31843	0.89	4.0E-82	BF139189.1	EST HUMAN	Q124HT0540-128900-365-108 HT0540 Homo sapiens cDNA
5951	18641	31228	0.99	4.0E-82	U026833.1	EST HUMAN	Q124HT0540-128900-365-108 HT0540 Homo sapiens cDNA
5951	18641	31228	0.99	4.0E-82	U026833.1	EST HUMAN	Human von Willebrand factor gene, exon 9

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (10p) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12025	24601	38495	7.32	4.0E-42	AB97390.1	EST_HUMAN	wp75409.x1 NCL CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2467524 3' similar to TR075276
12057	25337		3.69	4.0E-42	AF029701.2	NT	OP75276 P0011: Homo sapiens presentin-1 gene, exons 1 and 2
277	13373	28501	18.34	3.0E-42	4602189	NT	Homo sapiens amyloid beta (A4) precursor protein (protease non-II, Alzheimer disease) (APP), mRNA
704	13766	29701	2.78	3.0E-42	BC005705.1	EST_HUMAN	RC2-EN0120-010400-013-02 BNC120 Homo sapiens cDNA
788	13947	28794	10.4	3.0E-42	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
971	13927	28895	6.11	3.0E-42	4602189	NT	Homo sapiens amyloid beta (A4) precursor protein (protease non-II, Alzheimer disease) (APP), mRNA
1052	14106		53.82	3.0E-42	AA735948.1	EST_HUMAN	u23605.at Soares_ha25_NHT Homo sapiens cDNA clone 1343848 3'
1357	14382	27583	1.01	3.0E-42	AW978773.1	EST_HUMAN	RC2-EN0120-010400-013-02 P10001 Homo sapiens cDNA
1462	14495	27460	2.81	3.0E-42	AL13326.2	NT	Homo sapiens chromosome 21 segment H521C066
1977	14841	27837	1.95	3.0E-42	BC13322.1	EST_HUMAN	RC1-BH0005-250700-076-04 BN0003 Homo sapiens cDNA
2023	15043	28156	1.2	3.0E-42	4601022	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (phallary) receptor type 1 (ADCYAP1R1) mRNA
2085	15336		2.31	3.0E-42	U45531.1	NT	Homo sapiens neurocystic glycine kinase, receptor type 2 (NRYK2) mRNA
8492	21498	34877	2.71	3.0E-42	U45531.1	NT	Homo sapiens neurocystic glycine kinase, receptor type 2 (NRYK2) mRNA
8602	21668	35252	0.71	3.0E-42	11432889	NT	Homo sapiens protein 9 (GNTN9), mRNA
8602	21668	35252	0.71	3.0E-42	11432889	NT	Homo sapiens protein 9 (GNTN9), mRNA
10183	23108	36591	3.98	3.0E-42	AB026000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10183	23108	36591	3.98	3.0E-42	AB026000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
12109	24978	36577	1.6	3.0E-42	11432889	NT	Homo sapiens protein 9 (GNTN9), mRNA
12109	24978	36577	1.6	3.0E-42	11432889	NT	Homo sapiens protein 9 (GNTN9), mRNA
599	13966	26579	1.96	2.0E-42	AB023218.1	NT	Homo sapiens mRNA for KIAA0969 protein, partial cds
599	13966	26579	1.96	2.0E-42	AB023218.1	NT	Homo sapiens mRNA for KIAA0969 protein, partial cds
8492	21498	34877	2.71	3.0E-42	U45531.1	NT	Homo sapiens neurocystic glycine kinase, receptor type 2 (NRYK2) mRNA
2951	15049	28707	0.76	2.0E-42	AL163201.2	NT	Homo sapiens chromosome 21 segment H521C001
3960	19859	25802	1.07	2.0E-42	U67976.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4052	17059	25884	0.55	2.0E-42	U79833.1	NT	Human integrin membrane surface protein Spry4 mRNA, complete cds
4291	17260	30771	1.07	2.0E-42	4604118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4586	17610	30505	1.09	2.0E-42	AB026019.1	NT	Homo sapiens mRNA for KIAA1069 protein, partial cds
4586	17610	30505	1.09	2.0E-42	AB026019.1	NT	Homo sapiens mRNA for KIAA1069 protein, partial cds
4604	17621	30613	3.21	2.0E-42	AF045555.1	NT	Homo sapiens wiser1 (WBSR1) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds

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Probe ID	Exon NO.	ORF SEQ ID NO.	Expression Signal	Mod Similar (BLAST E Value)	Top Hit Accession No.	Top Hit Database Source
5117	18127	31002	1.93	2.0E-82	4407580	NT
5117	18127	31003	1.93	2.0E-82	4607680	NT
5181	18463	31953	3.50	2.0E-82	A30182701	NT
5249	19371	32670	0.98	2.0E-82	A47234631	NT
7435	20041	34400	0.99	2.0E-82	A14783281	EST_HUMAN
8104	21004	34070	0.98	2.0E-82	8922130	NT
8368	21463	34973	0.98	2.0E-82	11431845	NT
8688	21463	35038	0.97	2.0E-82	11321570	NT
9017	21463	35402	0.94	2.0E-82	7897340	NT
9017	21463	35403	0.97	2.0E-82	7897340	NT
10468	23300	36884	1.68	2.0E-82	Y08032.1	NT
10468	23300	38865	1.95	2.0E-82	Y08032.1	NT
11600	24538	39005	3.85	2.0E-82	11417159	NT
11600	24538	39006	3.85	2.0E-82	11417159	NT
11638	24575	39140	2.31	2.0E-82	U08793.1	NT
11638	24575	39141	2.31	2.0E-82	U08793.1	NT
12227	25062		1.94	2.0E-82	NP4980.1	EST_HUMAN
12760	26108		4.39	2.0E-82	A0011278.1	EST_HUMAN
13064	26508		1.93	2.0E-82	11418097	NT
594	13651	26574	1.27	1.0E-82	11545621	EST_HUMAN
1213	14281		1.98	1.0E-82	858819.1	EST_HUMAN
1290	14326	27268	1.91	1.0E-82	858819.1	EST_HUMAN
1291	14326	27267	1.07	1.0E-82	A0011102.1	EST_HUMAN
8294	22250	35539	1.00	1.0E-82	A00303788.1	NT
9001	22531	35403	1.24	1.0E-82	A00316508.1	NT
10211	22531	35403	1.94	1.0E-82	BP514568.1	EST_HUMAN
10355	23328	37691	1.97	1.0E-82	A1163202.1	NT
11097	24031	37691	1.97	9.0E-83	BF972200.1	EST_HUMAN
10677	25031	39454	1.93	9.0E-83	BE28347.1	EST_HUMAN
10677	25031	37058	1.95	8.0E-83	BE283973.1	EST_HUMAN
1413	14445	27117	1.65	8.0E-83	GN65951.1	EST_HUMAN
1691	15820	27702	0.98	8.0E-83	AW85522.1	EST_HUMAN
1359	14304	27394	0.96	7.0E-83	AW85522.1	EST_HUMAN
2876	15035		1.92	7.0E-83	AA58485.1	EST_HUMAN

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mod Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4832	17870		7.64	7.0E-43	BF221813.1	EST_HUMAN	7p37.07.AT NCI_QGAP_F28 Homo sapiens cDNA clone IMAGE3447853 3' similar to TRQ97318 Q97318 D-2207H1.4 ;
6199	19244	32476	0.73	7.0E-43	11429557	NT	Human sapiens KIAA0100 gene product (KIAA0100) mRNA
403	13476	28410	3.07	6.0E-43	M33320.1	NT	Human placenta Glycophorin 1b (GPIb) gene, exon 2-2b
1002	14830	27817	1.08	8.0E-43	AW57008.1	EST_HUMAN	H3103.AT Score_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE2934523 3' similar to
3030	16038	29009	0.64	6.0E-43	AW615405.1	EST_HUMAN	SW16EB_HAEN P4471 HYPOTHETICAL PROTEIN H0034. ;
3084	16121		0.87	6.0E-43	AF231916.1	NT	QV43T0234-181198-037405 ST0234 Homo sapiens cDNA
3083	16140	29051	1.03	6.0E-43	AA701457.1	EST_HUMAN	285505.AT Score2_fetal_liver脾脏 -INFL32 S1 Homo sapiens cDNA clone IMAGE435080 3'
3975	19620	28541	2.84	6.0E-43	11439241	NT	Homo sapiens hypothetical protein FL103719 (FL10379) mRNA
5197	18176	31954	1.2	6.0E-43	4827039	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 18 (TNFSF18) mRNA
5366	18471	31442	1.93	6.0E-43	4597869	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33MD) (VAPA) mRNA, and translated products
5367	18478	31443	1.92	6.0E-43	4597869	NT	Homo sapiens tyrosinase gene, exon 1-5b
5715	20465	34465	2.1	6.0E-43	U167070.1	NT	Homo sapiens mit protein kinase gene
10039	20963	36490	2.6	8.0E-43	U17853.1	NT	Homo sapiens myosin regulatory subunit 1 (MYO1B) (MYO1B2) mRNA
10127	20933	36581	0.78	6.0E-43	4593312	NT	Homo sapiens myosin regulatory subunit 1 (MYO1B) (MYO1B2) mRNA
10127	20933	36582	0.78	6.0E-43	11433942	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae P98 (PRF8) mRNA
11859	24741		2.01	6.0E-43	11433942	NT	ab14610.3 Sindbis virus (6937210) Homo sapiens cDNA clone IMAGE344810 3' similar to contains THR12 THR regulatory element
12178	25027		5.85	6.0E-43	AA489105.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
945	13968		1.42	6.0E-43	AF240786.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2056	15329		1	6.0E-43	AF060905.1	NT	Homo sapiens 26S proteasome regulatory subunit (SIU2) mRNA, complete cds
3502	16569	22610	0.97	6.0E-43	AL33207.2	NT	Novel human gene mapping to chromosome X
3926	16969	28979	1.02	6.0E-43	4985190	NT	Homo sapiens deoxyribonuclease I (DNASE1) mRNA
9115	18128	31000	14.32	6.0E-43	4957013	NT	Homo sapiens catalase (CAT) mRNA
9115	18128	31001	14.32	6.0E-43	4557013	NT	Homo sapiens catalase (CAT) mRNA
9245	18235	31124	0.93	6.0E-43	4503802	NT	Homo sapiens phosphatidyl-inositol 3-kinase, catalytic, gamma polypeptide (PIK3CG) mRNA
641	13107	28628	2.28	4.0E-43	AF224960.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, complete cds
3525	19571	29494		4.0E-43	BE680075.1	EST_HUMAN	U015116007.NH1_MSC_71 Homo sapiens cDNA clone IMAGE393105 5'
969	14050		8.39	3.0E-43	AA388311.1	EST_HUMAN	EST178542 Pileola 1 Homo sapiens cDNA similar to a mRr to endogenous retrovirus ERV9

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Table 4
Isotypes Expressed In Bone Marrow[illegible]

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Event SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11272	24224	37740	1.84	2.0E-43	AL134452.1	EST_HUMAN	DKFZ294T135.11 5'UT (synonym: hNR1) Homo sapiens cDNA clone DKFZ294T135.5'
11272	24224	37740	1.84	2.0E-43	AL134452.1	EST_HUMAN	DKFZ294T135.11 5'UT (synonym: hNR1) Homo sapiens cDNA clone DKFZ294T135.5'
12802	26428		4.81	2.0E-43	AB011936.1	NT	Homo sapiens gene for AFA, complete cds
1410	14443	27414	1.56	1.0E-43	4504329	NT	Homo sapiens hydroxylase-Coenzyme A dehydrogenase3-lysate-Coenzyme A hydrolase (trifunctional protein), beta subunit (H4H3) mRNA
1410	14443	27414	1.56	1.0E-43	4504329	NT	Homo sapiens hydroxylase-Coenzyme A dehydrogenase3-lysate-Coenzyme A hydrolase (trifunctional protein), beta subunit (H4H3) mRNA
1433	14453	27461	0.93	1.0E-43	AF105871.1	NT	Homo sapiens hydroxylase-Coenzyme A dehydrogenase3-lysate-Coenzyme A hydrolase (trifunctional protein), beta subunit (H4H3) mRNA
2656	19452	27462	0.93	1.0E-43	AF105871.1	NT	Homo sapiens hydroxylase-Coenzyme A dehydrogenase3-lysate-Coenzyme A hydrolase (trifunctional protein), beta subunit (H4H3) mRNA
3108	19253	29271	1.18	1.0E-43	BE633565.1	EST_HUMAN	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
3852	18923	29271	3.38	1.0E-43	7626349	NT	031807375F1.NH1.MGC-71 Homo sapiens cDNA clone IMAGE380874.5'
4273	17602	30162	2.37	1.0E-43	AF533768.1	NT	Homo sapiens cell recognition molecule Casp2 (NUA00885) mRNA
6854	18007	33203	1.53	1.0E-43	U027614.1	EST_HUMAN	Rattus norvegicus brain specific corticotrophin-binding protein CBP50 mRNA, partial cds
3810	18550	29769	3.98	7.0E-44	BE01208.1	EST_HUMAN	Human gene for mitochondrial adenosine/CoA dehydrogenase, exon 3
1258	14333	27204	4.11	8.0E-44	BE633894.1	EST_HUMAN	PROTEIN (HUMAN)
1258	14333	27256	4.11	8.0E-44	BE633894.1	EST_HUMAN	RC2-F10118-205500-01-1305 FN0118 Homo sapiens cDNA
2407	15414	28438	5.78	8.0E-44	AA177674.1	EST_HUMAN	aa8503.11 Stratiotes alba root cDNA FN1118 Homo sapiens cDNA
5311	18326		1.19	9.0E-44	AL042883.2	EST_HUMAN	DKFZ294T40322.11 434 (synonym: hNR3) Homo sapiens cDNA clone IMAGE571020.3'
5595	18962	31682	1.59	9.0E-44	AA87339.1	EST_HUMAN	aa77693.41 Somax, NFL, T, GRG, S1 Homo sapiens cDNA clone IMAGE17460500.3' similar to p34-H14338
5743	18937	32018	1.09	8.0E-44	11428718	NT	VITAMIN K-DEPENDENT PROTEIN 5 PRECURSOR (HUMAN)
5743	18937	32019	1.09	8.0E-44	11428718	NT	Homo sapiens acyl-LDL receptor, SREBP-cis-acting receptor expressed by endothelial cells (SREC), mRNA
7714	20871	34039	3.35	8.0E-44	BE010371.1	EST_HUMAN	Homo sapiens acyl-LDL receptor, SREBP-cis-acting receptor expressed by endothelial cells (SREC), mRNA
7950	20866	34059	0.69	8.0E-44	AF039391.1	NT	PMGL T0019-160000-004-F02 L T0019 Homo sapiens cDNA
8408	21377	34783	2.05	8.0E-44	BE770198.1	EST_HUMAN	Homo sapiens pre-mRNA splicing factor (PSF19) mRNA, complete cds
7115	13777	28712	0.81	5.0E-44	AA382811.1	EST_HUMAN	PMF-F10034-160000-004-F10 F10034 Homo sapiens cDNA
3227	18064		1.54	5.0E-44	AF109718.1	NT	EST86094 Testis 1 Homo sapiens cDNA 5' end
6227	19301	32534	0.49	5.0E-44	AA167978.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
							249807.11 Stratiotes alba neuron (6837233) Homo sapiens cDNA clone IMAGE531100.5' similar to
							TRC-68916 G48916 RETROTRANSCRIPTABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q.1

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Table 4
Single Exon Probes Expressed in Bone Marrow

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	OSF SEQ ID NO.	Expression Signal	Most Similar (100) Hit Database Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9701	22654	36108	0.99	2.0E-44	AJ120280.1	EST_HUMAN	AJ120280 HEMABT1 Homo sapiens cDNA clone HEMABT100339 5'
10089	22015	36491	0.95	2.0E-44	H2284.1	EST_HUMAN	ymd1e1.11 Soares infant brain 1MB Homo sapiens cDNA clone IMAGE:51383 5' similar to SP-APOL_RAT
12448	29206	31829	3.26	2.0E-44	BF448006.1	EST_HUMAN	P26844 BETA-2-GLYCOPROTEIN 1; nido3002.x1 Lipek8_symphidetic trunk Homo sapiens cDNA clone IMAGE:490251 3' similar to
12445	29206	31830	3.26	2.0E-44	BF448006.1	EST_HUMAN	TR-CDUGSS CDUGSS D776528.1; nido3002.x1 Lipek8_symphidetic trunk Homo sapiens cDNA clone IMAGE:490251 3' similar to
312	13404	25330	1.44	1.0E-44	AF114483.1	NT	Homo sapiens tyrosine 3-monooxygenase/thyrosinase 5-monooxygenase activation protein, zeta polypeptide (TYH4Z) mRNA
551	13621	26541	15.79	1.0E-44	4607692	NT	Homo sapiens tyrosine 3-monooxygenase/thyrosinase 5-monooxygenase activation protein, zeta polypeptide (TYH4Z) mRNA
721	13763	27922	0.95	1.0E-44	11427831	NT	Homo sapiens complement component 5 (C5) mRNA
1359	14351	27922	0.95	1.0E-44	AA384378.1	EST_HUMAN	mid8511.111 transgenic adult brain 31T Homo sapiens cDNA clone IMAGE:129885 3'
2070	15037	28105	2.51	1.0E-44	BE39731	EST_HUMAN	001306007.1 NH1_PGC_24 Homo sapiens cDNA clone IMAGE:362657 5'
2232	15246	28389	4.37	1.0E-44	11427831	EST_HUMAN	mid8511.111 transgenic adult brain 31T Homo sapiens cDNA clone IMAGE:129885 3'
3764	16605	29717	2.47	1.0E-44	AA720851.1	EST_HUMAN	001306007.1 NH1_PGC_24 Homo sapiens cDNA clone IMAGE:362657 5'
4448	17432	30650	3.92	1.0E-44	AJ220641.1	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
4728	17748	30650	2.95	1.0E-44	AL43514.2	EST_HUMAN	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
4728	17748	30640	2.95	1.0E-44	AL43514.2	EST_HUMAN	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
4949	17472	30950	2.12	1.0E-44	AJ220641.1	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
6026	19112	32314	0.86	1.0E-44	11434422	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
6314	19385	32927	1.38	1.0E-44	S77482.1	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
7094	20085	33394	1.44	1.0E-44	AL449784.1	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
7094	20085	33395	1.44	1.0E-44	AL449784.1	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
7314	20285	33526	2.56	1.0E-44	AL449784.1	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
7706	20695	34032	4.72	1.0E-44	8303604	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
7814	20763	34138	0.63	1.0E-44	11430840	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
7839	20793	34138	2.13	1.0E-44	11430840	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
8893	22946	36533	2.91	1.0E-44	5031640	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
10128	23004	36533	0.92	1.0E-44	AF224511.1	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
10150	18337	31265	2.85	1.0E-44	4607848	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
10150	18337	31265	2.85	1.0E-44	4607848	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
12121	20285	33526	2.67	1.0E-44	AL449784.1	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'
12324	25126		2.03	1.0E-44	11417812	NT	Homo sapiens 68 kDa cytosolic protein (AMT) cDNA clone IMAGE:129106 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12456	25201	31829	2.32	1.0E-84	11418185	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
12457	25202	31830	1.91	9.0E-85	AF163206.2	NT	Homo sapiens chromosome 21 segment HS21C080
1074	14110	27069	2.21	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Sclp mRNA, complete cds
1074	14110	27070	2.21	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Sclp mRNA, complete cds
1581	14614	27595	1.31	9.0E-85	M33282.1	NT	Human plasmidogen gene, exon 7
1581	14614	27596	1.31	9.0E-85	M33282.1	NT	Human plasmidogen gene, exon 7
1684	14715	27595	2.95	9.0E-85	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4280	17309	30188	1.11	9.0E-85	AF163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4613	17309	30821	1.05	9.0E-86	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HS2BP), mRNA
4650	17365	30855	1	9.0E-86	AF163288.2	NT	Homo sapiens chromosome 21 segment HS21C080
1138	14181	27132	13.33	7.0E-85	U50984.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11659	24837		9.76	7.0E-85	AF113210.1	NT	Homo sapiens MSTP200 mRNA, complete cds
11745	24830	38209	2.51	9.0E-85	1148873	NT	Homo sapiens DEADH (Atp-Glu-Ala-AspHis) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11745	24830	38210	2.51	9.0E-85	1148873	NT	Homo sapiens DEADH (Atp-Glu-Ala-AspHis) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2340	15350	28371	1.67	5.0E-85	AF16294.2	NT	Homo sapiens chromosome 21 segment HS21C084
5520	18925	31590	1.37	5.0E-85	BF035674.1	EST_HUMAN	60145846F1 NH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
5520	18925	31591	1.37	5.0E-85	BF035674.1	EST_HUMAN	60145846F1 NH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
13000	18344		6.19	5.0E-85	AF21189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1H-tetradom (CACNA1H) mRNA, complete cds
6271	19344	32576	1.42	4.0E-85	BF07090.1	EST_HUMAN	602084720F1 NH_MGC_83 Homo sapiens cDNA clone IMAGE:424087 5'
6271	19344	32577	1.42	4.0E-85	BF07090.1	EST_HUMAN	602084720F1 NH_MGC_83 Homo sapiens cDNA clone IMAGE:424087 5'
7013	20180	33456	0.88	4.0E-85	AF028118.1	EST_HUMAN	NF4001.v1 NC1_CGAP_NH11 Homo sapiens cDNA clone IMAGE:2296908 3'
10937	23957		1.35	4.0E-85	BE012693.1	EST_HUMAN	RC1-1819523-120200-011-c07 B10623 Homo sapiens cDNA
12575	25772		1.31	4.0E-85	Z118897.1	EST_HUMAN	HSDHGGC03 Stragene cDNA library Human heart, cat6950208 Homo sapiens cDNA clone HEGC03
1302	14930	27201	1.02	3.0E-85	AF098197.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1785	17858	27868	3.9	3.0E-85	BF7495.1	EST_HUMAN	yeS300.1 Bone's fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:121904 5'
4083	17851	30042	1.37	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
17851	17851	30042	1.37	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5275	18573	31465	0.65	3.0E-85	11439001	NT	Homo sapiens leucine rich protein (LRP), mRNA
5275	18573	31465	0.65	3.0E-85	11439001	NT	Homo sapiens leucine rich protein (LRP), mRNA
5203	18278	32511	0.65	3.0E-85	11422024	NT	Homo sapiens metal proteo-oncogene (metaloprotein growth factor receptor) (MET), mRNA
6237	18330	32560	5.69	3.0E-85	7892363	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA

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Table 4
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6267	10330	32951	5.59	3.0E-45	7662309	NT	Homo sapiens KIAA0759 gene product (KIA0759), mRNA
7140	21261		7.73	3.0E-45	U44048.1	NT	Homo sapiens KIAA0759 gene product (KIA0759), mRNA
7626	20588	33946	0.88	3.0E-45	11419870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase p125(FAK), KIAA0821 protein (KIAA0821), mRNA
8204	21174	34894	1.54	3.0E-45	U4468.1	NT	Homo sapiens DENN1 mRNA, complete cds
8883	21820	35240	1.06	3.0E-45	11023839	NT	Homo sapiens CGL-41 protein (LOC51109), mRNA
9329	22284	35725	3.37	3.0E-45	11430989	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9861	22818	36272	1.03	3.0E-45	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRPB), mRNA
9861	22818	36273	1.03	3.0E-45	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRPB), mRNA
10849	23789	37266	1.18	3.0E-45	AF008942.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11834	24717	38003	1.72	3.0E-45	5031660	NT	Homo sapiens EGF-like repeats and discoidin, like domain 3 (EDIL3), mRNA
12919	25495		2.14	3.0E-45	11418177	NT	Homo sapiens Ren GTPase activating protein 1 (RANGAP1), mRNA
664	14019	28970	0.87	2.0E-45	7657268	NT	Homo sapiens KIAA0629 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0629), mRNA
1041	14037	27039	2.52	2.0E-45	AF248540.1	NT	Homo sapiens interactor 2 (SIIC2) mRNA, complete cds
1418	14451	27424	8.48	2.0E-45	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1418	14451	27425	8.48	2.0E-45	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1418	14451	27426	8.48	2.0E-45	U19263.1	NT	Human DNA polymerase beta gene, exon 3, 12 and 13
2459	13232	28277	1.8	2.0E-45	U19263.1	NT	Human DNA polymerase beta gene, exon 3, 12 and 13
3035	18933	29011	14.9	2.0E-45	M59368.1	NT	Homo sapiens Ki-67 (p70-90), Ki-67 mRNA, complete cds
4331	17988	30270	4.93	2.0E-45	AF03680.1	NT	Homo sapiens phosphoglycerin (PG) mRNA
4948	17984	30854	0.98	2.0E-45	AL183284.2	NT	Homo sapiens chromosome 21, segment HS210884
5178	16191	31054	1.37	2.0E-45	4552212	NT	Homo sapiens arginase, liver (ARG3) mRNA
6628	22572	39022	2.87	2.0E-45	AF79020.1	EST	MSR1 repetitive element
10037	22654	39386	0.94	2.0E-45	AF144580.1	EST	MSR1 repetitive element
10535	23547	37948	1.31	2.0E-45	AF065394.1	EST	MSR1 repetitive element
2295	19307			1.0E-45	BE764306.1	EST	MSR1 repetitive element
2403	18410	28434	6.8	1.0E-45	BE18392.1	EST	MSR1 repetitive element
2403	18410	28435	6.8	1.0E-45	BE18392.1	EST	MSR1 repetitive element
8091	21027	34429	0.52	1.0E-45	BE062951.1	EST	MSR1 repetitive element
10171	22403	38542	2.41	1.0E-45	BE257917.1	EST	MSR1 repetitive element
10571	22403	38542	2.41	1.0E-45	BE257917.1	EST	MSR1 repetitive element
11289	24221	37745	2.01	1.0E-45	AA177865.1	EST	MSR1 repetitive element